

170160

STIC-Biotech/ChemLib

From: Myers, Carla
Sent: Tuesday, November 01, 2005 8:38 AM
To: STIC-Biotech/ChemLib
Subject: sequence search for 10788,779

Please search SEQ ID NO: 1-10 (these sequences are primers of 24 to 30 nucleotides)
and limit the length of the search hits to 50 nucleotides.

Please provide a printout of the first 40 results.

The CRF has been entered http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=10788779

Thank you-

Carla Myers
AU 1634
Remsen Bldg / Rm 2E79
Mailbox: REM 2C70
571-272-0747

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 11/15/05
Date completed: 11/21/05
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# 10 AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 104
WWW/Internet: _____
Other (Specify): _____

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 665.886 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGGATCGCTACGGCTCTGGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hlg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pt.*

10: gb_to.*

11: gb_sts.*

12: gb_by.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	6	I12894
2	16.2	67.5	26	6	BD271387 Sequence 1
3	16.2	67.5	26	6	AX049220 Sequence
4	16.2	67.5	26	6	AX049825 Sequence
5	16.2	67.5	26	6	AX050823 Sequence
6	16.2	67.5	26	6	AX511114 Sequence
7	16	66.7	38	11	BV142795 PZ02991 Z
8	16	66.7	38	11	BV142796 PZ02991 Z
9	16	66.7	38	11	BV142797 PZ02991 Z
10	16	66.7	38	11	BV142798 PZ02991 Z
11	16	66.7	38	11	BV142799 PZ02991 Z
12	16	66.7	38	11	BV142800 PZ02991 Z
13	16	66.7	38	11	BV142801 PZ02991 Z
14	15	62.5	33	6	AR079445 Sequence
15	15	62.5	33	6	AR168767 Sequence
16	15	62.5	33	6	AR217267 Sequence
17	15	62.5	33	6	AR264164 Sequence
18	15	62.5	33	6	AR404008 Sequence
19	15	62.5	33	6	AR406110 Sequence

20	14.6	60.8	24	6	AX444885
21	14.6	60.8	32	6	A98580
22	14.6	60.8	32	6	E38129
23	14.6	60.8	32	6	AR437122
c 24	14.4	60.0	32	6	AR143248
c 25	14.4	60.0	32	6	AR448674
c 26	14.4	60.0	32	6	BD085791
c 27	14	58.3	30	6	AX004095
c 28	13.8	57.5	36	6	AR123280
c 29	13.6	56.7	21	6	AR393694
c 30	13.6	56.7	21	6	AX092759
c 31	13.6	56.7	31	6	AX962045
c 32	13.6	56.7	40	6	AR095496
c 33	13.6	56.7	49	6	AR031823
c 34	13.4	55.8	24	6	AR177808
c 35	13.4	55.8	24	6	CQ875256
c 36	13.4	55.8	30	6	AR065612
c 37	13.4	55.8	30	6	AR448962
c 38	13.4	55.8	34	6	BD062912
c 39	13.4	55.8	44	6	AX457963
c 40	13.4	55.8	50	4	CST438207
c 41	13.4	55.8	50	6	CQ009087
c 42	13.2	55.0	19	6	AX129908
c 43	13.2	55.0	25	6	CQ864330
c 44	13.2	55.0	25	6	AX476206
c 45	13.2	55.0	25	6	AX476207

ALIGNMENTS

RESULT 1	I12894	Sequence 1 from patent US 5429923.	24 bp	DNA	linear	PAT 26-JUL-1995
LOCUS	I12894	Sequence 1 from patent US 5429923.	24	bp	DNA	linear
DEFINITION	I12894	Sequence 1 from patent US 5429923.				
ACCESSION	I12894	Sequence 1 from patent US 5429923.				
VERSION	I12894.1	GI:910871				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 24)					
AUTHORS	Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.					
TITLE	Method for detecting hypertrophic cardiomyopathy associated mutations					
JOURNAL	Patent: US 5429923-A 1 04-JUL-1995;					
FEATURES	Location/Qualifiers					
source	1..24					
ORIGIN	/organism="unknown"					
	/mol_type="unassigned DNA"					

Query Match	100.0%;	Score 24;	DB 6;	Length 24;
Best Local Similarity	100.0%;	Pred. No. 1.4;		
Matches	24;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	CAAGGATCGCTACGGCTCTGGAT 24		
Db	1	CAAGGATCGCTACGGCTCTGGAT 24		
RESULT 2	BD271387	Sequence 1 from patent US 5429923.	26 bp	DNA
LOCUS	BD271387	Sequence 1 from patent US 5429923.	26	bp
DEFINITION	BD271387	Sequence 1 from patent US 5429923.		
ACCESSION	BD271387	Sequence 1 from patent US 5429923.		
VERSION	BD271387.1	GI:33081155		
KEYWORDS	JP 2002543825-A/41.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	1 (bases 1 to 26)			
AUTHORS	Lu,P.S.			


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JOURNAL Patent: WO 0231512-A 362 18-APR-2002;
FEATURES   Arbor Vita Corporation (US)
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           /organism="synthetic construct"
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           /note="158KIF forward primer"

ORIGIN
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Best Local Similarity 85.7%; Pred. No. 9.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCTGG 22
    ||||| ||||| ||||| |||||
Db 2 AAGGATCCCTCCGGCTCCTCG 22

RESULT 7
BV142795      38 bp DNA linear STS 05-MAY-2004
LOCUS PZ02991 Zea mays ssp. mays Oh43 Zea mays Oh43 Zea mays STS genomic,
DEFINITION sequence tagged site.
ACCESSION BV142795
VERSION BV142795.1 GI:47024996
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 38)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS Contact: Brandon S. Gaut
TITLE Dept. Ecology and Evolutionary Biology
JOURNAL U.C. Irvine
COMMENT 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatgagaagtctctcaagcag
Primer B: gtacgtttattcgacaagcagc
STS size: 38
Protocol: PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 47 56 62 62 50 50 52 59 67 55 59 52 53
51 46 55 52 35 23 35 35 38 42 35 35 26 26 26 48 44 44
57 52 52.
Location/Qualifiers
1. .38
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="OH43"

FEATURES
source
/db_xref="taxon:4577"
/clone_lib="Zea mays Oh43"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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ORIGIN
Query Match      66.7%; Score 16; DB 11; Length 38;
Best Local Similarity 79.2%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| |||||
Db 10 CAAGAACCCTGCGGCGCGCGGAT 33

RESULT 8
BV142796      38 bp DNA linear STS 05-MAY-2004
LOCUS PZ02991 Zea mays ssp. mays Mol7(1) Zea mays Mol7(1) Zea mays STS
DEFINITION genomic, sequence tagged site.
ACCESSION BV142796
VERSION BV142796.1 GI:47024997
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 38)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS Contact: Brandon S. Gaut
TITLE Dept. Ecology and Evolutionary Biology
JOURNAL U.C. Irvine
COMMENT 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatgagaagtctctcaagcag
Primer B: gtacgtttattcgacaagcagc
STS size: 38
Protocol: PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 59 69 66 64 52 52 41 51 49 61 60 68 69
69 60 54 57 57 52 55 61 58 57 51 47 58 63 70 77 77 72 72 67
64 68 66.
Location/Qualifiers
1. .38
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/mol_type="genomic DNA"
/cultivar="Mol7(1)"
/db_xref="taxon:4577"
/clone_lib="Zea mays Mol7(1)"
/dev_stage="seedling"

FEATURES
source

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/note="Organ: leaf; genomic DNA from inbred line"  
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SYN      100%
ORIGIN
<1..538
Accession: J047, Genomic DNA from lambdoid phage
Query Match      66.7%; Score 16; DB 11; Length 38;
Best Local Similarity 79.2%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| |||||
Db 10 CAAGAACCGGTGCGGCGCGGGAT 33

```

[illegible]

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
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321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Tel: (949) 824-2181
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatggagaagttcctccaagcag
Primer B: gtacgtttttatgcagaagcgc
STS size: 38
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with AmpliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

[illegible]

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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Mol17(2)"
/db_xref="taxon:4577"
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/note="Organ: leaf; genomic DNA from inbred line"
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STS

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Query Match      66.7%; Score 16; DB 11; Length 38;
Best Local Similarity 79.2%; Pred. NO. 1.2e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db 10 CAAGAACCGCTCGGCGCGCGGAT 33
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RESULT	10
BV142798	
LOCUS	38 bp DNA linear STS 05-MAY-2004
DEFINITION	P202991 Zea mays ssp. mayas CML69 Zea mays STS genomic, sequence tagged site.
ACCESSION	BV142798
VERSION	BV142798.1 GI:47024999
KEYWORDS	STS.
SOURCE	Zea mays
ORGANISM	Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 38)
REFERENCE	Mcmullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S. MPZ-UCI Joint SNP Discovery Unpublished (2003)
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Tel: (949) 824-2181
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatgagagaagttcctcaagcag
Primer B: gtacgtttatttcacagcagcc
STS size: 38
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (sigma)
total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

[illegible]

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93 44 46. Location/Qualifiers
1..38
    organism="Zea mays"
    mol_type="genomic DNA"
    cultivar="CML69"
    db_xref="taxon:4577"
    clone_lib="Zea mays CML69"
    dev_stage="seedling"
    note="Organ: leaf; genomic DNA from inbred line"
<1..>38

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Query Match	66.7%	Score 16;	DB 11;	Length 38;
Best Local Similarity	79.2%	Pred. No. 1.2e+04;		

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
 ||||| ||||| ||||| ||||| |||||
 Db 10 CAAGAACCGCTCGCGCGCGGAT 33

RESULT 11
 BV142799
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays subsp. parviglumis
 Zea mays subsp. parviglumis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 38)
 McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
 Unpublished (2003)
 CONTACT: Brandon S. Gaut
 Dept.: Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel.: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: gagatgagaagtctcctcaagcag
 Primer B: gtacgtttattgacacagcgc
 STS size: 38
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with ampliTaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 84 77 75 80 73 65 61 68 85 79 77 77 72
 70 74 69 72 71 66 69 81 77 77 77 72 75 79 77 82 82 80 82 82
 85 85 85.

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 /cultivar="teol"
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 /clone.lib="Zea mays JSGyLOS 130"
 /dev_stage="seedling"
 /note="Organ: leaf; genomic DNA"
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STS
 ORIGIN
 Query Match 66.7%; Score 16; DB 11; Length 38;
 Best Local Similarity 79.2%; Pred. No. 1.2e+04;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
 ||||| ||||| ||||| ||||| |||||

Db
 10 CAAGAACCGCTCGCGCGCGGAT 33
 ||||| ||||| ||||| ||||| |||||

RESULT 12
 BV142800
 LOCUS
 DEFINITION

BV142800 38 bp DNA linear STS 05-MAY-2004
 PZ02991 Zea mays ssp. parviglumis USDA P1566686 Zea mays USDA
 P1566686 Zea mays subsp. parviglumis STS genomic, sequence tagged
 site.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BV142800.1 GI:47025001
 STS.
 Zea mays subsp. parviglumis
 Zea mays subsp. parviglumis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 38)
 McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
 Unpublished (2003)
 CONTACT: Brandon S. Gaut
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 Tel.: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: gagatgagaagtctcctcaagcag
 Primer B: gtacgtttattgacacagcgc
 STS size: 38
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with ampliTaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 52 67 56 55 55 55 60 55 64 37 40 40 40
 24 24 24 29 25 33 28 35 35 35 23 23 23 35 38 37 37 37 56 57
 57 58 57.

FEATURES
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 /mol_type="genomic DNA"
 /cultivar="teol"
 /db_xref="taxon:76912"
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 /dev_stage="seedling"
 /note="Organ: leaf; genomic DNA"
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STS
 ORIGIN
 Query Match 66.7%; Score 16; DB 11; Length 38;
 Best Local Similarity 79.2%; Pred. No. 1.2e+04;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
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 Db 10 CAAGAACCGCTCGCGCGCGGAT 33

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RESULT 13
BV142801
LOCUS
DEFINITION
  BV142801 38 bp DNA linear STS 05-MAY-2004
  PZ02991 Zea mays ssp. parviglumis Wilkes Site 6 Zea mays Wilkes
  Site 6 Zea mays subsp. parviglumis STS genomic, sequence tagged
  site.
ACCESSION
  BV142801
VERSION
  BV142801.1 GI:47025002
KEYWORDS
  STS.
SOURCE
  Zea mays subsp. parviglumis
  Zea mays subsp. parviglumis
  Zea mays subsp. parviglumis
  Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 38)
REFERENCE
  McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
  MP2-UCI Joint SNP Discovery
  Unpublished (2003)
COMMENT
  Contact: Brandon S. Gaut
  Dept. Ecology and Evolutionary Biology
  U.C. Irvine
  321 Steinhaus Hall, Irvine, CA 92697-2525, USA
  Tel: (949) 824-2564
  Fax: (949) 824-2181
  Email: bgaut@uci.edu
  Primer A: gagatggagaagtctctcaagcag
  Primer B: gtacgttttattcgacaagcagcc
  STS size: 38
Protocol:
  PCR amplification of genomic DNA
  Template: 50 ng
  Primer: each 0.5 uM
  dNTPs: each 200 uM
  Taq Polymerase: RedTaq (Sigma)
  Total Vol: 10 ul
  Amplicon sequencing
  ABI protocol - using d-Rhodamine terminator cycle
  sequencing ready reaction with ampliTaq DNA polymerase FS
  Sequence ran on ABI 3700 sequencer.
Buffer:
  Genomic DNA amplification
  RedTaq (Sigma)
  Sequencing buffer
  d-Rhodamine kit (ABI)
PHRED/PHRAP Quality Scores 44 46 40 46 56 56 40 40 40 30 30 30
33 19 19 27 34 42 43 38 42 36 44 44 44 44 44 44 44 48 48 43 36
42 38 29.
FEATURES
  source
  1. 38
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  /mol_type="genomic DNA"
  /cultiivar="teol7"
  /db xref="taxon:76912"
  /clone lib="Zea mays Wilkes Site 6"
  /dev stage="seedling"
  /note="Organ: leaf; genomic DNA"
  <1. >38
STS
ORIGIN
  Query Match 66.7%; Score 16; DB 11; Length 38;
  Best Local Similarity 79.2%; Pred. No. 1.2e+04;
  Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
  ||||| ||||| ||||| |||||
  Db 10 CAAGAACCGCTGCGCGCGCGGAT 33
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RESULT 14
AR079445
LOCUS
DEFINITION
  AR079445 33 bp DNA linear PAT 31-AUG-2000
  Sequence 12 from patent US 5965528.
ACCESSION
  AR079445
VERSION
  AR079445.1 GI:10006190
KEYWORDS
  .
SOURCE
  Unknown.
  ORGANISM
  Unclassified.
  1 (bases 1 to 33)
REFERENCE
  Murgita, R.A.
  TITLE
  Recombinant human alpha-fetoprotein as an immunosuppressive agent
  JOURNAL
  Patent: US 5965528-A 12 12-OCT-1999;
  FEATURES
  Location/Qualifiers
  source
  1. 33
  /organism="unknown"
  /mol_type="unassigned DNA"
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  Query Match 62.5%; Score 15; DB 6; Length 33;
  Best Local Similarity 78.3%; Pred. No. 3.7e+04;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 2 AAGATCGCTACGGCTCCTGGAT 24
  ||||| ||||| ||||| |||||
  Db 5 AAGATCCTTAGCTCTCCTGGAT 27
  ||||| ||||| ||||| |||||
RESULT 15
AR168767
LOCUS
DEFINITION
  AR168767 33 bp DNA linear PAT 17-DEC-2001
  Sequence 12 from patent US 6288034.
ACCESSION
  AR168767
VERSION
  AR168767.1 GI:17904858
KEYWORDS
  .
SOURCE
  Unknown.
  ORGANISM
  Unclassified.
  1 (bases 1 to 33)
REFERENCE
  Murgita, R.A.
  TITLE
  Recombinant human alpha-fetoprotein as an immunosuppressive agent
  JOURNAL
  Patent: US 6288034-A 12 11-SEP-2001;
  FEATURES
  Location/Qualifiers
  source
  1. 33
  /organism="unknown"
  /mol_type="unassigned DNA"
ORIGIN
  Query Match 62.5%; Score 15; DB 6; Length 33;
  Best Local Similarity 78.3%; Pred. No. 3.7e+04;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 2 AAGATCGCTACGGCTCCTGGAT 24
  ||||| ||||| ||||| |||||
  Db 5 AAGATCCTTAGCTCTCCTGGAT 27
  ||||| ||||| ||||| |||||
RESULT 16
AR217267
LOCUS
DEFINITION
  AR217267 33 bp DNA linear PAT 25-SEP-2002
  Sequence 13 from patent US 6416734.
ACCESSION
  AR217267
VERSION
  AR217267.1 GI:23316737
KEYWORDS
  .
SOURCE
  Unknown.
  ORGANISM
  Unclassified.
  1 (bases 1 to 33)
REFERENCE
  Murgita, R.A.
  TITLE
  Recombinant alpha-fetoprotein for treating and diagnosing cancers
  JOURNAL
  Patent: US 6416734-A 13 09-JUL-2002;
  FEATURES
  Location/Qualifiers

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source
1. .33
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 62.5%; Score 15; DB 6; Length 33;
Best Local Similarity 78.3%; Pred. No. 3.7e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCCTGGAT 24
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Db 5 AAGGATCCTTAGCTCTCTGGAT 27
||||| ||| |||||
RESULT 17
LOCUS AR264164 33 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 17 from patent US 6331611.
ACCESSION AR264164
VERSION AR264164.1 GI:28076254
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 33)
AUTHORS Murgita,R.A.
TITLE Expression and purification of cloned human alpha-fetoprotein
JOURNAL Patent: US 6331611-A 17 18-DEC-2001;
FEATURES
Location/Qualifiers
1. .33
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 62.5%; Score 15; DB 6; Length 33;
Best Local Similarity 78.3%; Pred. No. 3.7e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCCTGGAT 24
||||| ||| |||||
Db 5 AAGGATCCTTAGCTCTCTGGAT 27
||||| ||| |||||
RESULT 18
LOCUS AR404008 33 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6627440.
ACCESSION AR404008
VERSION AR404008.1 GI:40151939
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 33)
AUTHORS Murgita,R.A.
TITLE Recombinant human alpha-fetoprotein as a cell proliferative agent
JOURNAL Patent: US 6627440-A 12 30-SEP-2003;
FEATURES
Location/Qualifiers
1. .33
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 62.5%; Score 15; DB 6; Length 33;
Best Local Similarity 78.3%; Pred. No. 3.7e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCCTGGAT 24
||||| ||| |||||
Db 5 AAGGATCCTTAGCTCTCTGGAT 27
||||| ||| |||||
RESULT 19
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AR406110
LOCUS AR406110 33 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6630445.
ACCESSION AR406110
VERSION AR406110.1 GI:40155318
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 33)
AUTHORS Murgita,R.A.
TITLE Recombinant alpha-fetoprotein for treating cancers
JOURNAL Patent: US 6630445-A 12 07-OCT-2003;
FEATURES
Location/Qualifiers
1. .33
/organism="unknown"
/mol_type="genomic DNA"
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Query Match 62.5%; Score 15; DB 6; Length 33;
Best Local Similarity 78.3%; Pred. No. 3.7e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCCTGGAT 24
||||| ||| |||||
Db 5 AAGGATCCTTAGCTCTCTGGAT 27
||||| ||| |||||
RESULT 20
LOCUS AX444885 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1340 from Patent WO0216649.
ACCESSION AX444885
VERSION AX444885.1 GI:21692163
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 Gunderson,K.
AUTHORS Probes and decoder oligonucleotides
TITLE Patent: WO 0216649-A 1340 28-FEB-2002;
JOURNAL Illumina, Inc. (US)
FEATURES
Location/Qualifiers
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
ORIGIN
Query Match 60.8%; Score 14.6; DB 6; Length 24;
Best Local Similarity 81.0%; Pred. No. 6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 GGATCGCTACGGCTCCTGGAT 24
||||| ||| |||||
Db 2 GGTCGCTACGGCGGCTGGTT 22
||||| ||| |||||
RESULT 21
LOCUS A98580 32 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 5 from Patent EP0902092.
ACCESSION A98580
VERSION A98580.1 GI:6781632
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 32)
AUTHORS Wurst,W.D. and Prochiantz,A.D.
TITLE Method for the identification of target genes for transcription
```

factors
JOURNAL Patent: EP 0902092-A 5 17-MAR-1999;
GSF FORSCHUNGSZENTRUM UMWELT (DE); CENTRE NAT RECH SCIENT (FR)
FEATURES Location/Qualifiers
source 1..32
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 60.8%; Score 14.6; DB 6; Length 32;
Best Local Similarity 81.0%; Pred. No. 5.9e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 GGATCGCTACGGCTCCTGGAT 24
||||| ||||| ||||| |||||
Db 4 GGATCCCTACGCGCTTCTTGAT 24
RESULT 22
E38129
LOCUS 32 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for identifying target gene of transcription factor.
E38129
ACCESSION
E38129
VERSION GI:13027164
KEYWORDS JP 1999187876-A/5.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Borufugangu,B. and Alan,P.
TITLE Method for identifying target gene of transcription factor
JOURNAL Patent: JP 1999187876-A 5 13-JUL-1999;
GSF FORSCH ZENTRUM FUER UMWELT & GESUNDHEIT GMBH, CENTRE NATIONAL
DE LA RECHERCHE SCIENTIFIQUE
COMMENT OS Unidentified
PN JP 1999187876-A/5
PD 13-JUL-1999
PF 14-SEP-1998 JP 1998260205
PR 15-SEP-1997 DE 19740578.9
PI BORUFUGANGU BURUSUTO,ALAN FLOSIANZ
PC C12N15/09,C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..32
/organism='Unidentified'.
FEATURES source 1..32
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 60.8%; Score 14.6; DB 6; Length 32;
Best Local Similarity 81.0%; Pred. No. 5.9e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 GGATCGCTACGGCTCCTGGAT 24
||||| ||||| ||||| |||||
Db 4 GGATCCCTACGCGCTTCTTGAT 24
RESULT 23
AR437122
LOCUS 32 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6656735.
AR437122
ACCESSION
AR437122
VERSION GI:40200206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 32)
AUTHORS Wurst,W. and Prochiantz,A.
TITLE Method for identification of target genes of transcription factors
JOURNAL Patent: US 6656735-A 5 02-DEC-2003;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 60.8%; Score 14.6; DB 6; Length 32;
Best Local Similarity 81.0%; Pred. No. 5.9e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 GGATCGCTACGGCTCCTGGAT 24
||||| ||||| ||||| |||||
Db 4 GGATCCCTACGCGCTTCTTGAT 24
RESULT 24
AR143248/c
LOCUS 32 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 44 from patent US 6204232.
AR143248
ACCESSION
AR143248
VERSION GI:15104534
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Borchert,T.Vedel., Svendsen,A., Andersen,C., Nielsen,B.,
Nissen,T.Lauesgaard. and KJ.ae buttetd.rulff,slashedren.
TITLE .alpha.-amylase mutants
JOURNAL Patent: US 6204232-A 44 20-MAR-2001;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 60.0%; Score 14.4; DB 6; Length 32;
Best Local Similarity 75.0%; Pred. No. 7.4e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
||||| ||||| ||||| |||||
Db 31 CATTGATCGTACGCGGTCTGGTT 8
RESULT 25
AR448674/c
LOCUS 32 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 44 from patent US 6673589.
AR448674
ACCESSION
AR448674
VERSION GI:42677239
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Borchert,T.V., Svendsen,A., Andersen,C., Nielsen,B., Nissen,T.L.
TITLE .alpha.-amylase mutants
JOURNAL Patent: US 6673589-A 44 06-JAN-2004;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 60.0%; Score 14.4; DB 6; Length 32;
Best Local Similarity 75.0%; Pred. No. 7.4e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| |||||
Db 31 CATTGATCGTAACGGGCTCTGGTT 8

RESULT 26
BD085791/c
LOCUS Alpha-amylase variant. 32 bp DNA linear PAT 27-AUG-2002
ACCESSION BD085791
VERSION BD085791.1 GI:22631401
KEYWORDS JP 2001521739-A/36.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Borchert,T.V., Svendsen,A., Andersen,K., Nielsen,B.L., Nissen,T.L.
and Caelliph,S.
TITLE Alpha-amylase variant
JOURNAL Patent: JP 2001521739-A 36 13-NOV-2001;
COMMENT NOVO NORDISK AS
OS Unidentified
PN JP 2001521739-A/36
PD 13-NOV-2001
PF 30-OCT-1998 JP 2000519071
PR 30-OCT-1997 DK 1240/97,14-JUL-1998 DK PA 199800936 PI
TORBEN VEDEL BORCHERT,ALLAN SVENDSEN,KARSTEN ANDERSEN, PI BIYARNE
LENFELDT NIELSEN,TORBEN LAUESGIRLD NISSEN,SOREN PI CAELLIPH
PC C12N15/09,C11D3/386,C12N1/21,C12N9/28//C12N15/09,C12R1:10),
PC (C12N15/09,C12R1:07),C12N1/21,C12R1:10),C12N1/21,C12R1:08),
PC C12N1/21,C12R1:09),C12N15/00,C12R1:10),C12N15/00,C12N15/00,
PC C12R1:07)
CC Strandedness: Single;
CC Topology: linear;
CC /desc = 'Primer DA23'
FH Key Location/Qualifiers
FT source 1..32
FT Location/Qualifiers
source 1..32
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 60.0%; Score 14.4; DB 6; Length 32;
Best Local Similarity 75.0%; Pred. No. 7.4e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| |||||
Db 31 CATTGATCGTAACGGGCTCTGGTT 8

RESULT 27
AX004095/c
LOCUS AX004095 30 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 42 from Patent WO992322.
ACCESSION AX004095
VERSION AX004095.1 GI:9927701
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Osbourn,J.K.
TITLE Cysteine nose antibody libraries, means for their production and
uses thereof
JOURNAL Patent: WO 992322-A 42 14-MAY-1999;
CAMBRIDGE ANTIBODY TECH (GB); OSBOURN JANE KATHARINE (GB)
FEATURES
source 1..30
Location/Qualifiers

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 30;
Best Local Similarity 77.3%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGG 22
    ||||| ||||| ||||| |||||
Db 23 CAAGGACGGCTACGGCTTGCGG 2

RESULT 28
ARI23280
LOCUS ARI23280 36 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6169167.
ACCESSION ARI23280
VERSION ARI23280.1 GI:14108246
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Bartley,T.D. and Fox,G.M.
TITLE Antibodies to ligands for HEK4 receptors
JOURNAL Patent: US 6169167-A 11 02-JAN-2001;
FEATURES Location/Qualifiers
source 1..36
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 36;
Best Local Similarity 88.2%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTC 18
    ||||| ||||| |||||
Db 5 AAGGATCCCTATGGCTC 21

RESULT 29
AR393694/c
LOCUS AR393694 21 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 233 from patent US 6617122.
ACCESSION AR393694
VERSION AR393694.1 GI:40120501
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hayden,M.R., Brooks-Wilson,A.R. and Pimstone,S.N.
TITLE Process for identifying modulators of ABC1 activity
JOURNAL Patent: US 6617122-A 233 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCT 20
    ||||| ||||| |||||
Db 20 CAATGAGCGCTTTGGCTCCT 1
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RESULT 30
AX092759/c
LOCUS AX092759 21 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 171 from Patent WO0115676.
ACCESSION AX092759
VERSION AX092759.1 GI:13444816
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and
triglyceride levels
JOURNAL Patent: WO 0115676-A 171 08-MAR-2001;
UNIVERSITY University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
FEATURES
source
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCCT 20
| | | | | | | | | | | | | | | |
Db 20 CAATGAGCGCTTGGCTCCT 1
| | | | | | | | | | | | | | | |
RESULT 31
AX962045
LOCUS AX962045 31 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 68 from Patent WO03104275.
ACCESSION AX962045
VERSION AX962045.1 GI:40881455
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura,Y., Furukawa,Y., Tahara,H. and Tsunoda,T.
TITLE Genes and polypeptides relating to human colon cancers
JOURNAL Patent: WO 03104275-A 68 18-DEC-2003;
Oncotherapy Science, Inc. (JP) ; Japan as represented by the
president of the university of Tokyo (JP)
FEATURES
source
1..31
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="an artificially synthesized primer sequence"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 31;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCCT 20
| | | | | | | | | | | | | | | |
Db 7 CCAGGATGGCTGCAGCTCCT 26
| | | | | | | | | | | | | | | |
RESULT 32
AR095496/c
LOCUS AR095496 40 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 3 from patent US 6004780.
ACCESSION AR095496
VERSION AR095496.1 GI:10023423
KEYWORDS
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Soppet,D.R. and Li,H.
TITLE Growth factor HTT36
JOURNAL Patent: US 6004780-A 3 21-DEC-1999;
FEATURES
source
1..40
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCCT 20
| | | | | | | | | | | | | | | |
Db 23 CAGGGATGGCTGCGGATCCT 4
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RESULT 33
AR031823/c
LOCUS AR031823 49 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5866422.
ACCESSION AR031823
VERSION AR031823.1 GI:5946112
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 49)
AUTHORS Wayne,J. and Xu,S.-Y.
TITLE Method for cloning and producing the Tsp45I restriction
endonuclease in E. coli
JOURNAL Patent: US 5866422-A 17 02-FEB-1999;
FEATURES
source
1..49
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCCT 20
| | | | | | | | | | | | | | | |
Db 45 CCAGGGTAGCTACGGGTCAT 26
| | | | | | | | | | | | | | | |
RESULT 34
AR177808
LOCUS AR177808 24 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 8 from patent US 6313265.
ACCESSION AR177808
VERSION AR177808.1 GI:17920163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Phillips,G., Cunningham,B.A. and Crossin,K.L.
TITLE Neurite outgrowth-promoting polypeptides containing fibronectin
type III repeats and methods of use
JOURNAL Patent: US 6313265-A 8 06-NOV-2001;
FEATURES
source
1..24
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
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Query Match 55.8%; Score 13.4; DB 6; Length 24;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCGAT 24
||||| ||||| ||||| ||||| |||||
Db 2 AAGGATCGCTACCACTCTGGT 24

RESULT 35
CQ875256/c
LOCUS CQ875256 24 bp DNA linear PAT 27-SEP-2004
DEFINITION Sequence 162 from Patent WO2004075733.
ACCESSION CQ875256
VERSION CQ875256.1 GI:52748344
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Greinwald,J.H., Wenstrup,R.J., Aronow,B.J. and Pestian,J.P.
TITLE Construction of a deafness gene chip
JOURNAL Patent: WO 2004075733-A 162 10-SEP-2004;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide primer sequence"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 24;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
||||| ||||| ||||| ||||| |||||
Db 24 CAAGTATCTGTATGGCTCTAGGA 2

RESULT 36
AR065612
LOCUS AR065612 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5849534.
ACCESSION AR065612
VERSION AR065612.1 GI:5995828
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
AUTHORS Grotendorst,G.R. and Iida,N.
TITLE DNA encoding leukocyte derived growth factor-2 (LDGF-2)
JOURNAL Patent: US 5849534-A 11 15-DEC-1998;
FEATURES
source
1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 30;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
||||| ||||| ||||| ||||| |||||
Db 4 CGACGGTGGCGACGACTCTCTGGA 26

RESULT 37
AR448962
LOCUS AR448962 30 bp mRNA linear PAT 20-FEB-2004

DEFINITION Sequence 11 from patent US 6673893.
ACCESSION AR448962
VERSION AR448962.1 GI:42677748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Grotendorst,G.R. and Iida,N.
TITLE Leukocyte derived growth factor 2
JOURNAL Patent: US 6673893-A 11 06-JAN-2004;
FEATURES
source
1..30
/organism="unknown"
/mol_type="mRNA"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 30;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
||||| ||||| ||||| ||||| |||||
Db 4 CGACGGTGGCGACGACTCTCTGGA 26

RESULT 38
BD062912
LOCUS BD062912 34 bp DNA linear PAT 27-AUG-2002
DEFINITION Thermotable phosphatases.
ACCESSION BD062912
VERSION BD062912.1 GI:22608515
KEYWORDS JP 2001510983-A/12.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Mathur,E.J., Lee,E. and Bylina,E.
TITLE Thermotable phosphatases
JOURNAL Patent: JP 2001510983-A 12 07-AUG-2001;
COMMENT DIVERSA CORP
PN JP 2001510983-A/12
PD 07-AUG-2001
PF 19-JUN-1997 JP 1998503409
PR 19-JUN-1996 US 60/033752
PI ERIC J MATHUR,EDD LEE,EDWARD BYLINA
PC A61K38/46,C07H1/00,C07H21/02,C07H21/04,C12N9/14,C12N1/20, PC
C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source
1..34
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 34;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
||||| ||||| ||||| ||||| |||||
Db 2 CGAGGATCGCTTAAGGCTTCTCGA 24

RESULT 39
AX457963
LOCUS AX457963 44 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 5 from Patent WO0246456.
ACCESSION AX457963
VERSION AX457963.1 GI:21724858

```

ORIGIN
Query Match          55.8%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2  AAGGATCGCTACGGCTCCTGGAT  24
      |||||
Db       7  AAGAGTGGCTTGGGCTGCTGGAT  29
      |||||

```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 165.262 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGATCGTACGGCTCTCGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	2	AAQ91121
2	24	100.0	24	9	ACA63111
3	24	100.0	24	13	ADR05297
4	16.4	68.3	33	11	ADM68395
5	16.2	67.5	26	4	AAT16851
6	16.2	67.5	26	4	AAF17495
7	16.2	67.5	26	4	AAC99432
8	16.2	67.5	26	6	ABT06636
9	16.2	67.5	26	6	ABQ96682
10	15.2	63.3	24	10	ADJ80120
11	15.2	63.3	25	9	ACK06221
12	15.2	63.3	25	9	ACK05595
13	15	62.5	33	2	AAT35182
14	15	62.5	33	6	ABZ70298
15	15	62.5	36	2	AQ004591
16	14.6	60.8	24	6	ABQ01333
17	14.6	60.8	24	6	ABQ06613
18	14.6	60.8	24	6	ABQ06654
19	14.6	60.8	25	9	ACK06282
20	14.6	60.8	32	2	AAX22971

21	14.6	60.8	36	3	AAA76301
22	14.4	60.0	31	8	ACD54952
23	14.4	60.0	31	12	ADM63061
24	14.4	60.0	32	2	AAX59667
25	14.4	60.0	33	6	ABQ83921
26	14.4	60.0	33	6	ABK50283
27	14.4	60.0	33	8	ABX12001
28	14.2	59.2	25	9	ACI28366
29	14	58.3	26	10	AAD59416
30	14	58.3	30	2	AAX57219
31	14	58.3	32	12	ADO43696
32	14	58.3	33	6	ABX14381
33	13.8	57.5	22	3	AAZ35063
34	13.8	57.5	36	2	AAT34298
35	13.6	56.7	21	3	AAC69334
36	13.6	56.7	21	4	AAF93000
37	13.6	56.7	25	9	ACK06220
38	13.6	56.7	25	9	ACI04808
39	13.6	56.7	25	9	ACK05594
40	13.6	56.7	28	2	AAZ35681
41	13.6	56.7	31	6	ABS79090
42	13.6	56.7	31	6	ADE71167
43	13.6	56.7	31	10	ACD27669
44	13.6	56.7	31	12	ADI00667
45	13.6	56.7	33	6	ABZ21018

ALIGNMENTS

RESULT 1

AAQ91121
ID AAQ91121 standard; cDNA; 24 BP.

XX AAQ91121;

DT 19-FEB-1996 (first entry)

DE Beta-cardiac myosin heavy chain PCR primer A.

XX Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
KW diagnosis; primer; mutation; detection; ss.

OS Synthetic.

PN US5429923-A.

PD 04-JUL-1995.

PF 11-DEC-1992; 92US-00989160.

PR 11-DEC-1992; 92US-00989160.

XX (HARD) HARVARD COLLEGE.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA (GEO-) GEN HOSPITAL SHENYANG MILITARY AREA.

PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX WPI; 1995-245715/32.

DR Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
XX useful for testing asymptomatic individual(s).

PT Example 1; Col 10; 22pp; English.

XX AAQ91121-091130 are nested PCR primers used for the amplification and
CC identification of beta-cardiac myosin heavy-chain RNA. They are used in a
CC new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
CC the method involves detecting the presence or absence of specific HC-
CC associated mutations in the beta-cardiac myosin heavy-chain obtained from
CC a blood sample. The method may be used to diagnose familial or sporadic
CC HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
CC a broad applicability and may be used to detect mutations responsible for
CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
CC anaemia, Tay-Sachs disease and phenylketonuria
XX
SQ Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db 1 CAAGGATCGCTACGGCTCCTGGAT 24
|||||
RESULT 2
ACA63111
ID ACA63111 standard; DNA; 24 BP.
XX ACA63111;
AC
XX
DT 28-AUG-2003 (first entry)
XX
DE Human beta cardiac myosin heavy chain PCR primer A.
XX
KW Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
KW phenylketonuria; cystic fibrosis.
XX
OS Homo sapiens.
XX
XX US2003054343-A1.
PN
XX
PD 20-MAR-2003.
XX
XX 06-JUN-1995; 95US-00469172.
PF
XX
XX 11-DEC-1992; 92US-00989160.
PR
XX
XX (SEID/) SEIDMAN C.
PA (SEID/) SEIDMAN J.
PA (WATK/) WATKINS H.
PA (ROSE/) ROSENZWEIG A.
XX
XX Seidman C, Seidman J, Watkins H, Rosenzweig A;
PI
XX WPI; 2003-512374/48.
DR
XX
XX
PT Detecting a presence or absence of a mutation associated with
PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
PT hemophilia, by detecting a mutation in an amplified product of a beta
PT cardiac myosin heavy-chain DNA.
XX
XX
XX Example 1; Page 5; 22pp; English.
PS
XX
XX The invention relates to detecting the presence or absence of a mutation
CC associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
CC and FHC) comprises detecting a mutation associated with hypertrophic
CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy
CC chain DNA. The mutations associated with SHC/FHC are detected in the
CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-
CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
CC sample). FHC associated point mutation can be classified and used to
CC determine life expectancy in affected individuals e.g. using a Kaplan-
CC Meier curve for the classified type of FHC causing point mutation. Also
CC included are an RNA probe comprising ribonucleotides arranged in a
CC sequence which is complementary to at least a portion of beta-cardiac
CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
CC DNA. The method is useful for detecting the presence or absence of a
CC mutation associated with hypertrophic cardiomyopathy. This method is
CC especially useful for diagnosing SHC and FHC, as well as for determining
CC the estimated life expectancy of a person with familial hypertrophic
CC cardiomyopathy. In particular, the method is useful for determining an
CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
CC chain cDNA containing an FHC-associated mutation
XX
SQ Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db 1 CAAGGATCGCTACGGCTCCTGGAT 24
|||||
RESULT 3
ADR05297
ID ADR05297 standard; DNA; 24 BP.
XX
XX ADR05297;
AC
XX 21-OCT-2004 (first entry)
DT
XX
DE Human beta cardiac myosin heavy chain mutation detection primer A.
XX
KW Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
KW familial hypertrophic cardiomyopathy;
KW sporadic hypertrophic cardiomyopathy.
XX
OS Homo sapiens.
XX
XX US2004152121-A1.
PN
XX 05-AUG-2004.
PD
XX 27-FEB-2004; 2004US-00788779.
PF
XX 11-DEC-1992; 92US-00989160.
PR 06-JUN-1995; 95US-00469172.
PR
XX (SEID/) SEIDMAN C.
PA (SEID/) SEIDMAN J.
PA (WATK/) WATKINS H.
PA (ROSE/) ROSENZWEIG A.
XX
XX Seidman C, Seidman J, Watkins H, Rosenzweig A;
PI
XX WPI; 2004-592586/57.
DR
XX
XX
PT Detecting mutations associated with hypertrophic cardiomyopathy to
PT diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
PT myosin heavy-chain DNA and detecting the mutation in the amplified
PT product.
XX
XX Claim 18; SEQ ID NO 1; 22pp; English.
PS
XX The invention relates to detecting the presence or absence of a mutation
CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
CC amplified product, and detecting the presence or absence of a mutation
CC associated with hypertrophic cardiomyopathy in the amplified product,
CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
CC included are a set of DNA oligonucleotide primers for amplifying beta-
CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
 CC oligonucleotide primers being useful for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
 CC cardiomyopathy-associated mutation) and a kit for facilitating the
 CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
 CC holding an RNA probe completely hybridizable to the beta-cardiac myosin
 CC heavy chain DNA, where the RNA probe is capable of detecting a
 CC hypertrophic cardiomyopathy-associated mutation, a second container
 CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
 CC instructions for using the components of the kit to detect the presence
 CC or absence of a hypertrophic cardiomyopathy-associated mutation in
 CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
 CC detecting the presence or absence of a mutation associated with
 CC hypertrophic cardiomyopathy for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
 CC having hypertrophic cardiomyopathy relies on the presence of typical
 CC clinical symptoms and the demonstration of unexplained ventricular
 CC hypertrophy. The present invention is non-invasive and based, at least in
 CC part, on the discovery that hypertrophic cardiomyopathy is caused by
 CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
 CC reveals that there are no extensive studies involving a large number of
 CC families which established that this particular disease or disorder was
 CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
 CC The present sequence is a PCR primer used to amplify a region of the beta
 CC cardiac myosin heavy chain having a disease-related point mutation.

XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 24; DB 13; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAGATCGCTACGGCTCTCGAT 24
 |||||
 DB 1 CAAGATCGCTACGGCTCTCGAT 24

RESULT 4
 ADM68395/c
 ID ADM68395 standard; DNA; 33 BP.
 XX
 AC ADM68395;
 DT 03-JUN-2004 (first entry)
 XX
 DE PCR primer Seq ID6 related to human zinc finger protein 57_21.
 XX
 KW human; zinc finger protein 57_21; diabetes; cancer; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1376698-A.
 XX
 PD 30-OCT-2002.
 XX
 PF 22-MAR-2001; 2001CN-00105751.
 XX
 PR 22-MAR-2001; 2001CN-00105751.
 XX
 PA (BTOW-) BTOWNDOW GENE DEV INC SHANGHAI.
 XX
 XX Mao Y, Xie Y;
 XX
 XX WPI; 2003-184955/19.
 XX
 XX Polypeptide-human zinc finger protein -57.21.
 PT
 XX
 PS Example 5; SEQ ID NO 6; 34pp; Chinese.
 XX

CC This invention relates to a novel protein, human zinc finger protein
 CC 57_21, and the DNA sequence encoding it. The protein of the invention may
 CC be useful for the treatment of diseases such as diabetes and cancer. The
 CC present sequence is that of a PCR primer which was used in the

CC exemplification of the invention.

XX Sequence 33 BP; 8 A; 9 C; 9 G; 7 T; 0 U; 0 Other;
 SQ Query Match 68.3%; Score 16.4; DB 11; Length 33;
 Best Local Similarity 94.4%; Pred. No. 6.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AGGATCGCTACGGCTCTCT 20
 |||||
 DB 32 AGGATCGCTACGGCTCTCT 15

RESULT 5
 AAF16851
 ID AAF16851 standard; DNA; 26 BP.
 XX
 AC AAF16851;
 DT 12-MAR-2001 (first entry)
 XX
 DE KIAA0316 PDZ domain PCR primer #1.

XX Endothelial cell; haematopoietic cell; PDZ domain protein; PCR primer;
 KW PL domain protein; leukocyte activation; synapse formation;
 KW transmembrane neurotransmitter receptor; autoimmune disease;
 KW transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease; ss.

XX Homo sapiens.
 XX
 PN WO200069897-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WO-US013166.
 XX
 PR 14-MAY-1999; 99US-0134114P.
 PR 14-MAY-1999; 99US-0134117P.
 PR 14-MAY-1999; 99US-0134118P.
 PR 21-OCT-1999; 99US-0160860P.
 PR 29-OCT-1999; 99US-0162498P.
 PR 13-DEC-1999; 99US-0170453P.
 PR 14-JAN-2000; 2000US-0176195P.
 PR 14-FEB-2000; 2000US-0182296P.
 PR 11-APR-2000; 2000US-00547276.
 PR 11-APR-2000; 2000US-0196460P.
 PR 11-APR-2000; 2000US-0196527P.
 PR 11-APR-2000; 2000US-0196528P.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-025003/03.

XX New inhibitors of binding of a PDZ protein and PL protein for inhibiting
 PT cell-mediated response by hematopoietic cells, or for treating diseases
 PT characterized by inflammatory and humoral immune responses, e.g.
 PT inflammation, cancer.

XX Disclosure; Page 37; 139pp; English.

XX The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or haematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a PDZ
 CC domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a PCR primer for a PDZ
 CC domain. PDZ domains of proteins are named after three prototypical
 CC proteins: PSD95, Drosophila large disc protein and zonula Occludin 1
 CC protein. PDZ domain proteins are involved in synapse formation by

CC organising transmembrane neurotransmitter receptors through intracellular
CC interactions. The inhibitors identified by the present invention can be
CC used to treat a disease mediated by haematopoietic cells, e.g. autoimmune
CC disease, inflammation, allergy (e.g. drug allergies), inflammatory bowel
CC diseases, ulcerative colitis, ileitis, psoriasis, respiratory allergic
CC diseases (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes,
CC Hashimoto thyroiditis, osteoarthritis), atherosclerosis, cancers,
CC infectious diseases (e.g. viral infection), ischaemia, vasculitis and
CC Crohn's disease. The inhibitors can also be used to prevent
CC transplanted rejection of a solid organ transplant
XX
SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 4; Length 26;

Best Local Similarity 85.7%; Pred. No. 8.2e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGATCGCTACGGCTCTCTGG 22

Db 2 AAGGATCCCTCCGGCTCTCTGG 22

RESULT 6

AAFI7495

ID AAFI7495 standard; DNA; 26 BP.

XX AC

XX AAFI7495;

XX AC

DT 12-MAR-2001 (first entry)

XX XIAA0316

DE PDZ domain PCR primer #1.

XX Endothelial cell; haematopoietic cell; PDZ domain protein; PCR primer;

KW PL domain protein; leukocyte activation; synapse formation;

KW transmembrane neurotransmitter receptor; autoimmune disease;

KW transplanted rejection; inflammation; allergy;

KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;

KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;

KW ischaemia; vasculitis; Crohn's disease; ss.

XX Homo sapiens.

OS

XX WO200069898-A2.

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XX The present invention relates to a method for modulating a biological
CC function of an endothelial cell or haematopoietic cell, comprises
CC introducing into a cell an antagonist that inhibits binding between a PDZ
CC domain protein and a PL domain protein to result in inhibition of
CC leukocyte activation. The present sequence is a PCR primer for a PDZ
CC domain. PDZ domains of proteins are named after three prototypical
CC proteins: PSD95, Drosophila large disc protein and Zonula Occludin 1
CC protein. PDZ domain proteins are involved in synapse formation by
CC organising transmembrane neurotransmitter receptors through intracellular
CC interactions. The inhibitors identified by the present invention can be
CC used to treat a disease mediated by haematopoietic cells, e.g. autoimmune
CC disease, inflammation, allergy (e.g. drug allergies), inflammatory bowel
CC diseases, ulcerative colitis, ileitis, psoriasis, respiratory allergic
CC diseases (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes,
CC Hashimoto thyroiditis, osteoarthritis), atherosclerosis, cancers,
CC infectious diseases (e.g. viral infection), ischaemia, vasculitis and
CC Crohn's disease. The inhibitors can also be used to prevent
CC transplanted rejection of a solid organ transplant
XX
SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 4; Length 26;

Best Local Similarity 85.7%; Pred. No. 8.2e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGATCGCTACGGCTCTCTGG 22

Db 2 AAGGATCCCTCCGGCTCTCTGG 22

RESULT 7

AAC99432

ID AAC99432 standard; DNA; 26 BP.

XX AC

XX AAC99432;

XX DT

XX 07-MAR-2001 (first entry)

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Primer #41 used to amplify PDZ encoded domain.

Haematopoietic cell; PDZ; PL; autoimmune disease; inflammation; allergy;
asthma; multiple sclerosis; cancer; infection; primer; ss.

Synthetic.

WO200069898-A2.

PD

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(ARBO-) ARBOR VITA CORP.

Lu PS;

PI

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WPI; 2001-080245/09.

Modulating a biological function of an endothelial cell or hematopoietic

PT cell, useful for treating autoimmune diseases and infectious diseases, by
 PT administering an antagonist that inhibits binding between a PDZ protein
 PT and a PL protein.

PS Disclosure, Page 28-43; 141pp; English.

XX The present invention relates to a new method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell. The method
 CC involves introducing into a cell, an antagonist that inhibits binding
 CC between a PDZ protein and a PL protein. The inhibitor is used to treat a
 CC disease mediated by hematopoietic cells, e.g. autoimmune disease. It may
 CC also be used to prevent transplantation rejection of a solid organ
 CC transplant. The method may also be used in the treatment of inflammation,
 CC allergy, inflammatory bowel diseases, ulcerative colitis, ileitis,
 CC psoriasis, asthma, atopic dermatitis, autoimmune diseases (e.g.
 CC rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes,
 CC Hashimoto thyroiditis, osteoarthritis, graft rejection, transplantation
 CC rejection), atherosclerosis, cancers, infectious diseases, ischemia,
 CC vasculitis and Crohn's disease

SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 4; Length 26;

Best Local Similarity 85.7%; Pred. No. 8.2e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGATCGCTACGGCTCTCGG 22

DB 2 AAGGATCCTCGGCTCTCGG 22

RESULT 8

ABT06636

ID ABT06636 standard; DNA; 26 BP.

XX ABT06636;

XX 07-NOV-2002 (first entry)

DE PDZ domain PCR primer SEQ ID No 362.

XX Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
 KW inflammatory; humoral immune response; inflammation; PCR; primer; ss.

XX Unidentified.

XX WO200231512-A2.

XX 18-APR-2002.

XX 11-OCT-2001; 2001WO-US0321150.

XX 13-OCT-2000; 2000US-00688017.

XX (ARBO-) ARBOR VITA CORP.

XX Rabinowitz JD, Lu PS, Schweizer J;

XX WPI; 2002-416878/44.

XX Assays for determining the affinity of binding between a PDZ domain and a
 PT ligand, and determining the Ki of an inhibitor of the binding, comprises
 PT using a polypeptide comprising a PDZ domain and a non-PDZ domain.

XX Disclosure; Page 43; 164pp; English.

XX The invention relates to methods and reagents for determining the
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The
 CC invention also relates to methods and reagents for determining the Ki of
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an
 CC agent that enhances binding of a PDZ domain and a ligand, and determining
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by

CC determining the ligand bound with an immobilised polypeptide comprising a
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a
 CC disease characterised by leukocyte activation, e.g., an autoimmune
 CC disease that is characterised by inflammatory or humoral immune response,
 CC and for reducing inflammation in a subject. This sequence represents a
 CC PDZ domain protein related PCR primer of the invention

SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 26;

Best Local Similarity 85.7%; Pred. No. 8.2e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGATCGCTACGGCTCTCGG 22

DB 2 AAGGATCCTCGGCTCTCGG 22

RESULT 9

ABQ96682

ID ABQ96682 standard; DNA; 26 BP.

XX ABQ96682;

XX 28-OCT-2002 (first entry)

XX KIAA 0316 PDZ domain forward PCR primer 158KIP.

XX Molecular interaction; hematopoietic cell; immune response; T cell;
 KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;
 KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;
 KW immunosuppressive; antiinflammatory; anti-allergic; antiatherosclerotic;
 KW antiulcer; antipsoriatic; dermatological; antiasthmatic; cytostatic;
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;
 KW angiogenesis-dependent disorder; infectious disease; PCR primer; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200242422-A2.

XX 30-MAY-2002.

XX 09-NOV-2001; 2001WO-US044138.

XX 11-NOV-2000; 2000US-00710059.

XX 24-NOV-2000; 2000US-00721915.

XX 24-NOV-2000; 2000US-00722069.

XX 28-NOV-2000; 2000US-00724553.

XX (ARBO-) ARBOR VITA CORP.

XX Lu P, Rabinowitz JD, Schweizer J;

XX WPI; 2002-608221/65.

XX Modulating the biological function of an endothelial cell or

PT hematopoietic cell e.g., a T-cell or B-cell comprises introducing into
 PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ
 PT ligand protein in the cell.

XX Disclosure; Page 48-49; 207pp; English.

XX The present invention describes a method (M1) for modulating a biological
 CC function of an endothelial cell or hematopoietic cell. M1 comprises
 CC introducing into the cell, an agent that inhibits binding of a PDZ
 CC (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein)
 CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the

biological function. Also described is a method (M2) for determining whether a test compound is an inhibitor of binding between a PDZ protein and a PL protein. M1 is used for modulating a biological function of an endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an inflammatory or humoral immune response, or an autoimmune disease. An inhibitor (I) is useful for treating a disease characterised by leukocyte activation, where the disease is characterised by an inflammatory or humoral immune response, e.g., an autoimmune disease. The compounds e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating symptoms of) a variety of diseases and conditions characterised by inflammatory and humoral immune responses e.g., inflammation, allergy, inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis, diseases such as asthma, allergic rhinitis, scleroderma, respiratory allergic (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver, autologous, bone marrow, xenotransplantation), atherosclerosis, cancers, angiogenesis-dependent disorders, infectious diseases and ischaemia. ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used in the exemplification of the present invention

XX SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 26;

Best Local Similarity 85.7%; Pred. No. 8.2e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCGG 22

Db 2 AAGGATCGCTCGGCTCTCGG 22

RESULT 10

ADJ80120
ID ADJ80120 standard; DNA; 24 BP.

XX AC ADJ80120;

XX DT 06-MAY-2004 (first entry)

XX DE RE-DSB cassette internal primer, SEQ ID NO 79.

XX KW in vivo; site-directed mutagenesis; mutation;
XX KW integrative recombinant oligonucleotide; IRO; CORE-cassette; primer; ss;
XX KW counterselectable reporter.

XX OS Unidentified.

XX PN WO2003012036-A2.

XX PD 13-FEB-2003.

XX PF 26-JUL-2002; 2002WO-US023634.

XX PR 27-JUL-2001; 2001US-0308426P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Storici F, Resnick MA, Lewis LK;

XX DR WPI; 2003-289875/28.

XX PT In vivo mutagenesis enabling site-specific mutations, deletions and
XX FT insertions with integrative oligonucleotides, useful as diagnostic tools
XX FT where biological consequences are assessed in the creation of strains or
XX FT cell lines.

XX PS Disclosure; SEQ ID NO 79; 96pp; English.

XX CC The invention relates to a novel method for in vivo site-directed
XX CC mutagenesis which involves introducing a mutation into a target double-
XX CC stranded nucleic acid sequence having a first and second strand in a
XX CC cell. The method comprises introducing a double-stranded nucleic acid
XX CC cassette into a target nucleic acid sequence at an insertion point,

transforming the cell with a first oligonucleotide, and selecting for loss of the nucleic acid sequence encoding the reporter gene. The method employs using integrative recombinant oligonucleotides (IROs). The cassette is an Reporter (RE)-cassette and contains a first portion homologous to a nucleic acid sequence on a first side of the insertion point, a second portion homologous to a second nucleic acid sequence on a second side of the insertion point, and a nucleic acid sequence encoding a reporter located between the first portion and the second portion. The first oligonucleotide comprises a nucleic acid sequence homologous to one strand (the chosen strand) of the target nucleic acid sequence at a position on the first side of the insertion point, and a nucleic acid sequence homologous to the same strand of the target nucleic acid sequence at a position on the second side of the insertion point, and comprising at least one nucleotide that differs from the chosen strand of the target nucleic acid sequence. The loss of the nucleic acid sequence encoding the reporter gene indicates integration of the oligonucleotide sequence comprising at least one nucleotide that differs from the target nucleic acid sequence. The methods and compositions are useful as diagnostic tools where a series of strains or cell lines are created, each with the cassette at a different position within a gene, such that mutations can be introduced anywhere within the gene and the biological consequences assessed. They can also be used in targeted changes in the genome of various organisms, modification of large human genes and larger windows of site-directed mutagenesis. This polynucleotide represents a primer used in the method of the invention.

XX SQ Sequence 24 BP; 2 A; 9 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 63.3%; Score 15.2; DB 10; Length 24;

Best Local Similarity 85.0%; Pred. No. 2.4e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCTCGG 22

Db 3 AGGATCGCGCGCTCTCGG 22

RESULT 11

ACK06221/c
ID ACK06221 standard; DNA; 25 BP.

XX AC ACK06221;

XX DT 14-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 106202.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW Genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR WPI; 2003-567953/53.

XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX FT Southern, Northern or dot-blot hybridization to identify or detect the
XX FT sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 106202; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 7 A; 7 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 63.3%; Score 15.2; DB 9; Length 25;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTGGAT 24
 |||||
 Db 25 GGTCCCTACGGTCTCTGGAT 6

RESULT 12
 ACK05595/c
 ID ACK05595 standard; DNA; 25 BP.
 XX
 AC ACK05595;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 105576.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 105576; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its

CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 7 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 63.3%; Score 15.2; DB 9; Length 25;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTGGAT 24
 |||||
 Db 25 GGTCCCTACGGTCTCTGGAT 6

RESULT 13
 AAT35182
 ID AAT35182 standard; DNA; 33 BP.
 XX
 AC AAT35182;
 XX
 DT 27-NOV-1996 (first entry)
 XX
 DE Human alpha-foetoprotein DNA primer DomiI3.
 XX
 KW Alpha-foetoprotein; AFP; cell proliferation; bone marrow;
 KW autoimmune disease; breast cancer; prostate cancer; neoplasm; tumour;
 KW myelotoxicity; therapy; cell culture medium; primer; PCR;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN WO9622787-A1.
 XX
 PD 01-AUG-1996.
 XX
 PF 24-JAN-1996; 96WO-US0000996.
 XX
 PR 24-JAN-1995; 95US-00377309.
 PR 24-JAN-1995; 95US-00377311.
 PR 24-JAN-1995; 95US-00377316.
 PR 24-JAN-1995; 95US-00377317.
 PR 21-JUL-1995; 95US-00505012.
 XX
 PA (MURG/) MURGITA R A.
 XX
 PI Murgita RA;
 XX
 DR WPI; 1996-362459/36.
 XX
 PT New isolated recombinant human alpha-fetoprotein - used for treating
 PT autoimmune diseases or neoplasms, for inhibiting myelotoxicity or
 PT promoting bone marrow cell proliferation.
 XX
 PS Example; Page 40; 133pp; English.

```
XX PCR primers (AAT35179-85) were used to amplify cDNA coding for fragments
CC of human mature recombinant alpha-fetoprotein (AFP). Plasmid pII8, which
CC contains the coding region of AFP (see also AAT35173), was used as
CC template. Primer DomI13 (AAT35182) was used with primer DomI15 (AAT35181)
CC to amplify AFP domain II (AAR99224) cDNA, and with primer DomI25
CC (AAT35179) to amplify domain I+II (AAR99222) cDNA. The recombinant AFP
CC fragments have therapeutic appln
XX
XX Sequence 33 BP; 10 A; 6 C; 6 G; 11 T; 0 U; 0 Other;
SQ
Query Match 62.5%; Score 15; DB 2; Length 33;
Best Local Similarity 78.3%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
Db ||||| || |||||
5 AAGGATCGCTTAGCTCTCTCTGGAT 27
RESULT 14
ABZ70298
ID ABZ70298 standard; DNA; 33 BP.
XX
XX AC ABZ70298;
XX
XX DT 25-APR-2003 (first entry)
XX
XX DE Dihydropyrroline-5-carboxylic acid reductase 8.91 PCR primer #4.
XX
XX KW Dihydropyrroline-5-carboxylic acid reductase 8.91; enzyme; cancer;
XX HIV infection; anti-HIV; cytostatic; PCR; primer; ss.
XX
XX OS Unidentified.
XX
XX PN CN1363661-A.
XX
XX PD 14-AUG-2002.
XX
XX PF 05-JAN-2001; 2001CN-00105030.
XX
XX PR 05-JAN-2001; 2001CN-00105030.
XX
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX PI Mao Y, Xie Y;
XX
XX DR WPI; 2002-751775/82.
XX
XX PT Polypeptide-dihydropyrroline-5-carboxylic acid reductase 8.91 and
XX polynucleotide for coding it.
XX
XX PS Example 4; Page 17 (Disclosure); 32pp; Chinese.
XX
XX CC The present invention relates to dihydropyrroline-5-carboxylic acid
XX reductase 8.91 (see ABP59181). The protein can be used for treating
XX diseases such as cancer and HIV infection. The present sequence is a PCR
XX primer, which was used in an example from the invention
XX
XX SQ Sequence 33 BP; 6 A; 10 C; 6 G; 11 T; 0 U; 0 Other;
Query Match 62.5%; Score 15; DB 6; Length 33;
Best Local Similarity 78.3%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
Db ||||| ||||| |||||
1 CATGGATCCCTACTCTCTCTGGA 23
RESULT 15
AAQ04591/c
ID AAQ04591 standard; DNA; 36 BP.
```

```
XX AAQ04591;
AC
XX DT 27-SEP-1990 (first entry)
XX
XX DE Probe used to screen cDNA library of bovine heavy metal responsive
XX sequence.
XX
XX KW Metallothionein; bMT-II; operator; ds.
XX
XX OS Bos taurus.
XX
XX PN EP369458-A.
XX
XX PD 23-MAY-1990.
XX
XX PF 17-NOV-1989; 89EP-00121295.
XX
XX PR 18-NOV-1988; 88US-00274241.
XX
XX PA (PHIP ) PHILLIPS PETROLEUM CO.
XX
XX PI Williams ME, Murphy MF;
XX
XX DR WPI; 1990-157607/21.
XX
XX PT Bovine metallo-thionein regulatory region fragment - providing inducible
XX expression of polypeptide in presence of heavy metal.
XX
XX PS Example 5; Page 14; 9pp; English.
XX
XX CC Gene being screened is bovine metallothionein regulatory gene it can be
XX used as an operator linked to the coding region of an heterologous
XX sequence, and is induced in the presence of heavy metals esp. Cd and Zn
XX
XX SQ Sequence 36 BP; 6 A; 8 C; 16 G; 6 T; 0 U; 0 Other;
Query Match 62.5%; Score 15; DB 2; Length 36;
Best Local Similarity 78.3%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
Db ||||| ||||| |||||
28 CATGGATCCCACTGCTCTCTGCA 6
RESULT 16
ABQ01333
ID ABQ01333 standard; DNA; 24 BP.
XX
XX AC ABQ01333;
XX
XX DT 11-JUN-2002 (first entry)
XX
XX DE Oligonucleotide adapter/capture probe 1324.
XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX
XX OS Synthetic.
XX
XX PN WO200216649-A2.
XX
XX PD 28-FEB-2002.
XX
XX PF 27-AUG-2001; 2001WO-US026519.
XX
XX PR 25-AUG-2000; 2000US-0227948P.
XX
XX PR 29-AUG-2000; 2000US-0228854P.
XX
XX PA (ILLU-) ILLUMINA INC.
XX
XX PI Gunderson K;
XX
```



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XX 09-FEB-2000; 2000WO-US003374.
XX PF
XX 09-FEB-1999; 99US-0119515P.
XX PR
XX 26-OCT-1999; 99US-0161699P.
XX PR
XX (POWD-) POWDERJECT VACCINES INC.
XX PA
XX Macklin MD, Fuller DL;
XX PI
XX WPI; 2000-524486/47.
XX DR
XX Nucleic acid immunization utilizing antigens from Mycobacterium
XX PT tuberculosis to protect against tuberculosis.
XX PR
XX Example 1; Page 31; 63pp; English.
XX PS
XX The present sequence is a PCR primer for the Mycobacterium tuberculosis
XX CC MPT 63 gene. Once amplified, the gene can be used in DNA vaccines to
XX CC elicit an immune response in humans, thus enabling immunisation against
XX CC the bacterium. This gives protection from tuberculosis (TB) either by DNA
XX CC vaccine alone or by combining the vaccine with the present BCG version to
XX CC give an enhanced immune response
XX CC
XX Sequence 36 BP; 9 A; 14 C; 6 G; 7 T; 0 U; 0 Other;
SQ
    Query Match      60.8%; Score 14.6; DB 3; Length 36;
    Best Local Similarity 81.0%; Pred. No. 4.8e+03;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| ||
Db 1 GGATCCCTACGGCTCCCAAT 21
    ||||| ||||| ||||| ||

RESULT 22
ACD54952
ID ACD54952 standard; DNA; 31 BP.
XX
AC ACD54952;
XX
XX 24-SEP-2003 (first entry)
DT
DE HBV DNazyme sequence #691.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; ss.
XX
XX Hepatitis B virus.
XX
XX WO200281494-A1.
XX
XX 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
XX PR
XX 08-JUN-2001; 2001US-00877478.
XX PR
XX 08-JUN-2001; 2001US-0296876P.
XX PR
XX 24-OCT-2001; 2001US-0335059P.
XX PR
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX PA
XX (BLAT/) BLATT L.
XX PA
XX (MACE/) MACEJAK D.
XX PA
XX (MCSW/) MCSWIGGEN J.
XX PA
XX (MORR/) MORRISSEY D.
XX PA

PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
XX PT hepatocellular carcinoma, or condition associated with hepatitis C virus
XX PT infection.
XX
XX Example 1; Page 190; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
XX CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX CC inozymes, zinzymes, amberyzymes, and G-cleaver ribozymes. Also disclosed
XX CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX CC as oligonucleotides that specifically bind the Enhancer I region of HBV
XX CC DNA. The nucleic acids may be used to modulate the expression of HBV
XX CC genes and HBV viral replication. Also disclosed is a method for screening
XX CC compounds and/or potential therapies directed against HBV, and compounds
XX CC that modulate the expression and/or replication of HCV. The compounds and
XX CC methods of the invention are useful for the treatment of degenerative and
XX CC disease states related to HBV and HCV infection, replication and gene
XX CC expression such as cirrhosis, liver failure, and hepatocellular
XX CC carcinoma. The present sequence represents one of the HBV ribozyme,
XX CC inozyme, G-cleaver, zinzyme, DNazyme or amberyzyme sequences disclosed in
XX CC the present invention
XX
SQ Sequence 31 BP; 8 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
    Query Match      60.0%; Score 14.4; DB 8; Length 31;
    Best Local Similarity 75.0%; Pred. No. 5.9e+03;
    Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| ||
Db 6 CAAGGCTAGCTACAACGACTGGAT 29
    ||||| ||||| ||||| ||

RESULT 23
ADM63061
ID ADM63061 standard; DNA; 31 BP.
XX
AC ADM63061;
XX
XX 03-JUN-2004 (first entry)
DT
DE Hepatitis B virus (HBV) enzymatic nucleic acid #2653.
XX
XX Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
XX KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
XX KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
XX KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
XX Hepatitis B virus.
XX OS
XX US2004054156-A1.
XX FN
XX 18-MAR-2004.
XX PD
XX 15-JAN-2003; 2003US-00342902.
XX PF
XX 14-MAY-1992; 92US-00882712.
XX PR
XX 07-FEB-1994; 94US-00193627.
XX PR
XX 08-NOV-1999; 99US-00436430.
XX PR
XX 20-MAR-2000; 2000US-00531025.
XX PR

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PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00896347.
PR 08-JUN-2001; 2001US-00877478.
XX
XX (DRAP//) DRAPER K.
PA (BLAT//) BLATT L.
PA (MCSW//) MCSWIGGEN J A.
PA (MORR//) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
XX
XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
XX Disclosure; SEQ ID NO 5195; 122pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
CC RNA of the invention. Note: The sequence data for this patent is also
CC available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX Sequence 31 BP; 8 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 14.4; DB 12; Length 31;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db ||||| ||||| ||||| ||||| |||||
6 CAAGGCTAGCTACACGACTGGAT 29
RESULT 24
AAXS9667/c
ID AAX59667 standard; DNA; 32 BP.
XX
XX AAX59667;
AC
XX
XX 22-JUL-1999 (first entry)
DT
XX
XX Muragenic primer DA23 used to amplify termamyl-like alpha-amylase DNA.
DE
XX
XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
KW saccharification process; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX WO9923211-A1.
FN
XX
XX 14-MAY-1999.
PD
XX
XX 30-OCT-1998; 98WO-DK000471.
PF
XX
XX 30-OCT-1997; 97DK-00001240.
PR
XX 14-JUL-1998; 98DK-00000936.
PR
XX (NOVO ) NOVO-NORDISK AS.
PA
XX
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PI Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
PI Kjaerulff S;
XX
XX WPI; 1999-326987/27.
XX
XX New Termamyl-like alpha-amylase variants.
XX
XX Example 5; Page 48; 115pp; English.
XX
XX The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present PCR primer was used to construct the variants of
CC the invention
XX
XX Sequence 32 BP; 12 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 14.4; DB 2; Length 32;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db ||||| ||||| ||||| ||||| |||||
31 CATGTGATCGTAACGGGTCCTGGTT 8
RESULT 25
ABQ83921
ID ABQ83921 standard; DNA; 33 BP.
XX
XX ABQ83921;
AC
XX
XX 04-FEB-2003 (first entry)
DT
XX
XX Mouse polycomb gene enhancer 84-57.31 PCR primer 4 SEQ ID NO:6.
DE
XX
XX Mouse; polycomb gene enhancer 84-57.31; embryotic development deformity;
KW tumour; PCR primer; ss.
XX
XX Mus sp.
OS
XX
XX CNI342699-A.
FN
XX
XX 03-APR-2002.
PD
XX
XX 12-SEP-2000; 2000CN-00125168.
PF
XX
XX 12-SEP-2000; 2000CN-00125168.
PR
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-529776/57.
DR
XX
XX A novel mouse polycomb gene enhancer 84-57.31 polypeptide, and the
PT polynucleotide encoding it, useful for treating several diseases e.g.
PT embryotic development deformity and tumors.
XX
XX Example 5; Page 18 (Disclosure); 34pp; Chinese.
XX
XX The present invention describes mouse polycomb gene enhancer 84-57.31
CC (I). Also described is a process for preparing (I) using DNA
CC recombination techniques. (I) can be used for treating several diseases
CC e.g. embryotic development deformity and tumours. The present sequence
CC
```

CC represents a PCR primer for (1), which is used in an example from the
CC present invention

SQ Sequence 33 BP; 6 A; 13 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 6; Length 33;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24

Db 1 CATGGATCCCTACGTCACCTCGAT 24

RESULT 26

ABK50283

ID ABK50283 standard; DNA; 33 BP.

XX

AC ABK50283;

XX 15-JUL-2002 (first entry)

XX Human motor protein analogous protein 10.12 PCR primer #2.

DE Motor protein analogous protein 10.12;

XX protein metabolism disturbance related disease; Human;
KW membrane protein dysfunction related disease; ss;
KW cell withering dysfunction related disease; PCR; primer.

XX Homo sapiens.

OS CNI329083-A.

XX 02-JAN-2002.

XX 21-JUN-2000; 2000CN-00116665.

XX 21-JUN-2000; 2000CN-00116665.

XX (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.

XX Mao Y, Xie Y;

XX WPI; 2002-305418/35.

XX A novel polypeptide-human motor protein analogous protein 10.12 and

PT polynucleotide for coding this polypeptide.

XX Example 4; Page 22 (Disclosure); 38pp; Chinese.

XX The invention relates to a novel polypeptide-human motor protein

CC analogous protein 10.12, the polynucleotide encoding this polypeptide and

CC a method for producing this polypeptide by using recombinant DNA

CC technology. The invention also discloses the method for curing several

CC diseases, such as protein metabolism disturbance related disease,

CC membrane protein dysfunction related disease and cell withering

CC dysfunction related disease by using this polypeptide. Also disclosed is

CC an antagonist for resisting this polypeptide and its therapeutic action,

CC and the application of the polynucleotide encoding this novel human motor

CC protein analogous protein 10.12. The present sequence is a PCR primer

CC used to clone the cDNA encoding human motor protein analogous protein

CC 10.12

XX Sequence 33 BP; 10 A; 10 C; 6 G; 7 T; 0 U; 0 Other;

SQ Query Match 60.0%; Score 14.4; DB 6; Length 33;

Best Local Similarity 75.0%; Pred. No. 5.9e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24

Db 1 CATGGATCCCTAAGGTCCTCGAT 24

RESULT 27

ABX12001

ID ABX12001 standard; DNA; 33 BP.

XX

AC ABX12001;

XX 10-MAY-2003 (first entry)

XX Human starch precursor bindin 10.78 specific PCR primer, #2.

DE Human; PCR; ss; starch precursor bindin 10.78; cancer; HIV; infection;

XX antagonist; primer.

XX Homo sapiens.

OS CNI363564-A.

XX 14-AUG-2002.

XX 05-JAN-2001; 2001CN-00105033.

XX 05-JAN-2001; 2001CN-00105033.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2003-000305/01.

XX Polypeptide-human starch precursor bindin 10.78 and polynucleotide for

XX coding it.

XX Example 4; Page 18 (disclosure); 32pp; Chinese.

XX The invention discloses a human starch precursor bindin 10.78

CC polypeptide. Also disclosed are the polynucleotide for coding it, the

CC process for preparing the polypeptide by DNA recombination, the

CC application of the polypeptide in treating diseases (e.g. cancer, HIV

CC infection), the antagonist of the polypeptide and its medical action, and

CC the application of the polynucleotide. The sequence presented is the PCR

CC primer, #2, which was used to amplify human starch precursor bindin

CC 10.78 cDNA

XX Sequence 33 BP; 7 A; 13 C; 4 G; 9 T; 0 U; 0 Other;

SQ Query Match 60.0%; Score 14.4; DB 8; Length 33;

Best Local Similarity 75.0%; Pred. No. 5.9e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24

Db 1 CATGGATCCCTACCACTGGTT 24

RESULT 28

ACI28366

ID ACI28366 standard; DNA; 25 BP.

XX

AC ACI28366;

XX 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 28357.

DE EST; ss; probe; expressed sequence tag; microarray; gene expression;

XX genetic variation; biallelic marker; polymorphism; human;

XX cross-species comparison.

XX Homo sapiens.

OS US2003104410-A1.

XX

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PD 05-JUN-2003.
XX
XX
PF 15-MAR-2002; 2002US-00098263.
XX
XX PR 16-MAR-2001; 2001US-0276759P.
XX
XX PA (AFFY-) AFFYMETRIX INC.
XX
XX PI Mittmann MP;
XX
XX DR WPI; 2003-567953/53.
XX
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX
XX PS Claim 1; SEQ ID NO 28357; 9pp; English.
XX
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX SQ Sequence 25 BP; 8 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 7.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTCGA 23
Db 1 GATCTCTAAGGCTCCAGGA 19

          ||||| ||||| ||||| |||||
RESULT 29
AAD59416
ID AAD59416 standard; DNA; 26 BP.
XX
XX AC AAD59416;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE PCR primer fosR used in PCR analysis as internal positive control.
XX
XX KW Mouse; transgenic rodent; transgenic; voltage-gated potassium channel;
XX KW Kvbeta1.1; knock-in subunit; psychiatric; neurological disorder;
XX KW anxiolytic; PCR; primer; ss.
XX
XX OS Unidentified.
XX
XX FN US2003024001-A1.
XX
XX PD 30-JAN-2003.
XX

16-JUL-2002; 2002US-00196890.
XX
XX PR 27-JUL-2001; 2001US-0308485P.
XX
XX PR 09-NOV-2001; 2001US-0331140P.
XX
XX PA (AMHP ) WYETH.
XX
XX XX Kwak SP, Rhodes K, Marquis KL, Comery TA, Askew R, Brandt M;
XX PI Rosenzweig-Lipson S;
XX
XX DR WPI; 2003-456314/43.
XX
XX PT Novel transgenic rodent comprising knock-in Kv beta 1.1 subunit of A-type
XX PT potassium channel, which is unable to confer N-type inactivation of
XX PT channel but retains ability to co-associate with Kv1 family of alpha-
XX PT subunits.
XX
XX PS Example 1; Page 16; 40pp; English.
XX
XX CC The invention relates to a transgenic rodent comprising an endogenous
XX CC gene cluster encoding a mutated voltage-gated potassium channel Kvbeta1.1
XX CC subunit of an A-type potassium channel. Kvbeta1.1 subunit is a knock-in
XX CC subunit which is unable to confer N-type inactivation of the channel but
XX CC retains the ability to co-associate with Kv1 family of alpha-subunits.
XX CC The invention is useful as a model for psychiatric and neurological
XX CC disorders to identify anxiolytic compounds and pro-cognitive functions.
XX CC The invention is useful as a model for evaluating the efficacy of test
XX CC compounds that modulate Kvbeta1.1 activity. The invention also is useful
XX CC as a positive anxiolytic control. The present sequence is a PCR primer
XX CC used in PCR analysis as internal positive control
XX
XX SQ Sequence 26 BP; 4 A; 5 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 10; Length 26;
Best Local Similarity 77.3%; Pred. No. 9e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCGG 22
Db 1 CAAGGATCGCTTGGGCTCAGGG 22

          ||||| ||||| ||||| |||||
RESULT 30
AA57219/c
ID AA57219 standard; DNA; 30 BP.
XX
XX AC AA57219;
XX
XX DT 28-JUL-1999 (first entry)
XX
XX DE Cysteine noose library primer CL1.MUT.1.
XX
XX KW Cysteine noose; antibody variable domain; CDR; cytokine; agonist; primer;
XX KW complementarity determining region; antagonist; mimetic; antigen;
XX KW MIP-1 alpha receptor; treatment; HIV infection; CDR3; anti-HIV; ss.
XX
XX OS Synthetic.
XX
XX FN WO9923222-A1.
XX
XX PD 14-MAY-1999.
XX
XX PF 30-OCT-1998; 98WO-GB003255.
XX
XX PR 31-OCT-1997; 97GB-00023062.
XX
XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX PI Osbourn JK;
XX
XX DR WPI; 1999-313343/26.
XX
XX DR P-PSDB; AAY08379.
XX
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PT Cysteine noose antibody libraries and their production.

XX Example 6; Page 42; 64pp; English.

XX This invention describes the construction of libraries of antibody
CC variable domains containing modified complementarity determining regions
CC (CDRs) carrying a cysteine noose and which have cytokine agonist and
CC antagonist mechanisms of action. The method of the invention can be used
CC to obtain peptide ligand mimetics capable of binding a target antigen.
CC The binding members may also be used to provide agonists or antagonists
CC of targets such as cytokines. In particular specific binding members for
CC MIP-1 alpha receptors are useful for treatment of HIV infection and for
CC in vitro investigation of mechanisms of HIV infection. A selection of
CC peptide ligand mimetics from CDR3 cysteine noose libraries provide a
CC means to select a different and potentially more effective population of
CC peptide ligands than direct display of similar cysteine noose ligands on
CC the surface of bacteriophage. The products of the invention have anti-HIV
CC activity

XX SQ Sequence 30 BP; 5 A; 13 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 2; Length 30;

Best Local Similarity 77.3%; Pred. No. 9.1e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGG 22

Db 23 CAAGGATCGCTACGGCTCTCTGG 2

RESULT 31

ADO43696

ID ADO43696 standard; DNA; 32 BP.

XX AC ADO43696;

XX DT 29-JUL-2004 (first entry)

XX DE PCR primer used to isolate cDNA encoding HINF-P.

XX KW cellular proliferation; histone nuclear factor P; HINF-P; bone disorder;
XX cancer; immune disorder; cardiovascular disorder; viral infection; PCR;
XX primer; ss.

XX OS Unidentified.

XX FN WO2004038008-A2.

XX PD 06-MAY-2004.

XX PF 27-OCT-2003; 2003WO-US034188.

XX PR 25-OCT-2002; 2002US-0421166P.

XX PA (UYMA-) UNIV MASSACHUSETTS.

XX PI Stein GS, Van Wijnen AJ, Xie R, Stein JL, Mitra P;

XX DR WPI; 2004-365515/34.

XX PT Modulating cellular proliferation using a Histone Nuclear Factor P (HINF-
XX P) or Nuclear Protein or Ataxia-Telangiectasia locus (NPAT) polypeptide,
XX useful for diagnosing or treating cancer, immune disorders and/or viral
XX infections.

XX PS Example 3; Page 72; 117pp; English.

XX The specification describes a method for enhancing cellular
XX proliferation. The method comprises introducing into a cell a compound
XX that alters the expression or activity of a Histone Nuclear Factor P
XX (HINF-P) polypeptide to enhance proliferation of the cell. The method of
XX the invention is useful for the diagnosis, prevention and treatment of
XX diseases or conditions associated with aberrant expression or activity of

CC the HINF-P polypeptide, such as bone disorders, cancer, immune disorders,
CC cardiovascular disorders and viral infections. PCR primers ADO43696-
CC ADO43697 were used to isolate cDNA encoding HINF-P.

XX SQ Sequence 32 BP; 5 A; 11 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 12; Length 32;

Best Local Similarity 77.3%; Pred. No. 9.1e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGG 22

Db 2 CAGGATCGCTACGGCTCTCTGG 23

RESULT 32

ABX14381

ID ABX14381 standard; DNA; 33 BP.

XX AC ABX14381;

XX DT 03-MAR-2003 (first entry)

XX DE PCR primer #2 for cDNA encoding human zinc finger protein 11.88.

XX KW Human; zinc finger protein 11.88; cancer; HIV infection; PCR;
XX human immunodeficiency virus infection; primer; ss.

XX OS Homo sapiens.

XX FN CN1359917-A.

XX PD 24-JUL-2002.

XX PF 20-DEC-2000; 2000CN-00135106.

XX PR 20-DEC-2000; 2000CN-00135106.

XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX PI Mao Y, Xie Y;

XX DR WPI; 2002-733606/80.

XX PT Polypeptide-human zinc finger protein 11.88 and encoding polynucleotide.

XX FS Example 4; Page 17 (disclosure); 32pp; Chinese.

XX The present invention relates to the isolation of human zinc finger
XX protein 11.88, and the polynucleotide sequence encoding it. Also
XX described is the process for preparing the protein by DNA recombination
XX and the application of the polypeptide and polynucleotide in treating
XX various diseases such as cancer and human immunodeficiency virus (HIV)
XX infection. The present sequence represents a PCR primer used to clone
XX cDNA encoding human zinc finger protein 11.88

XX SQ Sequence 33 BP; 7 A; 8 C; 10 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 33;

Best Local Similarity 77.3%; Pred. No. 9.2e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGG 22

Db 1 CATGGATCCCTACGGCAGTTGG 22

RESULT 33

AAZ35063/C

ID AAZ35063 standard; DNA; 22 BP.

XX AC AAZ35063;

XX

DT 28-FEB-2000 (first entry)
 XX
 DE Feline CD86 gene PCR primer 8/97.31.
 XX
 XX CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator;
 KW therapy; PCR; primer; ss.
 XX
 XX Synthetic.
 OS Felis catus.
 XX
 XX WO9957295-A1.
 XX
 XX 11-NOV-1999.
 PD
 XX 30-APR-1999; 99WO-US009504.
 PF
 XX 01-MAY-1998; 98US-00071711.
 PR
 XX (SCHE) SCHERING-PLOUGH LTD.
 PA (SCHE) SCHERING-PLOUGH VETERINARY CORP.
 XX
 XX Winslow BJ, Cochran MD;
 XX
 XX WPI; 2000-062155/05.
 DR
 XX Novel recombinant virus useful as immunomodulators, particularly in
 PT vaccines.
 FT
 XX
 XX Example; Page 122; 230pp; English.
 PS
 CC This oligonucleotide represents primer 8/97.31 that was used in the PCR
 CC amplification of the feline CD70 (B7-2) (see AAZ34838) cDNA. The
 CC amplified gene was used in the construction of homology vector 1015.18.8A
 CC (LP1-CD86/IRE5-CD80), which was used to create recombinant racoonpox
 CC viruses (RPV) expressing feline CD80 and CD86. The invention relates to a
 CC recombinant virus, e.g. RPV, that contains at least one foreign nucleic
 CC acid, inserted into a nonessential genomic region, that encodes feline
 CC CD28, CD80, CD86 or CTLA-4 protein (see AAY32283-87), or their
 CC immunogenic fragments, and is expressed when the recombinant virus is
 CC introduced into a suitable host. The recombinant virus may further
 CC comprise a foreign nucleic acid encoding an immunogen derived from a
 CC feline pathogen. It is used to modulate an immune response in a feline,
 CC particularly as a vaccine
 XX
 XX Sequence 22 BP; 4 A; 5 C; 10 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 57.5%; Score 13.8; DB 3; Length 22;
 Best Local Similarity 88.2%; Pred. No. 1.1e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 8 CGCTACGGCTCTCGAT 24
 Db 21 CGCTCCGGATCTCGAT 5
 RESULT 34
 AAT34298
 ID AAT34298 standard; cDNA; 36 BP.
 AC
 AC AAT34298;
 XX
 DT 24-OCT-1996 (first entry)
 XX
 XX HEK4 binding protein PCR primer 819-28.
 DE
 XX HEK4 binding protein; HEK4 receptor; EPH-like receptor;
 KW protein tyrosine kinase; ligand; growth; differentiation; cancer;
 KW nervous system disorder; therapy; polymerase chain reaction; PCR; primer;
 KW antibody; ss.
 XX
 XX Synthetic.
 OS
 XX WO9623000-A1.
 PN

XX 01-AUG-1996.
 PD
 XX 16-JAN-1996; 96WO-US001079.
 PF
 XX 27-JAN-1995; 95US-00379802.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Bartley TD, Fox GM;
 XX
 XX WPI; 1996-362633/36.
 DR
 XX Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to
 PT modulate growth and differentiation of, e.g. liver and kidney cells, and
 PT to treat cancer and nervous system disorders.
 FT
 XX Example 5; Page 31; 65pp; English.
 PS
 XX PCR primers 819-31 (AAT34297) and 819-28 (AAT34298) were used to amplify
 CC a portion of HEK4 binding protein cDNA (see also AAT34292) coding for
 CC amino acids 1-179 of the protein (see also AAW00035). The PCR fragment
 CC was cloned into vector pCFM1656 and truncated HEK4 binding protein was
 CC expressed in Escherichia coli FMS (ATCC 53911) transformants. The protein
 CC was used as an antigen in rabbits. The antiserum recognised HEK4 binding
 CC protein in CHO cells in Western blot analysis
 XX
 XX Sequence 36 BP; 9 A; 9 C; 10 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 57.5%; Score 13.8; DB 2; Length 36;
 Best Local Similarity 88.2%; Pred. No. 1.1e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 AAGGATCGCTACGCTC 18
 Db 5 AAGATCCCTATGCTC 21
 RESULT 35
 AAC69334/c
 ID AAC69334 standard; DNA; 21 BP.
 AC
 AC AAC69334;
 XX
 XX 29-JAN-2001 (first entry)
 DT
 XX Human ABC1 gene intron 9 polymorphic site, SEQ ID NO:233.
 DE
 XX Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal; ds.
 XX
 XX Homo sapiens.
 OS
 XX WO200055318-A2.
 PN
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-IB000532.
 PF
 XX 15-MAR-1999; 99US-0124702P.
 PR 08-JUN-1999; 99US-0138048P.
 PR 17-JUN-1999; 99US-0139600P.
 PR 01-SEP-1999; 99US-0151977P.
 PR
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIORESEARCH INC.
 XX

PI	Hayden MR, Wilson AR, Pimstone SN;
XX	
DR	WPI; 2000-587528/55.
XX	
PT	New ABC1 polypeptide is useful for treating diseases associated with ABC1
PT	biological activity, e.g. Alzheimer's disease, Huntington's disease and
PT	cancer.
XX	
XX	Example; Fig 11; 229pp; English.
PS	
PS	
XX	
CC	The invention relates to the human ABC1 cholesterol transporter protein
CC	(B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC	a member of the ATP-binding cassette (ABC transporter) superfamily of
CC	proteins, and plays a crucial role in cholesterol transport, particularly
CC	intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC	involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC	located on chromosome 9q31, and mutations in this gene are associated
CC	with two genetic HDL (high density lipoprotein) deficiency disorders,
CC	tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC	are distinguishable in that TD is an autosomal recessive disorder, while
CC	FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC	cholesterol") in the blood correlate with a high risk of cardiovascular
CC	disease, particularly coronary artery disease, but also cerebrovascular
CC	disease, coronary restenosis, and peripheral vascular disease.
CC	Conversely, a high level of HDL has protective effects against
CC	cardiovascular disease. The invention provides genetic constructs and
CC	transgenic cells and non-human animals comprising human ABC1 nucleic
CC	acids, and methods of gene therapy for the treatment or prevention of
CC	cardiovascular disease comprising the administration of an expression
CC	vector encoding ABC1 or an active fragment thereof. The invention also
CC	encompasses compounds which mimic ABC1 activity, compounds which
CC	stimulate ABC1 expression and methods of screening for such compounds. It
CC	further relates to methods for determining whether a patient has an
CC	increased risk for cardiovascular disease due to polymorphisms in the
CC	ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
CC	prevent cardiovascular disease, especially coronary artery disease,
CC	cerebrovascular disease, coronary restenosis or peripheral vascular
CC	disease. They may also be used in the treatment of diseases associated
CC	with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC	disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC	The invention specifically excludes proteins with the exact amino acid
CC	sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC	acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC	present sequence represents a polymorphic site of the human ABC1 gene
XX	
SQ	Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
	Query Match 56.7%; Score 13.6; DB 3; Length 21;
	Best Local Similarity 80.0%; Pred. NO. 1.4e+04;
	Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	1 CAAGGATCGCTACGGCTCCT 20
Db	20 CAATGAGCGCTTTGGCTCCT 1
	RESULT 36
	ACK06220/C
ID	ACK06220 standard; DNA; 21 BP.
XX	
AC	ACK06220;
XX	
DT	17-OCT-2001 (first entry)
XX	
DE	Human microarray DNA oligonucleotide SEQ ID NO 106201.
XX	
KW	EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW	genetic variation; biallelic marker; polymorphism; human;
KW	cross-species comparison.
XX	
OS	Homo sapiens.
XX	
FN	US2003104410-A1.
XX	
PD	05-JUN-2003.
XX	
PF	15-MAR-2002; 2002US-00098263.
XX	
PR	16-MAR-2001; 2001US-0276759P.
PA	(AFFY-) AFFYMETRIX INC.
XX	
PI	Mittmann MP;
XX	
DR	WPI; 2003-567953/53.
XX	
PT	New array of nucleic acid probes, useful for in situ hybridization, in

PI	Hayden MR, Wilson AR, Pimstone SN;
XX	
DR	WPI; 2000-587528/55.
XX	
PT	New ABC1 polypeptide is useful for treating diseases associated with ABC1
PT	biological activity, e.g. Alzheimer's disease, Huntington's disease and
PT	cancer.
XX	
XX	Example; Fig 11; 229pp; English.
PS	
PS	
XX	
CC	The invention relates to the human ABC1 cholesterol transporter protein
CC	(B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC	a member of the ATP-binding cassette (ABC transporter) superfamily of
CC	proteins, and plays a crucial role in cholesterol transport, particularly
CC	intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC	involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC	located on chromosome 9q31, and mutations in this gene are associated
CC	with two genetic HDL (high density lipoprotein) deficiency disorders,
CC	tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC	are distinguishable in that TD is an autosomal recessive disorder, while
CC	FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC	cholesterol") in the blood correlate with a high risk of cardiovascular
CC	disease, particularly coronary artery disease, but also cerebrovascular
CC	disease, coronary restenosis, and peripheral vascular disease.
CC	Conversely, a high level of HDL has protective effects against
CC	cardiovascular disease. The invention provides genetic constructs and
CC	transgenic cells and non-human animals comprising human ABC1 nucleic
CC	acids, and methods of gene therapy for the treatment or prevention of
CC	cardiovascular disease comprising the administration of an expression
CC	vector encoding ABC1 or an active fragment thereof. The invention also
CC	encompasses compounds which mimic ABC1 activity, compounds which
CC	stimulate ABC1 expression and methods of screening for such compounds. It
CC	further relates to methods for determining whether a patient has an
CC	increased risk for cardiovascular disease due to polymorphisms in the
CC	ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
CC	prevent cardiovascular disease, especially coronary artery disease,
CC	cerebrovascular disease, coronary restenosis or peripheral vascular
CC	disease. They may also be used in the treatment of diseases associated
CC	with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC	disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC	The invention specifically excludes proteins with the exact amino acid
CC	sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC	acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC	present sequence represents a polymorphic site of the human ABC1 gene
XX	
SQ	Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
	Query Match 56.7%; Score 13.6; DB 3; Length 21;
	Best Local Similarity 80.0%; Pred. NO. 1.4e+04;
	Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	1 CAAGGATCGCTACGGCTCCT 20
Db	20 CAATGAGCGCTTTGGCTCCT 1
	RESULT 36
	AAF93000/C
ID	AAF93000 standard; DNA; 21 BP.
XX	
AC	AAF93000;
XX	
DT	17-MAY-2001 (first entry)
XX	
DE	Polymorphic sequence for ABC1 polymorphic site #19.
XX	

PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 106201; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 56.7%; Score 13.6; DB 9; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 5 GATCGCTACGGCTCCTGGAT 24
 ||||| ||||| ||||| |||||
 Db 25 GGTCCCTACGGGACCTGGAT 6
 RESULT 38
 AC104808/C
 ID AC104808 standard; DNA; 25 BP.
 XX
 AC AC104808;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 4799.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 EN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 DR New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX
 PS Claim 1; SEQ ID NO 4799; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 56.7%; Score 13.6; DB 9; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 AAGGATCGCTACGGCTCCTG 21
 ||||| ||||| ||||| |||||
 Db 23 AAGGAGGCAACGGTCTG 4
 RESULT 39
 ACK05594/C
 ID ACK05594 standard; DNA; 25 BP.
 XX
 AC ACK05594;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 105575.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 EN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 DR New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 105575; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used CC in monitoring gene expression levels by hybridisation to a DNA library, CC in analysis of genetic variation or in hybridisation of tag-labelled CC compounds. The nucleic acid probes are specifically designed for analysis CC of at least one target sequence. The method of analysis comprises CC hybridising at least one or more nucleic acids to at least two or more CC nucleic acid probes and detecting the hybridisation. The nucleic acid CC probes are attached to a solid support. The analysis comprises monitoring CC gene expression levels, identifying allelic markers or polymorphisms, CC or family members of a gene and a cross-species comparison. Each of the CC nucleic acids further comprises a tag sequence. The array of nucleic acid CC probes is useful in *in situ* hybridisation, in Southern, Northern or dot- CC blot hybridisation to identify or detect the sequence or specific CC mutations of any gene, in mapping the 5' termini of mRNA molecules by CC primer extensions or in screening cDNA or genomic libraries or subclones CC for additional subclones containing segments of DNA that have been CC isolated and previously sequenced. The sequence presented is one of the CC nucleic acid probes incorporated in the microarray. Note: The sequence CC data for this patent can also be obtained in electronic format directly CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 56.7%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. NO. 1.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5 GATCGCTACGGCTCTGGAT 24
| | | | | | | | | | | | | | | | | | | | | |
Db 25 GGTCCCTACGGGACCTGGAT 6

RESULT 40

AAZ35681
ID AAZ35681 standard; DNA; 28 BP.

XX AAZ35681;

XX 26-JAN-2000 (first entry)

XX IL-2/GM-CSF fusion protein construction oligonucleotide P4.

XX IL-2; interleukin 2; granulocyte macrophage colony stimulating factor;
KW GM-CSF; fusion protein; ss.

XX Synthetic.

OS Homo sapiens.

XX CN1225368-A.

XX 11-AUG-1999.

XX 05-FEB-1999; 99CN-00113461.

XX 05-FEB-1999; 99CN-00113461.

XX (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.

XX Wang X, Huang S, Gao J;

XX WPI; 1999-581110/50.

XX Interleukin -2/granulocyte-macrophage colony stimulating factor fusion protein.

XX Claim 5; Page 1; 17pp; Chinese.

XX The present invention describes an interleukin-2/granulocyte-macrophage colony stimulating factor fusion protein (IL-2/GM-CSF fusion protein).

CC The fusion protein is produced by genetic engineering technology by CC subcloning against IL-2 and end reform and a GM-CSF connection IL-2/GM- CC CSF expression plasmid is constructed. The fusion protein can be used to CC convert *Escherichia coli* obtaining high effect expression. The fused CC protein possesses IL-2 and GM-CSF dual activity. The present sequence CC represent an oligonucleotide used in the construction of the IL-2/GM-CSF CC fusion protein

SQ Sequence 28 BP; 3 A; 9 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 56.7%; Score 13.6; DB 2; Length 28;
Best Local Similarity 80.0%; Pred. NO. 1.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 4 GGATCGCTACGGCTCTGGGA 23
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GGATCCTTATCGCTCTGGGA 21

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Job time : 169.262 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1147.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGGATCGCTACGGCTCTCGAT 24

Scoring table:

IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	73.3	50	1	AU103062
2	15.2	63.3	41	9	CG716757
3	15	62.5	24	8	AZ812591
4	15	62.5	50	1	AU103061
5	15	62.5	50	1	AU103068
6	14.6	60.8	50	1	AU103064
7	14.6	60.8	50	1	AU103067
8	14.2	59.2	50	1	AU107042
9	14	58.3	44	8	AZ476398
10	14	58.3	40	1	AU102662
11	13.6	56.7	50	1	AU103063
12	13.4	55.8	40	1	AU1317060
13	13	54.2	39	9	AJ594860
14	13	54.2	44	5	B0589685
15	13	54.2	50	1	AU103069
16	13	54.2	50	1	AU104866
17	12.8	53.3	31	7	N94283
18	12.8	53.3	35	9	CL665533
19	12.8	53.3	50	1	AU107276
20	12.6	52.5	34	4	BJ064678
21	12.6	52.5	42	8	CC027439
22	12.6	52.5	50	1	AU103065
23	12.6	52.5	50	1	AU105726
24	12.6	52.5	50	1	AU105728

C 25	12.4	51.7	38	1	AJ655775
C 26	12.4	51.7	46	9	AG213917
C 27	12.4	51.7	47	8	AZ820416
C 28	12.4	51.7	49	1	A1159805
C 29	12.2	50.8	45	7	CF277394
30	12.2	50.8	48	8	BH907825
31	12.2	50.8	50	1	AU104805
32	12.2	50.8	50	1	AU104807
33	12.2	50.8	50	1	AU107142
34	12	50.0	30	9	AG195132
35	12	50.0	38	8	AZ492391
36	12	50.0	42	8	BH804014
37	12	50.0	49	1	AA087268
38	12	50.0	50	1	AU103066
39	12	50.0	50	1	AU104834
40	12	50.0	50	1	AU106612
41	12	50.0	50	1	AU106614
42	12	50.0	50	1	AU107039
43	11.8	49.2	23	8	AZ858813
44	11.8	49.2	34	9	CL522317
45	11.8	49.2	37	1	AA518952

ALIGNMENTS

RESULT 1
LOCUS AU103062 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU103062 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP19487, mRNA sequence.
ACCESSION AU103062
VERSION AU103062.1 GI:13552583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Seese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP19487"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 73.3%; Score 17.6; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 1 CAAGGATCGCTACGGCTCTCGAT 24
Db 10 CTAGGATCGGACGGGTCTCGAT 33

RESULT 2
CG716757
LOCUS
DEFINITION 1119046B12.1EL.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION CG716757
VERSION CG716757.1 GI:37745389
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 41)
AUTHORS Walbot,V.
JOURNAL Maize genomic sequences found using engineered RescueMu transposon
COMMENT Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119046 row: 7
Class: transposon-tagged.

FEATURES
source
1..41
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 63.3%; Score 15.2; DB 9; Length 41;
Best Local Similarity 85.0%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCTG 21
|||||
Db 13 AAGGATCGATCGGCACCTG 32

RESULT 3
AZ812591
LOCUS
DEFINITION 2M0079D21F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC2M0079D21 F, genomic survey sequence.
ACCESSION AZ812591
VERSION AZ812591.1 GI:12981989
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0079 row: D column: 21
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
source

1..24
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/strain="C57BL/6J"
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/clone="UUC2M0079D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 62.5%; Score 15; DB 8; Length 24;
Best Local Similarity 78.3%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCTCGAT 24
|||||
Db 1 ATGATCGCCATGGCTCTGGAT 23

RESULT 4
AUI03061

LOCUS
DEFINITION AUI03061 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone COLF1890, mRNA sequence.
ACCESSION AUI03061
VERSION AUI03061.1 GI:13552582
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Taunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
FEATURES             source
   source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COLF1890"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          62.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCGA 23
    |||||
Db 28 CTAGATCGGACGGGAAGTGA 50

RESULT 5
AUI03068
LOCUS
DEFINITION
AUI03068 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSI02929, mRNA sequence.
ACCESSION
AUI03068
VERSION
AUI03068.1 GI:13552589
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Taunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
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Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCGA 23
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Db 28 CTAGATCGGACGGGAAGTGA 50

RESULT 5
AUI03068
LOCUS
DEFINITION
AUI03068 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSI02929, mRNA sequence.
ACCESSION
AUI03068
VERSION
AUI03068.1 GI:13552589
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Taunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
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EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
FEATURES             source
   source
1..50
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/db_xref="taxon:9606"
/clone="HSI02929"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          62.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCGA 23
    |||||
Db 28 CTAGATCGGACGGGAAGTGA 40

RESULT 6
AUI03064
LOCUS
DEFINITION
AUI03064 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC00745, mRNA sequence.
ACCESSION
AUI03064
VERSION
AUI03064.1 GI:13552585
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Taunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
FEATURES             source
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1..50
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="HRC00745"
/clone_lib="Sugano Homo sapiens cDNA library"

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Query Match          60.8%; Score 14.6; DB 1; Length 50;
Best Local Similarity 81.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCTCGA 23
    |||||
Db 1 AGGATCGGACGGGAAGTGA 21

RESULT 7
AUI03067
LOCUS
DEFINITION
AUI03067 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC09549, mRNA sequence.
ACCESSION
AUI03067
VERSION
AUI03067.1 GI:13552588
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)

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ORIGIN
Query Match          62.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCGA 23
    |||||
Db 18 CTAGATCGGACGGGAAGTGA 40

RESULT 6
AUI03064
LOCUS
DEFINITION
AUI03064 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC00745, mRNA sequence.
ACCESSION
AUI03064
VERSION
AUI03064.1 GI:13552585
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Taunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
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EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
FEATURES             source
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="HRC00745"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          60.8%; Score 14.6; DB 1; Length 50;
Best Local Similarity 81.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCTCGA 23
    |||||
Db 1 AGGATCGGACGGGAAGTGA 21

RESULT 7
AUI03067
LOCUS
DEFINITION
AUI03067 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC09549, mRNA sequence.
ACCESSION
AUI03067
VERSION
AUI03067.1 GI:13552588
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)

```

AUTHORS
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. fine, large-scale
 mapping of mRNA start sites

TITLE
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL
 EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE
 21270072

PUBMED
 11375929

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="HRC09549"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 60.8%; Score 14.6; DB 1; Length 50;
 Best Local Similarity 81.0%; Pred. No. 4.9e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCTGGA 23
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 Db 1 AGGATCGCGACGGAACTGGA 21
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RESULT 8
 AUI07042/c

LOCUS
 AUI07042 50 bp mRNA linear EST 28-JAN-2004

DEFINITION
 AUI07042 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 KAT06852, mRNA sequence.

ACCESSION
 AUI07042

VERSION
 AUI07042.1 GI:13556563

KEYWORDS
 EST.

SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens

REFERENCE
 1 (bases 1 to 50)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

TITLE
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL
 EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE
 21270072

PUBMED
 11375929

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
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 /db_xref="taxon:9606"
 /clone="KAT06852"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 59.2%; Score 14.2; DB 1; Length 50;
 Best Local Similarity 84.2%; Pred. No. 7.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTGGA 23
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 Db 34 GATAACTAGGCTCCTGGA 16
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RESULT 9
 AZ476398

LOCUS
 AZ476398 44 bp DNA linear GSS 04-OCT-2000

DEFINITION
 IM0295B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0295B16 F, genomic survey sequence.

ACCESSION
 AZ476398

VERSION
 AZ476398.1 GI:10634523

KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 44)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE
 Unpublished (2000)

JOURNAL
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu

COMMENT
 Insert Length: 10000 Std Error: 0.00
 Plate: 0295 row: B column: 16
 Seq primer: CGTTGTAACACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 44.

FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0295B16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

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Query Match      58.3%; Score 14; DB 8; Length 44;
Best Local Similarity 77.3%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGG 22
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Db 23 CAAGCATCACTCCGGTGCCTGG 44

RESULT 10
AUI02662/c
LOCUS      AUI02662      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION AUI02662 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS07035, mRNA sequence.
ACCESSION  AUI02662
VERSION     AUI02662.1 GI:13552183
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yuzuki@ims.u-tokyo.ac.jp
Sakaki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES             source
    source            1..50
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                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clones="HRC00126"
                        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      56.7%; Score 13.6; DB 1; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTGGA 23
    ||||| ||||| ||||| |||||
Db 1 GGATCGCGACGGGAACCTGGA 20

RESULT 12
AUI317060
LOCUS      AUI317060      40 bp      mRNA      linear      EST 17-DEC-1998
DEFINITION uk72a02.y1 Schiller mouse At720 Mus musculus cDNA clone
            IMAGE:1974506 5' similar to SW:HEMN SYN3 P73245 PROBABLE
            OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE ; mRNA sequence.
ACCESSION  AUI317060
VERSION     AUI317060.1 GI:4032327
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 40)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Scheilberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
            The WashU-HMI Mouse EST Project
            Unpublished (1996)
            Contact: Marra M/Mouse EST Project
            WashU-HMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:991246
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
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ORIGIN
Query Match      58.3%; Score 14; DB 1; Length 50;
Best Local Similarity 77.3%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCTGGA 23
    ||||| ||||| ||||| |||||
Db 49 AAGTCTCGCATTCGGCTCCTGGA 28

RESULT 11
AUI03063
LOCUS      AUI03063      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION AUI03063 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC00126, mRNA sequence.
ACCESSION  AUI03063
VERSION     AUI03063.1 GI:13552584
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,

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Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
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EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

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                        /organism="Homo sapiens"
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                        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      56.7%; Score 13.6; DB 1; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTGGA 23
    ||||| ||||| ||||| |||||
Db 1 GGATCGCGACGGGAACCTGGA 20

RESULT 12
AUI317060
LOCUS      AUI317060      40 bp      mRNA      linear      EST 17-DEC-1998
DEFINITION uk72a02.y1 Schiller mouse At720 Mus musculus cDNA clone
            IMAGE:1974506 5' similar to SW:HEMN SYN3 P73245 PROBABLE
            OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE ; mRNA sequence.
ACCESSION  AUI317060
VERSION     AUI317060.1 GI:4032327
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 40)
AUTHORS     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Scheilberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
            The WashU-HMI Mouse EST Project
            Unpublished (1996)
            Contact: Marra M/Mouse EST Project
            WashU-HMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:991246
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
            Location/Qualifiers
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                                /mol_type="mRNA"
                                /db_xref="taxon:10090"
                                /clones="IMAGE:1974506"

FEATURES             source
    source            1..40
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /db_xref="taxon:10090"
                        /clones="IMAGE:1974506"

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/cell_line="pituitary cell line"
 /lab_host="SOLR"
 /note="Organ: pituitary; Vector: pBluescript SK-
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 cDNA was prepared from cell line AtT-20 using primer
 5'-CAGAGAGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An SCORI
 adaptor was used on the 5' end of the cDNA as follows:
 5'-AATTGGCAGAG-3'. The library was size-selected and
 went through one round of amplification. Average insert
 size is 1.7 kb, with a range from 0.4-12 kb. This library
 was constructed by Dr. Martin Schiller (Johns Hopkins
 University)."

ORIGIN

Query Match 55.8%; Score 13.4; DB 1; Length 40;
 Best Local Similarity 73.9%; Pred. No. 1.7e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGATCGCTACGGCTCTCGA 23
 ||||| ||||| ||||| ||||| |||||
 Db 13 CAAGAAACGCTGCAGTACTGCA 35

RESULT 13

AJ594860/c

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 406G07, genomic survey sequence.

ACCESSION

AJ594860

VERSION

GSS; left border; T-DNA flanking sequence.

KEYWORDS

Arabidopsis thaliana (thale cress)

SOURCE

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

TITLES

JOURNAL

COMMENT

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
 http://dbgap.versailles.inra.fr/publiclines/. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (http://www.genoplante.com and
 http://genoplante-info.infobiogen.fr).

FEATURES

source

1. 39
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassillewskija"
 /db_xref="taxon:3702"
 /clone="406G07"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature

1. 39
 /note="T-DNA flanking sequence
 left border"

ORIGIN

Query Match 54.2%; Score 13; DB 9; Length 39;
 Best Local Similarity 76.2%; Pred. No. 2.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGATCGCTACGGCTCTCTG 21
 ||||| ||||| ||||| ||||| |||||
 Db 22 CAAGCATCTCTTCAGTCTCATG 2

RESULT 14

BQ589685

LOCUS

DEFINITION BQ589685 44 bp mRNA linear EST 06-DEC-2002
 E012680-024-020-L13-SP6 MP12-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-020-L13 5-PRIME, mRNA sequence.

ACCESSION

BQ589685

VERSION

BQ589685.1 GI:26119268

KEYWORDS

EST.

SOURCE

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weissshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weissshaar@mpiz-koeln.mpg.de
 Insert Length: 44 Std Error: 0.00
 Plate: 20 row: 1 column: 13
 Seq primer: SP6, CATACGATTAGGTGACACTATAG.
 Location/Qualifiers
 1. 44
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:190477"
 /db_xref="taxon:161934"
 /clone="024-020-L13"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCAGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 54.2%; Score 13; DB 5; Length 44;
 Best Local Similarity 76.2%; Pred. No. 2.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGATCGCTACGGCTCTCTG 21
 ||||| ||||| ||||| ||||| |||||
 Db 5 CACTGATGCCACGGCTCCCG 25

RESULT 15
 AUI03069
 LOCUS
 DEFINITION AUI03069 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HUV00521, mRNA sequence.
 ACCESSION AUI03069
 VERSION AUI03069
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 PUBMED 11375929
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 source
 1..50
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="HUV00521"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;
 Best Local Similarity 76.2%; Pred. No. 2.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 AGGATCGCTACGGCTCTCGGA 23
 ||||| ||| |||||
 Db 1 AGGATCGCGACTGGGAACCTGGA 21

RESULT 16
 AUI04866
 LOCUS
 DEFINITION AUI04866 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 CAS03624, mRNA sequence.
 ACCESSION AUI04866
 VERSION AUI04866
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 PUBMED 11375929
 COMMENT Contact: Yutaka Suzuki
 Department of Virology

Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).
 FEATURES
 source
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CAS03624"
 /clone_lib="Sugano Homo sapiens cDNA library"
 ORIGIN
 Query Match 54.2%; Score 13; DB 1; Length 50;
 Best Local Similarity 76.2%; Pred. No. 2.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CAAGGATCGCTACGGCTCTCG 21
 ||||| ||| |||||
 Db 25 CAAGGATCATTTACTTTTCTG 45

RESULT 17

N94283
 LOCUS
 DEFINITION N94283 31 bp mRNA linear EST 05-APR-1996
 zz26f01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
 IMAGE:293689 5' similar to gb:X56807_cds2 DESMOCOLLIN 3A/3B
 PRECURSOR (HUMAN); mRNA sequence.
 N94283
 ACCESSION N94283.1 GI:1266592
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 31)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Ruchling,T., Soares,M., Tan,F.,
 Trevasaki,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: mob.REGA+ET
 High quality sequence stop: 1.

FEATURES
 source

Location/Qualifiers
 1..31
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="CDB:3801536"
 /db_xref="taxon:9606"
 /clone="IMAGE:293689"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFLS"
 /note="Organ: Liver and Spleen; Vector: pTV73D (Pharmacia)
 with a modified polylinker; Site.1: Pac 1; Site.2: Eco RI;
 1st strand cDNA was primed with a Pac 1 - oligo(dT) primer
 [5' AACTGGAAGAATTAAATAAGATCTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors


```

/tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"

ORIGIN
Query Match      52.5%; Score 12.6; DB 4; Length 34;
Best Local Similarity 68.2%; Pred. No. 4e+05;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AAGGATCGTACGGCTCTCGGA 23
|||||
Db 10 AAGGATCGTACGGCTCTCGGA 31

RESULT 21
LOCUS CC027439
DEFINITION CC027439 42 bp DNA linear GSS 01-APR-2003
3591_1_5_1_D10.1BL.Y.1 3591 - RescueMu Grid P Zea mays genomic,
genomic survey sequence.
ACCESSION CC027439
VERSION CC027439.1 GI:29442296
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE clade; Panicoideae; Andropogoneae; Zea.
JOURNAL 1 (bases 1 to 42)
COMMENT Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3591_1_5_1 row: 4
Class: transposon-tagged.
Location/Qualifiers
1. 42
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid P was grown at Molokai in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Query Match      52.5%; Score 12.6; DB 8; Length 42;
Best Local Similarity 78.9%; Pred. No. 4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGATCGCTACGGCTCC 19
|||||

```

```

Db 23 CAAGATCGCTTCGTTCC 41

RESULT 22
LOCUS AU103065
DEFINITION AU103065 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC01582, mRNA sequence.
ACCESSION AU103065
VERSION AU103065.1 GI:13552586
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yszukui@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC01582"
/clone_lib="Sugano Homo sapiens cDNA library"

FEATURES
source
Query Match      52.5%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GATCGTACGGCTCTCGGA 23
|||||
Db 1 GATCGTACGGCTCTCGGA 19

RESULT 23
LOCUS AU105726
DEFINITION AU105726 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HST05236, mRNA sequence.
ACCESSION AU105726
VERSION AU105726.1 GI:13555247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 11375929
COMMENT Contact: Yutaka Suzuki

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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES             source
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        /location/Qualifiers
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="HS105236"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          52.5%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GATCGCTACGCTCCTCGA 23
    |||||
Db 25 GGTGGCTCAGGCTCCTCGA 43

RESULT 24
AU105728             50 bp mRNA linear EST 28-JAN-2004
LOCUS                HUVA0074, mRNA sequence.
DEFINITION            AU105728 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION             AU105728
VERSION               AU105728.1 GI:13555249
KEYWORDS              EST.
SOURCE                Homo sapiens (human)
ORGANISM              Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS              Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
                    Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
                    Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
                    Diverse transcriptional initiation revealed by fine, large-scale
                    mapping of mRNA start sites
                    ENEO Rep. 2 (5), 388-393 (2001)
JOURNAL              ENEO Rep. 2 (5), 388-393 (2001)
MEDLINE              21270072
PUBMED               11375929
COMMENT              Contact: Yutaka Suzuki
                    Department of Virology
                    Institute of Medical Science, University of Tokyo
                    4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                    Email: yuzuki@ims.u-tokyo.ac.jp
                    Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
                    Sugano,S. Construction and characterization of a full
                    length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                    149-156 (1997).

FEATURES             source
    source
        1..50
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="HUVA0074"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          52.5%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GATCGCTACGCTCCTCGA 23
    |||||
Db 7 GGTGGCTCAGGCTCCTCGA 25

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RESULT 25
AJ655775/c           38 bp mRNA linear EST 28-JUN-2004
LOCUS                KN277 Sus scrofa cDNA clone C0005191_B05, mRNA sequence.
DEFINITION            AJ655775
ACCESSION             AJ655775
VERSION               AJ655775.1 GI:493339807
KEYWORDS              EST.
SOURCE                Sus scrofa (pig)
ORGANISM              Sus scrofa
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS              Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
                    Development of cDNA and EST resources for studying reproduction and
                    embryo development in pigs and cattle
                    Unpublished (2004)
JOURNAL              Contact: Anderson SI
COMMENT              Genomics and Bioinformatics
                    Roslin Institute
                    Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
                    Single pass sequencing. Bases called and trimmed with phred
                    v0.020425.c. Vector identified by cross match with the -minscore 20
                    and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI
                    R. Site2: NotI 5' Seq Primer M13p Normalised library constructed
                    from pooled early embryos, from 8- cell stage to blastocysts.
                    Clones available from UK Centre for Functional Genomics in Farm
                    Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
                    www.arkgenomics.org.

FEATURES             source
    source
        1..38
        /organism="Sus scrofa"
        /mol_type="mRNA"
        /db_xref="taxon:9823"
        /clone="C0005191_B05"
        /tissue type="embryo"
        /clone_lib="KN277"
        /notes="Vector: pBluescriptII(SK+); Site_1: EcoRI; Site_2:
        NotI; Single pass sequencing. Normalised library
        constructed from pooled early embryos, from 8-cell stage
        to blastocysts."

ORIGIN
Query Match          51.7%; Score 12.4; DB 1; Length 38;
Best Local Similarity 72.7%; Pred. No. 4.9e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGCTCCTCGA 23
    |||||
Db 29 AGGATCGCTAGGCGCATCGA 8

RESULT 26
AG213917/c           46 bp DNA linear GSS 09-AUG-2003
LOCUS                AG213917
DEFINITION            AG213917
                    flanking sequence of Tos17 insertion in rice strain ND9022, genomic
                    survey sequence.
ACCESSION             AG213917
VERSION               AG213917.1 GI:323611107
KEYWORDS              GSS.
SOURCE                Oryza sativa (japonica cultivar-group)
ORGANISM              Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS              Miyao,A., Tanaka,K., Murata,K., Sawaki,H., Takeda,S., Abe,K.,
                    Shinzuka,Y., Onosato,K. and Hirochika,H.
                    Target Site Specificity of the Tos17 Retrotransposon Shows a
                    Preference for Insertion within Genes and against Insertion in
                    Retrotransposon-Rich Regions of the Genome
                    Plant Cell 15 (8), 1771-1780 (2003)
JOURNAL

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MEDLINE      22779046
PUBMED      12897251
REFERENCE    2 (bases 1 to 46)
AUTHORS      Miyao,A., Kato,M. and Hirochika,H.
TITLE        Direct Submission
JOURNAL      Submitted (16-APR-2002) Akio Miyao, National Institute of
              Agrobiological Sciences, Molecular Genetics, 2-1-2, Kannondai,
              Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp,
              URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,
              Fax:81-298-38-7020)
FEATURES
  Location/Qualifiers
    1..46
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="genomic DNA"
      /strain="ND9022"
      /cultivar="Nipponbare"
      /db_xref="taxon:39947"
      /clone="T11738"
      /clone_lib="PCR product directly amplified from rice
      genomic DNA"
      /note="The 3' end of retrotransposon Tos17 was found
      immediately upstream of this sequence."
ORIGIN
Query Match      51.7%; Score 12.4; DB 9; Length 46;
Best Local Similarity 72.7%; Pred. No. 4.9e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AAGGATCGCTACGGCTCCTGGA 23
      ||||| ||||| ||||| |||||
Db      44 AGGGATTGATGAGGCTCATGGA 23

RESULT 27
AZ820416/c
LOCUS      AZ820416      47 bp      DNA      linear      GSS      20-FEB-2001
DEFINITION      2M092F16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M092F16 R, genomic survey sequence.
ACCESSION      AZ820416
VERSION      AZ820416.1 GI:12990420
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: F column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers
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    /db_xref="taxon:10090"
    /clone="UUGC2M092F16"

MEDLINE      22779045
PUBMED      12897251
REFERENCE    2 (bases 1 to 46)
AUTHORS      Miyao,A., Kato,M. and Hirochika,H.
TITLE        Direct Submission
JOURNAL      Submitted (16-APR-2002) Akio Miyao, National Institute of
              Agrobiological Sciences, Molecular Genetics, 2-1-2, Kannondai,
              Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp,
              URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,
              Fax:81-298-38-7020)
FEATURES
  Location/Qualifiers
    1..46
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      /mol_type="genomic DNA"
      /strain="ND9022"
      /cultivar="Nipponbare"
      /db_xref="taxon:39947"
      /clone="T11738"
      /clone_lib="PCR product directly amplified from rice
      genomic DNA"
      /note="The 3' end of retrotransposon Tos17 was found
      immediately upstream of this sequence."
ORIGIN
Query Match      51.7%; Score 12.4; DB 9; Length 46;
Best Local Similarity 72.7%; Pred. No. 4.9e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AAGGATCGCTACGGCTCCTGGA 23
      ||||| ||||| ||||| |||||
Db      44 AGGGATTGATGAGGCTCATGGA 23

RESULT 27
AZ820416/c
LOCUS      AZ820416      47 bp      DNA      linear      GSS      20-FEB-2001
DEFINITION      2M092F16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M092F16 R, genomic survey sequence.
ACCESSION      AZ820416
VERSION      AZ820416.1 GI:12990420
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: F column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers
  1..47
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    /db_xref="taxon:10090"
    /clone="UUGC2M092F16"

MEDLINE      22779045
PUBMED      12897251
REFERENCE    2 (bases 1 to 46)
AUTHORS      Miyao,A., Kato,M. and Hirochika,H.
TITLE        Direct Submission
JOURNAL      Submitted (16-APR-2002) Akio Miyao, National Institute of
              Agrobiological Sciences, Molecular Genetics, 2-1-2, Kannondai,
              Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp,
              URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,
              Fax:81-298-38-7020)
FEATURES
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    1..46
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="genomic DNA"
      /strain="ND9022"
      /cultivar="Nipponbare"
      /db_xref="taxon:39947"
      /clone="T11738"
      /clone_lib="PCR product directly amplified from rice
      genomic DNA"
      /note="The 3' end of retrotransposon Tos17 was found
      immediately upstream of this sequence."
ORIGIN
Query Match      51.7%; Score 12.4; DB 9; Length 46;
Best Local Similarity 72.7%; Pred. No. 4.9e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AAGGATCGCTACGGCTCCTGGA 23
      ||||| ||||| ||||| |||||
Db      44 AGGGATTGATGAGGCTCATGGA 23

RESULT 27
AZ820416/c
LOCUS      AZ820416      47 bp      DNA      linear      GSS      20-FEB-2001
DEFINITION      2M092F16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M092F16 R, genomic survey sequence.
ACCESSION      AZ820416
VERSION      AZ820416.1 GI:12990420
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: F column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers
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    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M092F16"

MEDLINE      22779045
PUBMED      12897251
REFERENCE    2 (bases 1 to 46)
AUTHORS      Miyao,A., Kato,M. and Hirochika,H.
TITLE        Direct Submission
JOURNAL      Submitted (16-APR-2002) Akio Miyao, National Institute of
              Agrobiological Sciences, Molecular Genetics, 2-1-2, Kannondai,
              Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp,
              URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,
              Fax:81-298-38-7020)
FEATURES
  Location/Qualifiers
    1..46
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="genomic DNA"
      /strain="ND9022"
      /cultivar="Nipponbare"
      /db_xref="taxon:39947"
      /clone="T11738"
      /clone_lib="PCR product directly amplified from rice
      genomic DNA"
      /note="The 3' end of retrotransposon Tos17 was found
      immediately upstream of this sequence."
ORIGIN
Query Match      51.7%; Score 12.4; DB 9; Length 46;
Best Local Similarity 72.7%; Pred. No. 4.9e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AAGGATCGCTACGGCTCCTGGA 23
      ||||| ||||| ||||| |||||
Db      44 AGGGATTGATGAGGCTCATGGA 23

RESULT 27
AZ820416/c
LOCUS      AZ820416      47 bp      DNA      linear      GSS      20-FEB-2001
DEFINITION      2M092F16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M092F16 R, genomic survey sequence.
ACCESSION      AZ820416
VERSION      AZ820416.1 GI:12990420
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: F column:
```

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pYT3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

```

ORIGIN
Query Match          51.7%; Score 12.4; DB 1; Length 49;
Best Local Similarity 72.7%; Pred. No. 5e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCG 22
    ||||| ||||| |||||
Db 34 CTAGAACCTCGGGCTCCTCG 13

RESULT 29
CF277394          45 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
14ETL--02-O14.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-O14,
mRNA sequence.
ACCESSION
CF277394.1 GI:33654780
VERSION
CF277394
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 45)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
source
1..45
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--02-O14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match          50.8%; Score 12.2; DB 7; Length 45;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCT 20
    ||||| ||||| |||||
Db 8 GGATCGCGCCGGCTCCT 24

RESULT 30
BH907825          48 bp DNA linear GSS 04-SEP-2002
LOCUS
DEFINITION
SALK_044281.17.00.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044281.17.00.n, genomic
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pYT3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
```

```

survey sequence.
BH907825          50 bp mRNA linear EST 28-JAN-2004
VERSION
BH907825.1 GI:22720758
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 48)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g08240.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
source
1..48
/organism="Arabidopsis thaliana"
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/ecotye="Col-0"
/db_xref="taxon:3702"
/clone="SALK_044281.17.00.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          50.8%; Score 12.2; DB 8; Length 48;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTC 18
    ||||| ||||| |||||
Db 21 AAGGATCCTCAGGCTC 37

RESULT 31
AU104805          50 bp mRNA linear EST 28-JAN-2004
LOCUS
DEFINITION
AU104805 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS10961, mRNA sequence.
ACCESSION
AU104805
VERSION
AU104805.1 GI:13554326
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
11375929
Contact: Yutaka Suzuki
```

```

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES             source
    1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone_lib="CASI0961"
    /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          50.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCC 19
Db 33 AGCCTCGCTATGGCTCC 49

RESULT 32
AUI04807
LOCUS             AUI04807 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION       HRC08216, mRNA sequence.
ACCESSION        AUI04807
VERSION          AUI04807
KEYWORDS         EST.
SOURCE           Homo sapiens (human)
ORGANISM         Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE        1 (bases 1 to 50)
AUTHORS          Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
                  Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
                  Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
                  Diverse transcriptional initiation revealed by fine, large-scale
                  mapping of mRNA start sites
                  EMBO Rep. 2 (5), 388-393 (2001)
                  21270072
                  PUBMED
                  Contact: Yutaka Suzuki
                  Department of Virology
                  Institute of Medical Science, University of Tokyo
                  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                  Email: yusuzuki@ims.u-tokyo.ac.jp
                  Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
                  Sugano, S. Construction and characterization of a full
                  length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                  149-156 (1997).

FEATURES             source
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    /mol_type="mRNA"
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    /clone_lib="Sugano Homo sapiens cDNA library"

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Query Match          50.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCC 19
Db 32 AGCCTCGCTATGGCTCC 48

```

```

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES             source
    1..50
    /organism="Homo sapiens"
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    /clone_lib="ZRV6C680"
    /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          50.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTG 21
Db 22 GACAGCTACGGCTCCG 6

RESULT 34
AGI95132
LOCUS             AGI95132 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION       Pan troglodytes DNA, clone: RP43-073N21.T7, genomic survey
sequence.
ACCESSION        AGI95132
VERSION          AGI95132.1 GI:45227308
KEYWORDS         GSS.
SOURCE           Pan troglodytes (chimpanzee)
ORGANISM         Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE        1 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
                  Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
                  BAC end sequences of Library RP-43
                  2 (bases 1 to 30)
                  Unpublished
                  Direct Submission
                  Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
                  Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
                  52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

FEATURES             source
    1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone_lib="HRC08216"
    /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          50.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCC 19
Db 32 AGCCTCGCTATGGCTCC 48

```

(E-mail:redstone@mail.kribb.re.kr, URL:http://pfs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS

Sequencing: T7
LIBRARY

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. .30
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clones="RP43-073N21.T7"
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/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

FEATURES source

ORIGIN

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Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGATCGCTACGGCTCTCTG 21
|||||
Db 4 AGGAATCCCTGCTGCTCTG 23

RESULT 35

AZ492391
LOCUS

DEFINITION AZ492391 38 bp DNA linear GSS 05-OCT-2000
clone UUGC1M0326D04 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
survey sequence.

ACCESSION AZ492391

VERSION AZ492391.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 38)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0326 row: D column: 04

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 38.

Location/Qualifiers

FEATURES source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6j"
/db_xref="taxon:10090"
/clones="UUGC1M0326D04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 50.0%; Score 12; DB 8; Length 38;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCTCTG 22
|||||
Db 3 AGGACACTACTGCCCTGG 22

RESULT 36

BH804014
LOCUS

DEFINITION BH804014 42 bp DNA linear GSS 25-APR-2002
1008097B08.2EL_x2 1008 - RescueMu Grid I Zea mays genomic, genomic
survey sequence.

ACCESSION BH804014

VERSION BH804014.1

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 42)

Walbot, V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1008097 row: 13

Class: transposon-tagged.

Location/Qualifiers

FEATURES source

1. .42
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA."

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmdb.iastate.edu and follow the links for 'RescueMu.' Grid 1 was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BstXI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 50.0%; Score 12; DB 8; Length 42;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCTGG 22
Db 8 AGGTACGTACGGCGCTGG 27

RESULT 37
AA087268
LOCUS
DEFINITION
49 bp mRNA linear EST 23-OCT-1996
mol2g10.r1 Life Tech mouse embryo 10 5dpc 10665016 Mus musculus
CDNA clone IMAGE:553410 5' similar to TR:G285961 G285961 MRNA 1,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
JOURNAL
COMMENT

The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: mousest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:334202

Possible reversed clone: similarity on wrong strand

Seq primer: -28M13 rev1 from Amersham

High quality sequence stop: 1.

FEATURES

Location/Qualifiers
1..49
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:553410"
/tissue_type="embryo"
/dev_stage="10.5dpc embryos"
/lab_host="DH10B"
/clone_lib="Life Tech mouse embryo 10 5dpc 10665016"
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site: 1;
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dt. 10.5dpc embryos. pCMV-SPORT2 vector."

ORIGIN

Query Match 50.0%; Score 12; DB 1; Length 49;
Best Local Similarity 75.0%; Pred. No. 7.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GATCGTACGGCTCTCGGAT 24
Db 21 GACCGGTACGGCTCTCGTT 40

RESULT 38
AU103066
LOCUS

DEFINITION
50 bp mRNA linear EST 28-JAN-2004
AU103066 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC03739, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yzukui@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HRC03739"

/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 50.0%; Score 12; DB 1; Length 50;
Best Local Similarity 75.0%; Pred. No. 7.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCTCGGA 23

Db 12 GGATCGGACGGGAACCTGGA 31

RESULT 39

LOCUS

DEFINITION
50 bp mRNA linear EST 28-JAN-2004
AU104834 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNG00343, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yzukui@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HRC03739"

/clone_lib="Sugano Homo sapiens cDNA library"

Db 3 AGCAGCGCTCCGGGCGCTGG 22

Search completed: November 18, 2005, 21:12:34
Job time : 1150.98 secs

PUBMED
COMMENT

11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezukui@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG00343"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 50.0%; Score 12; DB 1; Length 50;
Best Local Similarity 75.0%; Pred.No. 7.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTGAT 24
||| ||| |
Db 48 GAAGGCTTCAGCACCTGAT 29
|||||||

RESULT_40	AUI06612	50 bp	mrna	linear	EST 28-JAN-2004
LOCUS	AUI06612				
DEFINITION	AUI06612 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC00105, mRNA sequence.				
ACCESSION	AUI06612				
VERSION	AUI06612.1	GI:13556133			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 50)				
AUTHORS	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.				
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites				
JOURNAL	ENBO Rep. 2 (5), 388-393 (2001)				
MEDLINE	21270072				
PUBMED	11375929				

```

13.75523
Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC00105"
/clone_lib="Sugano Homo sapiens cDNA library"

FEATURES
source
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC00105"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 50.0%; Score 12; DB 1; Length 50;
Best Local Similarity 75.0%; Pred No. 7.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCTGG 22
|||||

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 46.6312 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGGATCGTACGGCTCTGGAT 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	1	US-07-989-160-1
2	16.2	67.5	25	4	US-09-396-196G-60856
3	15	62.5	33	2	US-08-377-309-12
4	15	62.5	33	3	US-09-186-723-12
5	15	62.5	33	3	US-08-505-012-17
6	15	62.5	33	3	US-09-186-949A-13
7	15	62.5	33	4	US-08-758-757-12
8	15	62.5	33	4	US-09-187-978-12
9	15	62.5	33	4	US-10-115-701A-12
10	15	62.5	33	4	US-09-940-308A-12
11	15	62.5	33	4	US-09-940-308A-12
12	15	62.5	33	5	PCT-US96-00996-17
13	14.6	60.8	32	4	US-09-152-361A-5
14	14.4	60.0	32	3	US-09-183-412-44
15	14.4	60.0	32	4	US-09-769-864-44
16	14.2	59.2	25	4	US-09-396-196G-70013
17	14.2	59.2	25	4	US-09-396-196G-70024
18	14	58.3	25	4	US-09-396-196G-4290
19	13.8	57.5	36	3	US-08-379-802-11
20	13.8	57.5	36	3	US-09-048-129-11
21	13.8	57.5	36	3	US-09-048-079-11
22	13.6	56.7	21	4	US-09-526-193A-233
23	13.6	56.7	25	4	US-09-396-196G-108958
24	13.6	56.7	25	4	US-08-396-196G-108959
25	13.6	56.7	40	3	US-08-827-336-3
26	13.6	56.7	40	3	US-09-357-905-3
27	13.6	56.7	49	2	US-08-960-756-17

28	13.4	55.8	24	3	US-08-506-296B-8	Sequence 8, Appl
29	13.4	55.8	30	2	US-08-465-095-11	Sequence 11, Appl
30	13.4	55.8	30	4	US-08-179-656A-11	Sequence 11, Appl
31	13.4	55.8	30	5	PCT-US94-00300-11	Sequence 11, Appl
32	13.2	55.0	19	4	US-09-696-791-1126	Sequence 1126, Ap
33	13.2	55.0	25	4	US-09-396-196G-126395	Sequence 126395,
34	13.2	55.0	27	3	US-09-347-878-72	Sequence 72, Appl
35	13.2	55.0	27	4	US-09-546-013-91	Sequence 91, Appl
36	13.2	55.0	31	3	US-09-134-078-38	Sequence 38, Appl
37	13	54.2	18	3	US-08-211-882-15	Sequence 15, Appl
38	13	54.2	18	3	US-09-633-659-15	Sequence 15, Appl
39	13	54.2	18	4	US-10-073-718-15	Sequence 15, Appl
40	13	54.2	25	4	US-09-396-196G-22766	Sequence 22766, A
41	13	54.2	25	4	US-09-396-196G-41969	Sequence 41969, A
42	13	54.2	25	4	US-09-396-196G-62126	Sequence 62126, A
43	13	54.2	27	4	US-09-768-319-1	Sequence 1, Appl
44	13	54.2	30	3	US-09-067-091-4	Sequence 4, Appl
45	13	54.2	30	3	US-09-230-222-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-07-989-160-1
; Sequence 1, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-07-989-160-1

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAGGATCGTACGGCTCTGGAT 24
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```
RESULT 6
US-09-186-949A-13
; Sequence 13, Application US/09186949A
; Patent No. 6416734
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Alpha-Fetoprotein For
; TITLE OF INVENTION: Treating and Diagnosing Cancers
; FILE REFERENCE: 06727/004002
; CURRENT APPLICATION NUMBER: US/09/186,949A
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/758,757
; PRIOR FILING DATE: 1996-12-03
; PRIOR APPLICATION NUMBER: US 08/377,311
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Based on Homo sapiens
US-09-186-949A-13

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
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Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 7
US-08-758-757-12
; Sequence 12, Application US/08758757
; Patent No. 6534479
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: RECOMBINANT ALPHA-FETOPROTEIN FOR
; TITLE OF INVENTION: TREATING AND DIAGNOSIS
; FILE REFERENCE: 06727/004001
; CURRENT APPLICATION NUMBER: US/08/758,757
; CURRENT FILING DATE: 1996-12-03
; EARLIER APPLICATION NUMBER: 08/377,311
; EARLIER FILING DATE: 1995-01-24
; EARLIER APPLICATION NUMBER: 08/758,757
; EARLIER FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-758-757-12

Query Match      62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
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Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 8
US-09-187-978-12
; Sequence 12, Application US/09187978A
; Patent No. 6627440
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
```

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; TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS A
; TITLE OF INVENTION: CELL PROLIFERATIVE AGENT
; FILE REFERENCE: 06727/006002
; CURRENT APPLICATION NUMBER: US/09/187,978A
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: 08/377,316
; EARLIER FILING DATE: 1995-01-24
; EARLIER APPLICATION NUMBER: 08/879,469
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-187-978-12

Query Match      62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
   ||||| || |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 9
US-10-115-701A-12
; Sequence 12, Application US/10115701A
; Patent No. 6630445
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Alpha-Fetoprotein for
; TITLE OF INVENTION: Treating and Diagnosing Cancers
; FILE REFERENCE: 06727/004003
; CURRENT APPLICATION NUMBER: US/10/115,701A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/758,757
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 08/758,757
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 08/758,757
; PRIOR FILING DATE: 1996-12-03
; PRIOR APPLICATION NUMBER: 08/377,311
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-115-701A-12

Query Match      62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
   ||||| || |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 10
US-09-940-308A-12
; Sequence 12, Application US/09940308A
; Patent No. 6656909
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; TITLE OF INVENTION: an Immunosuppressive Agent
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308A
; CURRENT FILING DATE: 2001-08-27
```

; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-940-308A-12

Query Match 62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||||| || |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 11

US-09-940-308A-12
; Sequence 12, Application US/09940308A
; Patent No. 6774108
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-940-308A-12

Query Match 62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||||| || |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 12

PCT-US96-00996-17
; Sequence 17, Application PC/TUS9600996
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF CLONED
; TITLE OF INVENTION: HUMAN ALPHA-FETOPROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00996
; FILING DATE: 24-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,317
; FILING DATE: 24-JAN-1995
; CLASSIFICATION:
; APPLICATION NUMBER: 08/377,311
; FILING DATE: 24-JAN-1995
; CLASSIFICATION:
; APPLICATION NUMBER: 08/377,309
; FILING DATE: 24-JAN-1995
; CLASSIFICATION:
; APPLICATION NUMBER: 08/377,316
; FILING DATE: 24-JAN-1995
; CLASSIFICATION:
; APPLICATION NUMBER: 08/505,012
; FILING DATE: 21-JULY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06727/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-8906
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-00996-17

Query Match 62.5%; Score 15; DB 5; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||||| || |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 13

US-09-152-361A-5
; Sequence 5, Application US/09152361A
; Patent No. 6656735
; GENERAL INFORMATION:
; APPLICANT: Wurst, Wolfgang
; APPLICANT: Prochaintz, Alain
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; APPLICANT: Centre National de la Recherche Scientifique
; TITLE OF INVENTION: Method for Identification of Target Genes of
; FILE REFERENCE: 080314-000000US
; CURRENT APPLICATION NUMBER: US/09/152,361A
; CURRENT FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: DE 197 40 578.9
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer for
; OTHER INFORMATION: Isolation of 60 amino acid homodomain of chicken
; OTHER INFORMATION: Engrailed 2 (EnHD) protein from plasmid containing
; OTHER INFORMATION: chicken cDNA sequence

US-09-152-361A-5

Query Match 60.8%; Score 14.6; DB 4; Length 32;
Best Local Similarity 81.0%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCTCTGGAT 24
||| ||||| ||||| |||||
Db 4 GGATCCCTACGGCTTCTTGGAT 24

RESULT 14

US-09-183-412-44/c
; Sequence 44, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-183-412-44

Query Match 60.0%; Score 14.4; DB 3; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGAT 24
||| ||||| ||||| |||||
Db 31 CATTGATCGTAACGGGTCCTGGTT 8

RESULT 15

US-09-769-864-44/c
; Sequence 44, Application US/09769864
; Patent No. 6673589
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44

; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-769-864-44

Query Match 60.0%; Score 14.4; DB 4; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGAT 24
||| ||||| ||||| |||||
Db 31 CATTGATCGTAACGGGTCCTGGTT 8

RESULT 16

US-09-396-196G-70013
; Sequence 70013, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70013
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-70013

Query Match 59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCTCTGGA 23
||| ||||| ||||| |||||
Db 6 GATCGGACTGCTCGGGA 24

RESULT 17

US-09-396-196G-70024
; Sequence 70024, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70024
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-70024

Query Match 59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCTCGGA 23
|||||
Db 4 GATCGGACTGCTCCGGGA 22

RESULT 18

US-09-396-196G-4290/c
; Sequence 4290, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4290

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-4290

Query Match 58.3%; Score 14; DB 4; Length 25;

Best Local Similarity 77.3%; Pred. No. 1.9e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCGG 22

|||||

Db 22 CTAGGATCTCGGAGCCTGG 1

RESULT 19

US-08-379-802-11

; Sequence 11, Application US/08379802

; Patent No. 6057124

GENERAL INFORMATION:

; APPLICANT: Bartley, Timothy D.

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Ligands for EPH-Like Receptor

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/08/379,802

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-325

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-379-802-11

Query Match 57.5%; Score 13.8; DB 3; Length 36;

Best Local Similarity 88.2%; Pred. No. 2.6e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTC 18

|||||

Db 5 AAGGATCCCTATGGCTC 21

RESULT 20

US-09-048-129-11

; Sequence 11, Application US/09048129

; Patent No. 6063903

GENERAL INFORMATION:

; APPLICANT: Bartley, Timothy D.

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Ligands for EPH-Like Receptor

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/048,129

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/379,802

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-325

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-048-129-11

Query Match 57.5%; Score 13.8; DB 3; Length 36;

Best Local Similarity 88.2%; Pred. No. 2.6e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTC 18

|||||

Db 5 AAGGATCCCTATGGCTC 21

RESULT 21

US-09-048-079-11

; Sequence 11, Application US/09048079

; Patent No. 6169167

GENERAL INFORMATION:

; APPLICANT: Bartley, Timothy D.

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Ligands for EPH-Like Receptor

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,079
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/379,802
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-325
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-048-079-11

Query Match 57.5%; Score 13.8; DB 3; Length 36;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTC 18
Db 5 AAGGATCGCTACGGCTC 21

RESULT 22
US-09-526-193A-233/c
; Sequence 233, Application US/09526193A
; Patent No. 6617122
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Pimstone, Simon N.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: CHOLESTEROL LEVELS
; FILE REFERENCE: 50110/002005
; CURRENT APPLICATION NUMBER: US/09/526,193A
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-193A-233

Query Match 56.7%; Score 13.6; DB 4; Length 21;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCT 20
Db 20 CAATGAGCGCTTGGCTCCT 1

RESULT 23
US-09-396-196G-108958
; Sequence 108958, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108958
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-108958

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTGGA 23
Db 4 GAATCGCTACGGTCCAGGA 23

RESULT 24
US-09-396-196G-108959
; Sequence 108959, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-108959

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTGGA 23
Db 1 GAATCGCTACGGTCCAGGA 20

RESULT 25
US-08-827-336-3/c
; Sequence 3, Application US/08827336
; Patent No. 6004780
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL
; TITLE OF INVENTION: GROWTH FACTOR HTTR36

;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
;; STREET: 9410 KEY WEST AVENUE
;; CITY: ROCKVILLE
;; STATE: MARYLAND
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/827,336
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROOKES, ANDY, A.
;; REGISTRATION NUMBER: 36,373
;; REFERENCE/DOCKET NUMBER: PF230
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-309-8504
;; TELEFAX: 301-309-8512
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 40 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-827-336-3

Query Match 56.7%; Score 13.6; DB 3; Length 40;
Best Local Similarity 80.0%; Pred.No.3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCT 20
Db 23 CAGGGATGGCTGCGGATCCT 4

RESULT 26
US-09-357-905-3/c
; Sequence 3, Application US/09357905
; Patent No. 6413933
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL
; TITLE OF INVENTION: GROWTH FACTOR HTTR36
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/357,905
; FILING DATE: 21-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/827,336
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDY, A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF230

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-309-8504
;; TELEFAX: 301-309-8512
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 40 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-357-905-3

Query Match 56.7%; Score 13.6; DB 3; Length 40;
Best Local Similarity 80.0%; Pred.No.3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCT 20
Db 23 CAGGGATGGCTGCGGATCCT 4

RESULT 27
US-08-960-756-17/c
; Sequence 17, Application US/08960756
; Patent No. 5866422
; GENERAL INFORMATION:
; APPLICANT: WAYNE, JAY
; APPLICANT: XU, SHUANG-YONG
; TITLE OF INVENTION: METHOD FOR CLONING AND
; TITLE OF INVENTION: PRODUCING THE Tsp45I RESTRICTION ENDONUCLEASE IN E. COLI
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: New England Biolabs, Inc.
; STREET: 32 Tozer Road
; CITY: Beverly
; STATE: MA
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,756
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 978-927-5054
; TELEFAX: 978-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA
US-08-960-756-17

Query Match 56.7%; Score 13.6; DB 2; Length 49;
Best Local Similarity 80.0%; Pred.No.3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCT 20

Db 45 CCAGGCTAGCTACGGCTCAT 26
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RESULT 28
US-08-506-296B-8
; Sequence 8, Application US/08506296B
; Patent No. 6313265

; GENERAL INFORMATION:
; APPLICANT: Phillips, Greg
; APPLICANT: Cunningham, Bruce A.
; APPLICANT: Crossin, Kathryn L.
; TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
; TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: U.S.
; ZIP: 92037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/506,296B
; FILING DATE: 24-JUL-1995
; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 488.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-506-296B-8

Query Match 55.8%; Score 13.4; DB 3; Length 24;
Best Local Similarity 73.9%; Pred. No. 3.8e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTGGAT 24
|||||

Db 2 AAGGATCGCTACCGCCCTTGT 24
|||||

RESULT 29
US-08-465-095-11
; Sequence 11, Application US/08465095
; Patent No. 5849534

; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Iida, Naoka
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,095
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,656
; FILING DATE: 07-JAN-1994
; APPLICATION NUMBER: 08/001,177
; FILING DATE: 07-JAN-1993
; APPLICATION NUMBER: 07/472,377
; FILING DATE: 01-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GZI-003C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-465-095-11

Query Match 55.8%; Score 13.4; DB 2; Length 30;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCGGA 23
|||||

Db 4 CGACGTGGCGACGACTCTCGGA 26
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RESULT 30
US-08-179-656A-11
; Sequence 11, Application US/08179656A
; Patent No. 6673893
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Iida, Naoka
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,656A
; FILING DATE: 07-JAN-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/001,177
; FILING DATE: 07-JAN-1993
; APPLICATION NUMBER: 07/472,377
; FILING DATE: 01-FEB-1990
; ATTORNEY/AGENT INFORMATION:

Query Match 55.8%; Score 13.4; DB 5; Length 30;
Best Local Similarity 73.9%; Pred. NO. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels

GENERAL INFORMATION:

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; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
; OTHER INFORMATION: of Human SAH hydrolase (mutant R431A)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (13)..(15)
; OTHER INFORMATION: Codon change from CGC to GCC
US-09-347-878-72

Query Match 55.0%; Score 13.2; DB 3; Length 27;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTG 21
Db 3 GGATCACTACGCCTACTG 20

RESULT 35
US-09-546-013-91
; Sequence 91, Application US/09546013
; Patent No. 6610504
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong-Shen
; TITLE OF INVENTION: METHODS FOR ASSAYING S-ADENOSYLMETHIONINE-DEPENDENT Methyltransfe
; FILE REFERENCE: 10937-1652
; CURRENT APPLICATION NUMBER: US/09/546,013
; CURRENT FILING DATE: 2000-04-10
; EARLIER APPLICATION NUMBER: 09/347,878
; EARLIER FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 09/457,205
; EARLIER FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
; OTHER INFORMATION: of Human SAH hydrolase (mutant R431A)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (13)..(15)
; OTHER INFORMATION: Codon change from CGC to GCC
US-09-546-013-91

Query Match 55.0%; Score 13.2; DB 4; Length 27;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTG 21
Db 3 GGATCACTACGCCTACTG 20

RESULT 36
US-09-134-078-38
; Sequence 38, Application US/09134078
; Patent No. 6368844
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; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lies A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-134-078-38

Query Match 55.0%; Score 13.2; DB 3; Length 31;
Best Local Similarity 83.3%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCT 20
Db 4 AGGATCGCTACCGCTCCT 21

RESULT 37
US-08-211-882-15/c
; Sequence 15, Application US/08211882
; Patent No. 6153737
; GENERAL INFORMATION:
; APPLICANT: Manoharan et al.
; TITLE OF INVENTION: Derivatized Oligonucleotides Having
; TITLE OF INVENTION: Improved Uptake And Other Properties
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6153737ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,882
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; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/782,374
; FILING DATE: 24-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0649
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-211-882-15

Query Match 54.2%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTACGGCTCC 19
Db 15 TCGCTACGGCTCC 3

RESULT 38
US-09-633-659-15/c
; Sequence 15, Application US/09633659
; Patent No. 6395492
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Bennett, Clarence Frank
; TITLE OF INVENTION: Derivatized Oligonucleotides Having Improved Uptake And
; TITLE OF INVENTION: Other Properties
; FILE REFERENCE: ISIS4470
; CURRENT APPLICATION NUMBER: US/09/633,659
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 08/211,882
; PRIOR FILING DATE: 1994-04-22
; PRIOR APPLICATION NUMBER: 07/782,374
; PRIOR FILING DATE: 1991-10-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6395492el Sequence
US-09-633-659-15

Query Match 54.2%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTACGGCTCC 19
Db 15 TCGCTACGGCTCC 3

RESULT 39
US-10-073-718-15/c
; Sequence 15, Application US/10073718
; Patent No. 6831166
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Bennett, Clarence Frank
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; TITLE OF INVENTION: Derivatized Oligonucleotides Having Improved Uptake and Other Pro
; FILE REFERENCE: ISIS-5024
; CURRENT APPLICATION NUMBER: US/10/073,718
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 09/633659
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 6153737
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/211882
; PRIOR FILING DATE: 1994-04-22
; PRIOR APPLICATION NUMBER: PCT/US92/09196
; PRIOR FILING DATE: 1992-10-23
; PRIOR APPLICATION NUMBER: 07/782374
; PRIOR FILING DATE: 1991-10-24
; PRIOR APPLICATION NUMBER: 07/566977
; PRIOR FILING DATE: 1990-08-13
; PRIOR APPLICATION NUMBER: PCT/US91/000243
; PRIOR FILING DATE: 1991-01-11
; PRIOR APPLICATION NUMBER: 08/463359
; PRIOR FILING DATE: 1990-01-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6831166el Sequence
US-10-073-718-15

Query Match 54.2%; Score 13; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTACGGCTCC 19
Db 15 TCGCTACGGCTCC 3

RESULT 40
US-09-396-196G-22766/c
; Sequence 22766, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22766
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; OTHER INFORMATION: No. 6821724el Sequence
US-09-396-196G-22766

Query Match 54.2%; Score 13; DB 4; Length 25;
Best Local Similarity 76.2%; Pred. No. 5.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTG 21
Db 21 CACGGGTGGCTATAGTCTCTG 1

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGATCGTACGCTCTCGAT 24

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Searched: 9794790 seqs, 4134909567 residues

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Listing first 45 summaries

Database : Published Applications NA:**

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28:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	US-08-469-172-1	Sequence 1, Appli
2	24	100.0	24	US-10-788-779-1	Sequence 1, Appli
3	16.2	67.5	25	US-10-809-189-60856	Sequence 60856, A
4	16.2	67.5	26	US-10-938-249-375	Sequence 375, App
5	16.2	67.5	26	US-11-131-054-362	Sequence 362, App

6	16.2	67.5	26	26	US-11-131-042-362	Sequence 362, App
7	15.8	65.8	25	26	US-11-036-317-219546	Sequence 219546,
8	15.2	63.3	24	20	US-10-484-989-79	Sequence 79, Appl
9	15.2	63.3	25	16	US-10-098-263B-105576	Sequence 105576,
10	15.2	63.3	25	16	US-10-098-263B-106202	Sequence 106202,
11	15.2	63.3	25	22	US-10-719-900-572806	Sequence 572806,
12	15.2	63.3	25	24	US-10-719-956-368379	Sequence 368379,
13	15	62.5	25	24	US-10-719-956-44525	Sequence 44525, A
14	15	62.5	25	24	US-10-719-956-44526	Sequence 44526, A
15	15	62.5	25	26	US-11-036-317-783296	Sequence 783296,
16	15	62.5	25	26	US-11-036-317-869432	Sequence 869432,
17	15	62.5	33	9	US-09-940-308-12	Sequence 12, Appl
18	15	62.5	33	12	US-09-940-308-12	Sequence 12, Appl
19	15	62.5	33	14	US-10-115-701A-12	Sequence 12, Appl
20	15	62.5	33	22	US-10-838-476-12	Sequence 156635,
21	14.8	61.7	25	26	US-11-036-317-166635	Sequence 1340, Ap
22	14.6	60.8	24	10	US-09-940-185-1340	Sequence 106263,
23	14.6	60.8	25	16	US-10-098-263B-106263	Sequence 72142, A
24	14.6	60.8	25	26	US-11-036-317-72142	Sequence 421165,
25	14.6	60.8	25	26	US-11-036-317-421165	Sequence 936457,
26	14.6	60.8	25	26	US-11-036-317-936457	Sequence 238398,
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28	14.4	60.0	25	22	US-10-719-900-298476	Sequence 177036,
29	14.4	60.0	25	22	US-10-956-157-177036	Sequence 5195, Ap
30	14.4	60.0	25	22	US-09-877-478-5195	Sequence 5195, Ap
31	14.4	60.0	31	10	US-10-342-902-5195	Sequence 10086, A
32	14.4	60.0	31	19	US-10-669-841-10086	Sequence 44, Appl
33	14.4	60.0	31	20	US-09-769-864-44	Sequence 44, Appl
34	14.4	60.0	32	9	US-10-665-667-44	Sequence 44, Appl
35	14.4	60.0	32	19	US-10-980-923-44	Sequence 28357, A
36	14.4	60.0	32	22	US-10-098-263B-28357	Sequence 70013, A
37	14.2	59.2	25	16	US-10-809-189-70013	Sequence 70024, A
38	14.2	59.2	25	22	US-10-809-189-70024	Sequence 168189,
39	14.2	59.2	25	22	US-10-956-157-168189	Sequence 230829,
40	14.2	59.2	25	22	US-10-719-956-260417	Sequence 260417,
41	14.2	59.2	25	24	US-10-719-956-260417	Sequence 488626,
42	14.2	59.2	25	24	US-10-719-956-488626	Sequence 276920,
43	14.2	59.2	25	24	US-11-036-317-276920	Sequence 334044,
44	14.2	59.2	25	26	US-11-036-317-334044	
45	14.2	59.2	25	26	US-11-036-317-334044	

ALIGNMENTS

RESULT 1
US-08-469-172-1
; Sequence 1, Application US/08469172
; Publication No. US2003005433A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-469-172-1

Query Match 100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGATCGTACGGCTCCTGGAT 24
   |||||
Db 1 CAAGATCGTACGGCTCCTGGAT 24

RESULT 2
US-10-788-779-1
; Sequence 1, Application US/10788779
; Publication No. US2004015121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-788-779-1

Query Match 100.0%; Score 24; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGATCGTACGGCTCCTGGAT 24
   |||||
Db 1 CAAGATCGTACGGCTCCTGGAT 24

RESULT 3
US-10-809-189-60856
; Sequence 60856, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60856
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-60856

Query Match 67.5%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGATCGTACGGCTCCTGGAT 24
   |||||
Db 1 GCATGGCTATGGCTCCTGGAT 21

RESULT 4
US-10-938-249-375
; Sequence 375, Application US/10938249
; Publication No. US20050037969A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; Cells
; FILE REFERENCE: 020054-001130US
; CURRENT APPLICATION NUMBER: US/10/938,249
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/724,553
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
```

```
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 543
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: forward primer 158KIF
US-10-938-249-375
```

```
Query Match          67.5%; Score 16.2; DB 22; Length 26;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 AAGGATCGCTACGGCTCTCGG 22
    ||||| || ||||| ||
Db 2 AAGGATCCCTCCGGCTCTCG 22
```

```
RESULT 5
US-11-131-054-362
; Sequence 362, Application US/11131054
; Publication No. US20050214869A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 020054-001110US
; CURRENT APPLICATION NUMBER: US/11/131,054
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: US/09/688,017
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 362
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 158KIF forward primer
US-11-131-054-362
```

```
Query Match          67.5%; Score 16.2; DB 26; Length 26;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 AAGGATCGCTACGGCTCTCGG 22
    ||||| || ||||| ||
Db 2 AAGGATCCCTCCGGCTCTCG 22
```

```
RESULT 6
US-11-131-042-362
; Sequence 362, Application US/11131042
; Publication No. US20050221388A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 020054-001110US
; CURRENT APPLICATION NUMBER: US/11/131,042
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: US/09/688,017
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 362
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 158KIF forward primer
US-11-131-042-362
```

```
Query Match          67.5%; Score 16.2; DB 26; Length 26;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 AAGGATCGCTACGGCTCTCGG 22
    ||||| || ||||| ||
Db 2 AAGGATCCCTCCGGCTCTCG 22
```

```
RESULT 7
US-11-036-317-219546
; Sequence 219546, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
```

```
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-219546

Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGATCGCTACGGCTCC 19
DB 1 CAAGGACCGCTACAGCTCC 19

RESULT 8
US-10-484-989-79
; Sequence 79, Application US/10484989
; Publication No. US20040171154A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Storici, Francesca
; APPLICANT: Resnick, Michael A.
; APPLICANT: Lewis, Lysle Kevin
; TITLE OF INVENTION: SYSTEMS FOR IN VIVO SITE-DIRECTED MUTAGENESIS USING
; FILE REFERENCE: 4239-67608
; CURRENT APPLICATION NUMBER: US/10/484,989
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/308,426
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/23634
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-484-989-79

Query Match      63.3%; Score 15.2; DB 20; Length 24;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGGATCGCTACGGCTCTGG 22
DB 3 AGGATCGCGCGGCTCCGG 22

RESULT 9
US-10-098-263B-105576/c
; Sequence 105576, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105576
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105576

Query Match      63.3%; Score 15.2; DB 16; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GATCGCTACGGCTCTGGAT 24
DB 25 GGTCCTACGGGTCCTGGAT 6

RESULT 10
US-10-098-263B-106202/c
; Sequence 106202, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-106202

Query Match      63.3%; Score 15.2; DB 16; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GATCGCTACGGCTCTGGAT 24
DB 25 GGTCCTACGGGTCCTGGAT 6

RESULT 11
US-10-719-900-572806
; Sequence 572806, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 572806
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-572806

Query Match      63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GGATCGCTACGGCTCTGGA 23
DB 5 GGACCGCTACGGCCCCAGGA 24
```

```
RESULT 12
US-10-719-956-368379
; Sequence 368379, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 368379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-368379

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5 GATCGTACGGCTCTCGGAT 24
      ||| |||| |||| |||| ||||
Db      1 GATGGTACCGCTTCTGGAT 20

RESULT 13
US-10-719-956-44525
; Sequence 44525, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-44525

Query Match      62.5%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGTACGGCTCTCGGAT 24
      ||| |||| |||| |||| ||||
Db      1 AAGGACCGCTACATCTCCAAGAT 23

RESULT 14
US-10-719-956-44526
; Sequence 44526, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-44526

Query Match      62.5%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGTACGGCTCTCGGAT 24
      ||| |||| |||| |||| ||||
Db      1 AAGGACCGCTACATCTCCAAGAT 23

RESULT 15
US-11-036-317-783296/c
; Sequence 783296, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 783296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-783296

Query Match      62.5%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CAAGATCGTACGGCTCTCGGA 23
      ||| |||| |||| |||| ||||
Db      23 CAAGACCTCTCCGGCTCCTAGA 1

RESULT 16
US-11-036-317-869432
; Sequence 869432, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 869432
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-869432

Query Match      62.5%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGTACGGCTCTCGGAT 24
      ||| |||| |||| |||| ||||
Db      3 AAGGCAAGCTTCGGCTCTCGCT 25
```



```
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 166635
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-166635
```

```
Query Match      61.7%; Score 14.8; DB 26; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 AAGGATCGCTACGGCTCC 19
    ||||| ||||| ||||| |||||
DB 1 AAGGACCGCTACAGTCC 18
```

```
RESULT 22
US-09-940-185-1340
; Sequence 1340, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69603-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1340
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-1340
```

```
Query Match      60.8%; Score 14.6; DB 10; Length 24;
Best Local Similarity 81.0%; Pred. No. 7.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 4 GGATCGCTACGGCTCTGTGAT 24
    ||||| ||||| ||||| |||||
DB 2 GGTTCGCTACGGCGGCTGTT 22
```

```
RESULT 23
US-10-098-263B-106263
; Sequence 106263, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106263
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-106263
```

```
Query Match      60.8%; Score 14.6; DB 16; Length 25;
Best Local Similarity 81.0%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 AAGGATCGCTACGGCTCTCTGG 22
    ||||| ||||| ||||| |||||
DB 5 AACGATCTCTAAGGCTCCAGG 25
```

```
RESULT 24
US-11-036-317-72142
; Sequence 72142, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 72142
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-72142
```

```
Query Match      60.8%; Score 14.6; DB 26; Length 25;
Best Local Similarity 81.0%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 AAGGATCGCTACGGCTCTCTGG 22
    ||||| ||||| ||||| |||||
DB 4 AAGGATCCCTCAGGCTCTCTGG 24
```

```
RESULT 25
US-11-036-317-421165
; Sequence 421165, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 421165
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-421165
```

```
Query Match      60.8%; Score 14.6; DB 26; Length 25;
Best Local Similarity 81.0%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 CAAGGATCGCTACGGCTCTCTG 21
    ||||| ||||| ||||| |||||
DB 2 CATGGAACGGACGGCTCCAG 22
```

```
RESULT 26
US-11-036-317-936457
; Sequence 936457, Application US/11036317
```

```
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 936457
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-936457

Query Match      60.8%; Score 14.6; DB 26; Length 25;
Best Local Similarity 81.0%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAGGATCGCTACGGCTCTCTGG 22
    ||||| ||||| ||||| |||||
Db  5 AAGGCAAGCTTCGGCTCTCTGG 25

RESULT 27
US-10-719-900-298398
; Sequence 298398, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 298398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-298398

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  1 CAAGGAGCTCTTCGGCTCTGGAT 24

RESULT 28
US-10-719-900-298476
; Sequence 298476, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 298476
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-298476

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  1 CAAGGAGCTCTTCGGCTCTGGAT 24
```

```
; ORGANISM: Mus musculus
US-10-719-900-298476

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  1 CAAGGATGGCGACGTTTACTGCGAT 24

RESULT 29
US-10-719-900-564538
; Sequence 564538, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 564538
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-564538

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  2 CTATGATGGCTACCGCATCTGGAT 25

RESULT 30
US-10-956-157-177036
; Sequence 177036, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 177036
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-177036

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  1 CAGTGATCGCTACTGCAACTTGAT 24

RESULT 31
US-09-877-478-5195
; Sequence 5195, Application US/09877478
```


Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5195
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-877-478-5195

Query Match 60.0%; Score 14.4; DB 10; Length 31;
Best Local Similarity 75.0%; Pred. No. 9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGCTCTCGAT 24
||||| ||||| ||||| |||||
Db 6 CAAGGCTAGCTACAACGACTGGAT 29

RESULT 32
US-10-342-902-5195
Sequence 5195, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MEH00-845-I)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430

PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5195
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-342-902-5195

Query Match 60.0%; Score 14.4; DB 19; Length 31;
Best Local Similarity 75.0%; Pred. No. 9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGCTCTCGAT 24
||||| ||||| ||||| |||||
Db 6 CAAGGCTAGCTACAACGACTGGAT 29

RESULT 33
US-10-669-841-10086
Sequence 10086, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: James, McSwiggen
APPLICANT: David, Morrissey
APPLICANT: Pamela, Pavco
APPLICANT: Patrice, Lee
APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
FILE REFERENCE: 400/042US (MBH02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR FILING DATE: 2000-02-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10086
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-669-841-10086

Query Match 60.0%; Score 14.4; DB 20; Length 31;
Best Local Similarity 75.0%; Pred. No. 9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| |||||
Db 6 CAAGGATAGCTACAACGACTGGAT 29
    ||||| ||||| ||||| |||||

RESULT 34
US-09-769-864-44/c
; Sequence 44, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-769-864-44

Query Match 60.0%; Score 14.4; DB 9; Length 32;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| |||||
Db 31 CATTGATCGTAACGGGCTCTGGTT 8
    ||||| ||||| ||||| |||||

RESULT 35
US-10-665-667-44/c
; Sequence 44, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-665-667-44

Query Match 60.0%; Score 14.4; DB 19; Length 32;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| |||||
Db 31 CATTGATCGTAACGGGCTCTGGTT 8
    ||||| ||||| ||||| |||||

RESULT 36
US-10-980-923-44/c
; Sequence 44, Application US/10980923
; Publication No. US20050084937A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/980,923
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/10/665,667
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-980-923-44

Query Match 60.0%; Score 14.4; DB 22; Length 32;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| |||||
Db 31 CATTGATCGTAACGGGCTCTGGTT 8
    ||||| ||||| ||||| |||||

RESULT 37
US-10-098-263B-28357
; Sequence 28357, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 28357
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-28357

Query Match 59.2%; Score 14.2; DB 16; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTGGA 23
    ||||| ||||| ||||| |||||
```

Db 1 GATCTTAAGGCTCCAGGA 19

RESULT 38

US-10-809-189-70013
; Sequence 70013, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70013
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-70013

Query Match 59.2%; Score 14.2; DB 22; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGTACGGCTCCTCGGA 23
|||||
Db 6 GATCGGACTGCTCCGGGA 24

RESULT 39

US-10-809-189-70024
; Sequence 70024, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70024
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-70024

Query Match 59.2%; Score 14.2; DB 22; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGTACGGCTCCTCGGA 23
|||||
Db 4 GATCGGACTGCTCCGGGA 22

RESULT 40

US-10-956-157-168189/c

; Sequence 168189, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 168189
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-168189

Query Match 59.2%; Score 14.2; DB 22; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGATCCCTACGGCTCCT 20
|||||
Db 21 AAGGATCCCTAGGGCTACT 3

Search completed: November 18, 2005, 15:41:02
Job time : 324.586 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 832.357 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-2
Perfect score: 30
Sequence: 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	6	I12895 Sequence 2
C 2	16.6	55.3	34	6	E59888 Method for
C 3	15.6	52.0	23	6	AX59517 Sequence
4	15.6	52.0	41	6	AR359198 Sequence
C 5	15.6	52.0	45	6	E31326 Process for
C 6	15.6	52.0	45	6	AR301265 Sequence
7	15.6	52.0	50	6	E31327 Process for
8	15.6	52.0	50	6	AR301266 Sequence
9	15.4	51.3	29	6	BD222501 Novel met
10	15.4	51.3	29	6	AX647902 Sequence
C 11	15.4	51.3	30	6	BD103433 A carcino
12	15.4	51.3	33	6	AX453416 Sequence
13	15.2	50.7	42	6	E51173 Method for
14	15.2	50.7	42	6	E51191 Process for
15	15.2	50.7	42	6	AR399392 Sequence
16	15.2	50.7	42	6	AX137508 Sequence
17	15	50.0	29	6	BD240955 A novel h
18	15	50.0	29	6	AR437642 Sequence
19	14.8	49.3	25	6	AR173178 Sequence

20	14.8	49.3	37	6	AR183091	Sequence
21	14.6	48.7	24	6	AX956456	Sequence
22	14.6	48.7	31	6	AR137780	Sequence
23	14.6	48.7	31	6	BD192813	Improved
24	14.6	48.7	44	6	AX955017	Sequence
25	14.4	48.0	27	6	AX033626	Sequence
26	14.4	48.0	31	6	AR071455	Sequence
27	14.4	48.0	33	6	AR071444	Sequence
28	14.4	48.0	40	6	AR152460	Sequence
29	14.4	48.0	40	6	AX456419	Sequence
C 30	14.4	48.0	44	6	AR143578	Sequence
C 31	14.4	48.0	44	6	AR168947	Sequence
C 32	14.4	48.0	44	6	AR232695	Sequence
C 33	14.4	48.0	44	6	AR262637	Sequence
C 34	14.4	48.0	44	6	AR316574	Sequence
C 35	14.4	48.0	45	6	BD188256	bHLH-PAS
C 36	14.4	48.0	45	6	AX456402	Sequence
37	14.2	47.3	20	6	AX477123	Sequence
38	14.2	47.3	20	6	AX526499	Sequence
39	14.2	47.3	28	6	CQ878078	Sequence
40	14.2	47.3	28	6	AR184482	Sequence
41	14.2	47.3	30	6	I36158	Sequence 42
42	14.2	47.3	31	6	CQ855152	Sequence
43	14.2	47.3	34	6	E10783	PCR primer
44	14.2	47.3	39	6	AR121200	Sequence
45	14.2	47.3	39	6	AR160328	Sequence

ALIGNMENTS

RESULT 1
LOCUS I12895 I12895 30 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 2 from patent US 5429923.
ACCESSION I12895
VERSION I12895.1 GI:910872
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 2 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30
|||||
Db 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30

RESULT 2
LOCUS E59888/c E59888 34 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for detecting micromutated DNA.
ACCESSION E59888
VERSION E59888.1 GI:18622724
KEYWORDS JP 2000308489-A/4.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
REFERENCE 1 (bases 1 to 34)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

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AUTHORS      Yokota, H. and Goto, K.
TITLE        Method for detecting micromutated DNA
JOURNAL      DAI ICHI SEIYAKU CO LTD
COMMENT      OS Pseudomonas aeruginosa
              PD 07-NOV-2000
              PF 28-APR-1999 JP 1999121957
              PI HIROSHI YOKOTA, KOSHICHI GOTO
              PC
C12N15/09, C12Q1/68// (C12N15/09, C12R1:385), (C12Q1/68, C12R1:385), PC
C12N15/00, C12N15/00, C12R1:385)
PC          (C12N15/00, C12R1:385)
CC          Key Location/Qualifiers
FH          1. .34
FT          source
FEATURES     Location/Qualifiers
              1. .34
              /organism="Pseudomonas aeruginosa"
              /mol_type="genomic DNA"
              /db_xref="taxon:287"
ORIGIN
Query Match      55.3%; Score 16.6; DB 6; Length 34;
Best Local Similarity 82.6%; Pred. No. 1.4e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      8 CAGGTAGGCAGACTTGTGCAGCCT 30
        |||||
Db      27 CAGGAGGCAGACTTGCAGCCT 5

RESULT 3
AX659517/c
LOCUS      AX659517 23 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 72 from Patent WO03000897.
ACCESSION  AX659517
VERSION     AX659517.1 GI:29161733
KEYWORDS    Oryza sativa
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
AUTHORS     Paszkowski, U., Briggs, S., Cooper, B., Goff, S., Moughamer, T.,
              Glazebrook, J., Katagiri, F., Kreis, J., Provart, N., Riecke, D. and
              Zhu, T.
TITLE       Identification and characterization of phosphate transporter genes
JOURNAL     Patent: WO 03000897-A 72 03-JAN-2003;
              Syngenta Participations AG (CH)
FEATURES     Location/Qualifiers
              1. .23
              /organism="Oryza sativa"
              /mol_type="unassigned DNA"
              /db_xref="taxon:4530"
ORIGIN
Query Match      52.0%; Score 15.6; DB 6; Length 23;
Best Local Similarity 81.8%; Pred. No. 4.5e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      8 CAGGTAGGCAGACTTGTGCAGC 29
        |||||
Db      23 CAATAGGCAGACTTGTGACC 2

RESULT 4
AX359198
LOCUS      AR359198 41 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6593124.

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ACCESSION    AR359198
VERSION      AR359198.1 GI:33765364
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 41)
AUTHORS      Lupton, S.D., Allen, J.M. and Feldhaus, A.L.
TITLE        Hybrid genes for expression of stimulatory factors in activated T
              cells
JOURNAL      Patent: US 6593124-A 14 15-JUL-2003;
FEATURES     Location/Qualifiers
              1. .41
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN
Query Match      52.0%; Score 15.6; DB 6; Length 41;
Best Local Similarity 81.8%; Pred. No. 4.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 CGGATCCAGGTAGGCAGACTTG 23
        |||||
Db      8 CGGATCCAGGAGGCTGCCCTG 29

RESULT 5
E31326/c
LOCUS      E31326 45 bp DNA linear PAT 18-JUN-2001
DEFINITION Process for producing novel microbial transglutaminase.
ACCESSION  E31326
VERSION     E31326.1 GI:13025716
KEYWORDS    JP 1999075876-A/25.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE    1 (bases 1 to 45)
AUTHORS      Keiichi, I., Nami, N., Tetsuya, M. and Katsuya, S.
TITLE        Process for producing novel microbial transglutaminase
JOURNAL      Patent: JP 1999075876-A 25 23-MAR-1999;
              AJINOMOTO CO INC
COMMENT      OS Unidentified
              PN JP 1999075876-A/25
              PD 23-MAR-1999
              PF 29-JUN-1998 JP 1998181951
              PR
              PI KEIICHI YOKOYAMA, NAMI NAKAMURA, TETSUYA MIWA, KATSUYA SEGURO
              C12N15/09, C12N1/21, C12N9/10// (C12N1/21, C12R1:19), (C12N9/10, PC
              C12R1:19),/00
              PC C12N15/00
              CC Strandedness: Single;
              CC Topology: Linear;
              FH Key Location/Qualifiers
              FT source 1. .45
              /organism="Unidentified".
FEATURES     Location/Qualifiers
              1. .45
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
ORIGIN
Query Match      52.0%; Score 15.6; DB 6; Length 45;
Best Local Similarity 81.8%; Pred. No. 4.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC 26
        |||||
Db      42 ATCCAGGTAGGCAGATTCATCA 21

RESULT 6
AR301265/c

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LOCUS AR301265 45 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 26 from patent US 6538122.
ACCESSION AR301265
VERSION AR301265.1 GI:31689038
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Yokoyama,K., Nakamura,N., Miwa,T. and Seguro,K.
TITLE Process for producing microbial transglutaminase
JOURNAL Patent: US 6538122-A 26 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..45
/mol_type="genomic DNA"
ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 45;
Best Local Similarity 81.8%; Pred. No. 4.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 5 ATCCAGGTAGGCAGACTTGTC A 26
||||| ||||| ||||| |||||
Db 42 ATCCAGGTAAGCAGATTCATCA 21
||||| ||||| ||||| |||||

RESULT 7
E31327 E31327 50 bp DNA linear PAT 18-JUN-2001
LOCUS E31327
DEFINITION Process for producing novel microbial transglutaminase.
ACCESSION E31327
VERSION E31327.1 GI:13025717
KEYWORDS JP 199075876-A/26.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Keiichi,Y., Nami,N., Tetsuya,M. and Katsuya,S.
TITLE Process for producing novel microbial transglutaminase
JOURNAL Patent: JP 199075876-A 26 23-MAR-1999;
COMMENT AJINOMOTO CO INC
OS Unidentified
PN JP 199075876-A/26
PD 23-MAR-1999
PF 29-JUN-1998 JP 1998181951
PR
PI KEIICHI YOKOYAMA, NAMI NAKAMURA, TETSUYA MIWA, KATSUYA SEGURO PC
C12N15/09, C12N1/21, C12N9/10// (C12N1/21, C12R1:19), (C12N9/10, PC
C12R1:19),
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..50
FT Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 50;
Best Local Similarity 81.8%; Pred. No. 4.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 5 ATCCAGGTAGGCAGACTTGTC A 26
||||| ||||| ||||| |||||
Db 13 ATCCAGGTAAGCAGATTCATCA 34
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RESULT 8
LOCUS AR301266 50 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 27 from patent US 6538122.
ACCESSION AR301266
VERSION AR301266.1 GI:31689039
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Yokoyama,K., Nakamura,N., Miwa,T. and Seguro,K.
TITLE Process for producing microbial transglutaminase
JOURNAL Patent: US 6538122-A 27 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..50
/mol_type="genomic DNA"
ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 50;
Best Local Similarity 81.8%; Pred. No. 4.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 5 ATCCAGGTAGGCAGACTTGTC A 26
||||| ||||| ||||| |||||
Db 13 ATCCAGGTAAGCAGATTCATCA 34
||||| ||||| ||||| |||||

RESULT 9
BD222501 BD222501 29 bp DNA linear PAT 17-JUL-2003
LOCUS BD222501
DEFINITION Novel methods for the identification of ligand and target biomolecules.
ACCESSION BD222501
VERSION BD222501.1 GI:33032271
KEYWORDS JP 2002521652-A/17.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Halkier,T., Jespersen,L. and Jensen,A.
TITLE Novel methods for the identification of ligand and target
JOURNAL Patent: JP 2002521652-A 17 16-JUL-2002;
COMMENT M AND E BIOTECH AS
OS Artificial Sequence
PN JP 2002521652-A/17
PD 16-JUL-2002
PF 16-JUL-1999 JP 2000561352
PR 20-JUL-1998 DK PA 199800956, 29-JUL-1998 US 60/094868 PI
TORBEN HALKIER, LENE JESPERSEN, ALLAN JENSEN
PC G01N33/50, G01N33/50, C12N15/00, C12Q1/02, C12Q1/25, G01N33/15, PC
G01N33/68//
PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/00, C12N5/00 CC
Description of Artificial Sequence: Synthetic DNA primer FH Key
Location/Qualifiers
FT source 1..29
FT Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 29;
Best Local Similarity 76.0%; Pred. No. 5.4e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GGATCCAGGTAGGCAGACTTGTC A 27
||||| ||||| ||||| |||||
Db 3 GGATCCATGAAGACAGAGATGCCAG 27
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RESULT 10
AX647902
LOCUS AX647902 29 bp DNA linear PAT 03-MAR-2003
DEFINITION Sequence 18 from Patent EP1270746.
ACCESSION AX647902
VERSION AX647902.1 GI:28802733
SOURCE
SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT
other sequences; artificial sequences.
REFERENCE
1 Jensen,A., Halkier,T. and Jespersen,L.
AUTHORS Methods for the identification of ligand and target biomolecules
TITLE Patent: EP 1270746-A 18 02-JAN-2003;
JOURNAL Innoxell A/S (DK)
FEATURES
Location/Qualifiers
source
1. .29
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA primer"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 29;
Best Local Similarity 76.0%; Pred. No. 5.4e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGCAGACTTGTCTCAG 27
|||||
Db 3 GGATCCATGAAGACAGAGTGCCAG 27

RESULT 11
BD103433/c
LOCUS BD103433 30 bp DNA linear PAT 27-AUG-2002
DEFINITION A carcinostatic or antiviral agent containing IRG27 protein or
gene.
ACCESSION BD103433
VERSION BD103433.1 GI:22649007
KEYWORDS WO 0187349-A/5.
SOURCE
SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS Enjoji,T., Todo,N. and Imamura,M.
TITLE A carcinostatic or antiviral agent containing IRG27 protein or gene
JOURNAL Patent: WO 0187349-A 5 22-NOV-2001;
SUMITOMO PHARMACEUTICALS CO LTD,TAKASHI ENJOJI,NAOKI TODO, MOTOAKI
IMAMURA
COMMENT OS Artificial Sequence
PN WO 0187349-A/5
PD 22-NOV-2001
PF 18-MAY-2001 WO 2001JP004155
PI TAKASHI ENJOJI,NAOKI TODO,MOTOAKI IMAMURA
PC A61K48/00,A61K38/17,A61P31/12,A61P35/00//C12N15/12,C07K16/18
CC Description of Artificial Sequence: a sequence of primer 4U
CC a sequence of 5'-upstream region for IRG27 gene. FH Key
CC Location/Qualifiers
FT source
1. .30
/organism='Artificial Sequence'.
FT Location/Qualifiers
source
1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 30;
Best Local Similarity 94.1%; Pred. No. 5.4e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 14 GGCGAGCTTGTCTCAGCCT 30
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Db 22 GGCAAACTTGTCTCAGCCT 6

RESULT 12
AX453416
LOCUS AX453416 33 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 5 from Patent WO0244212.
ACCESSION AX453416
VERSION AX453416.1 GI:21712729
KEYWORDS
SOURCE
SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Deleersnijder,W., Blockx,H. and de Moor,L.
TITLE Human g-protein coupled receptor and uses thereof
JOURNAL Patent: WO 0244212-A 5 06-JUN-2002;
SOLVAY PHARMACEUTICALS B V (NL)
FEATURES
Location/Qualifiers
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1. .33
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.4e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGCAGACTTGTCTCAG 27
|||||
Db 3 GGATCCAGCTCTGAAGCTTGTCTCAG 27

RESULT 13
E51173
LOCUS E51173 42 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for transforming plant and transformed plant.
ACCESSION E51173
VERSION E51173.1 GI:18629490
KEYWORDS JP 2001046073-A/10.
SOURCE
SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 42)
AUTHORS Nakashita,H., Yamaguchi,I., Yoshioka,K. and Doi,Y.
TITLE Method for transforming plant and transformed plant
JOURNAL Patent: JP 2001046073-A 10 20-FEB-2001;
RIKAGAKU KENKYUSHO,HIDEO NAKASHITA
COMMENT OS Artificial Sequence
PN JP 2001046073-A/10
PD 20-FEB-2001
PF 09-AUG-1999 JP 1999225832
PI HIDEO NAKASHITA,ISAMU YAMAGUCHI,KEIKO YOSHIOKA,YOSHIHARU DOI
PC C12N15/09,A01H5/00,C12N5/10,C12N9/02,C12N9/10,C12P7/62, PC
C12N15/00,C12N5/00
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CC Location/Qualifiers
FH Key
FT source
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/organism='Artificial Sequence'.
FT Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 50.7%; Score 15.2; DB 6; Length 42;
Best Local Similarity 71.4%; Pred. No. 6.6e+04;

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Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
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 Db 3 CGGATCCAGGGAGGGAATCATGGCGACC 30

RESULT 14
 AX137508
 LOCUS AX137508 42 bp DNA linear PAT 31-JAN-2002
 DEFINITION Sequence 10 from Patent EP1076095.
 ACCESSION AX137508
 VERSION AX137508.1 GI:14273702
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 42)
 AUTHORS Nakashita,H., Yamaguchi,I., Yoshioka,K. and Doi,Y.
 TITLE Process for producing polyester
 JOURNAL Patent: JP 2001046074-A 10 20-FEB-2001;
 RIKAGAKU KENKYUSHO
 COMMENT OS Artificial Sequence
 PN JP 2001046074-A/10
 PD 20-FEB-2001
 PF 09-AUG-1999 JP 1999225839
 PR
 PI HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIOHARU DOI
 PC C12N15/09,A01H5/00,C12N5/10,C12N9/02,C12N9/10,C12P7/62, PC
 C12N15/00,C12N5/00
 CC

Query Match 50.7%; Score 15.2; DB 6; Length 42;
 Best Local Similarity 71.4%; Pred. No. 6.6e+04;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
 |||||
 Db 3 CGGATCCAGGGAGGGAATCATGGCGACC 30

FEATURES
 source Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 50.7%; Score 15.2; DB 6; Length 42;
 Best Local Similarity 71.4%; Pred. No. 6.6e+04;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
 |||||
 Db 3 CGGATCCAGGGAGGGAATCATGGCGACC 30

RESULT 15
 AR399392
 LOCUS AR399392 42 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 10 from patent US 6620601.
 ACCESSION AR399392
 VERSION AR399392.1 GI:40141254
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 42)
 AUTHORS Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
 TITLE Methods for transformation of plants, transformed plants and processes for preparation of polyesters
 JOURNAL Patent: US 6620601-A 10 16-SEP-2003;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 50.7%; Score 15.2; DB 6; Length 42;
 Best Local Similarity 71.4%; Pred. No. 6.6e+04;

Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
 |||||
 Db 3 CGGATCCAGGGAGGGAATCATGGCGACC 30

RESULT 16
 AX137508
 LOCUS AX137508 42 bp DNA linear PAT 30-MAY-2001
 DEFINITION Sequence 10 from Patent EP1076095.
 ACCESSION AX137508
 VERSION AX137508.1 GI:14273702
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
 TITLE Methods for transformation of plants, transformed plants and processes for preparation of polyesters
 JOURNAL Patent: EP 1076095-A 10 14-FEB-2001;
 Riken (JP)

FEATURES
 source Location/Qualifiers
 1..42
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="synthetic DNA"

ORIGIN

Query Match 50.7%; Score 15.2; DB 6; Length 42;
 Best Local Similarity 71.4%; Pred. No. 6.6e+04;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
 |||||
 Db 3 CGGATCCAGGGAGGGAATCATGGCGACC 30

RESULT 17

BD240955
 LOCUS BD240955 29 bp DNA linear PAT 17-JUL-2003
 DEFINITION A novel human lysozyme gene, its encoded polypeptide and the method for preparing them.

ACCESSION BD240955
 VERSION BD240955.1 GI:33050725
 KEYWORDS JP 2002523097-A/4.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 29)
 AUTHORS Yu,L., Fu,Q., Zhao,Y., Zhang,H. and Bi,A.
 TITLE A novel human lysozyme gene, its encoded polypeptide and the method for preparing them
 JOURNAL Patent: JP 2002523097-A 4 30-JUL-2002;
 COMMENT LONG YU
 OS Unidentified
 PN JP 2002523097-A/4
 PD 30-JUL-2002
 PF 30-AUG-1999 JP 2000567703
 PR 31-AUG-1998 CN 98 1 11044.4
 PI LONG YU, QIANG FU, YONG ZHAO, HONGLAI ZHANG, ANDING BI
 PC C12N15/09,A61K38/43,A61K39/395,A61P31/04,A61P35/00, PC
 C07K16/40,
 PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/36,C12P21/08//C12Q1/68,
 PC (C12N1/21,C12R1:19), (C12N5/10,C12R1:91), (C12N9/36,C12R1:19),
 PC (C12N9/36,C12R1:91), C12N15/00,C12N5/00,A61K37/48, (C12N5/00, PC
 C12R1:91)

CC Primer
 FH Key
 FT source

Location/Qualifiers
 1..29

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FEATURES
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    FT
      Location/Qualifiers
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          /mol_type="genomic DNA"
          /db_xref="taxon:32644"
ORIGIN
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    Best Local Similarity 50.0%; Score 15; DB 6; Length 29;
    Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy
    1 GCGGATCCAGGTAGGCAGACTTG 23
    |||||
  Db
    3 GCGGATCCATGAAGGCATCCGTG 25
    |||||
RESULT 18
AR437642 AR437642 29 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 5 from patent US 6660512.
ACCESSION AR437642
VERSION AR437642.1 GI:40202794
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 29)
  Unclassified.
  AUTHORS
  Yu.L., Fu.Q., Zhao.Y., Zhang.H. and Bi.A.
  TITLE
  Human lysozyme gene, it's encoded polypeptide and the method of
  preparing them
  JOURNAL
  Patent: US 6660512-A 5 09-DEC-2003;
  FEATURES
    source
      Location/Qualifiers
        1..29
          /organism="unknown"
          /mol_type="genomic DNA"
ORIGIN
  Query Match
    Best Local Similarity 50.0%; Score 15; DB 6; Length 29;
    Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy
    1 GCGGATCCAGGTAGGCAGACTTG 23
    |||||
  Db
    3 GCGGATCCATGAAGGCATCCGTG 25
    |||||
RESULT 19
AR173178 AR173178 25 bp DNA linear PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 20 from patent US 6303750.
ACCESSION AR173178
VERSION AR173178.1 GI:17912669
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 25)
  Unclassified.
  AUTHORS
  Friedman.S.M., Crow.M.K., Li.Y., Tumang.J.R. and Sun.G.-R.
  TITLE
  Conserved T-cell receptor sequences
  JOURNAL
  Patent: US 6303750-A 20 16-OCT-2001;
  FEATURES
    source
      Location/Qualifiers
        1..25
          /organism="unknown"
          /mol_type="unassigned DNA"
ORIGIN
  Query Match
    Best Local Similarity 49.3%; Score 14.8; DB 6; Length 25;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  Qy
    9 AGGTAGGCAGACTTGTCA 26
    |||||

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Db
  4 AGGTCGACAGACTTGTCA 21
  |||||
RESULT 20
AR183091 AR183091 37 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 68 from patent US 6340461.
ACCESSION AR183091
VERSION AR183091.1 GI:20226684
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 37)
  Unclassified.
  Terman,D.Stephen.
  TITLE
  Superantigen based methods and compositions for treatment of
  diseases
  JOURNAL
  Patent: US 6340461-A 68 22-JAN-2002;
  FEATURES
    source
      Location/Qualifiers
        1..37
          /organism="unknown"
          /mol_type="unassigned DNA"
ORIGIN
  Query Match
    Best Local Similarity 49.3%; Score 14.8; DB 6; Length 37;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  Qy
    9 AGGTAGGCAGACTTGTCA 26
    |||||
  Db
    16 AGGACAGACAGACTTGTCA 33
    |||||
RESULT 21
AX956456 AX956456 24 bp DNA linear PAT 08-JAN-2004
LOCUS
DEFINITION Sequence 6 from Patent WO03097869.
ACCESSION AX956456
VERSION AX956456.1 GI:40784965
KEYWORDS
SOURCE
ORGANISM
Rosa sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE
  1
  Suess,K.H.
  AUTHORS
  Microsatellite markers for genetic analyses and the differentiation
  of roses
  JOURNAL
  Patent: WO 03097869-A 6 27-NOV-2003;
  Con/Cipio GmbH (DE)
  FEATURES
    source
      Location/Qualifiers
        1..24
          /organism="Rosa sp."
          /mol_type="unassigned DNA"
          /db_xref="taxon:36598"
ORIGIN
  Query Match
    Best Local Similarity 48.7%; Score 14.6; DB 6; Length 24;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  Qy
    9 AGGTAGGCAGACTTGTCCGCC 29
    |||||
  Db
    2 AGGTAGGCAGAGAGTCACAGAC 22
    |||||
RESULT 22
AR137780 AR137780 31 bp DNA linear PAT 16-JUN-2001
LOCUS
DEFINITION Sequence 14 from patent US 6197558.
ACCESSION AR137780
VERSION AR137780.1 GI:14479289

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KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.

REFERENCE
AUTHORS      Unclassified.
TITLE        1 (bases 1 to 31)
JOURNAL      Fotheringham, I.G.
FEATURES     Transaminase biotransformation process
              Patent: US 6197558-A 14 06-MAR-2001;
              Location/Qualifiers
              1..31
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      48.7%; Score 14.6; DB 6; Length 31;
Best Local Similarity 69.0%; Pred. No. 1.3e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTGTGACCC 29
    |||||
Db 2 GCGGATCCATCATGGCTGACTGCGACCC 30
    |||||

RESULT 23
BD192813
LOCUS      BD192813          31 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Improved transaminase biotransformation process.
ACCESSION  BD192813
VERSION     BD192813.1 GI:33002552
KEYWORDS   JP 2002514921-A/14.
SOURCE     Staphylococcus aureus
ORGANISM   Staphylococcus aureus
REFERENCE  Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS    Fotheringham, I.G.
TITLE      Improved transaminase biotransformation process
JOURNAL    Patent: JP 2002514921-A 14 21-MAY-2002;
           NSC TECHNOLOGIES LLC
COMMENT    PN JP 2002514921-A/14
           PD 21-MAY-2002
           PF 19-MAY-1998 JP 1998550503
           PR 19-MAY-1997 US 08/858111
           PI IAN G FOTHERINGHAM
           PC C12P13/04, C12P7/26, C12P7/62, C12N15/63, C12N9/88, C12N9/10 CC
Strandedness: Single;
CC Topology: Linear;
FH Key = 'synthetic oligonucleotide'
   Location/Qualifiers
FEATURES   1..31
           /organism="Staphylococcus aureus"
           /mol_type="genomic DNA"
           /db_xref="taxon:1280"

ORIGIN
Query Match      48.7%; Score 14.6; DB 6; Length 31;
Best Local Similarity 69.0%; Pred. No. 1.3e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTGTGACCC 29
    |||||
Db 2 GCGGATCCATCATGGCTGACTGCGACCC 30
    |||||

RESULT 24
AX955017
LOCUS      AX955017          44 bp      DNA      linear      PAT 08-JAN-2004
DEFINITION Sequence 13 from Patent WO03093468.
ACCESSION  AX955017
VERSION     AX955017.1 GI:40784254
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens

REFERENCE
AUTHORS      Unclassified.
TITLE        1 (bases 1 to 31)
JOURNAL      Miller, W.Allen, and Wang, S.
FEATURES     Cap-independent translation sequences derived from barley yellow
              dwarf virus
              Patent: US 5910628-A 19 08-JUN-1999;
              Location/Qualifiers
              1..31
              /organism="unknown"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Molday, R.S., Ahn, J. and Hauswirth, W.S.
TITLE        Expression system for large functional proteins
JOURNAL      Patent: WO 03093468-A 13 13-NOV-2003;
              University of British Columbia (CA)
FEATURES     Location/Qualifiers
              1..44
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

ORIGIN
Query Match      48.7%; Score 14.6; DB 6; Length 44;
Best Local Similarity 81.0%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTTGTG 23
    |||||
Db 24 GAATCCAGAGACAGACTTGTG 44
    |||||

RESULT 25
AX033626
LOCUS      AX033626          27 bp      DNA      linear      PAT 21-SEP-2000
DEFINITION Sequence 1 from Patent EP1029923.
ACCESSION  AX033626
VERSION     AX033626.1 GI:10280344
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Method for conveying bnyvv resistance to sugar beet plants
TITLE      Patent: EP 1029923-A 1 23-AUG-2000;
JOURNAL    HAVE D J VAN DER BV (NL)
FEATURES   1..27
           Location/Qualifiers
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="primer P1"

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Query Match      48.0%; Score 14.4; DB 6; Length 27;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGT 24
    |||||
Db 2 GCGGATCCATCATGGCAGACTTCGT 25
    |||||

RESULT 26
AR071455
LOCUS      AR071455          31 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 19 from patent US 5910628.
ACCESSION  AR071455
VERSION     AR071455.1 GI:7222343
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 31)
AUTHORS    Miller, W.Allen, and Wang, S.
TITLE      Cap-independent translation sequences derived from barley yellow
JOURNAL    Patent: US 5910628-A 19 08-JUN-1999;
FEATURES   Location/Qualifiers
           1..31
           /organism="unknown"
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ORIGIN /mol_type="unassigned DNA"

Query Match 48.0%; Score 14.4; DB 6; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTC 25
||||| ||| ||| ||| |||
Db 8 CGGATCCTGGGAAACAGGCTTGAC 31
||||| ||| ||| ||| |||

RESULT 27
LOCUS AR071444 33 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 8 from patent US 5910628.
ACCESSION AR071444
VERSION AR071444.1 GI:7222332
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Miller,W.Allen. and Wang,S.
TITLE Cap-independent translation sequences derived from barley yellow dwarf virus
JOURNAL Patent: US 5910628-A 8 08-JUN-1999;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 48.0%; Score 14.4; DB 6; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTC 25
||||| ||| ||| ||| |||
Db 9 CGGATCCTGGGAAACAGGCTTGAC 32
||||| ||| ||| ||| |||

RESULT 28
LOCUS AR152460/c 40 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 28 from patent US 6235263.
ACCESSION AR152460
VERSION AR152460.1 GI:15119992
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Wong,A.K.C., Bartel,P.L., Teng,D.H.-P. and Tavtigian,S.V.
TITLE Carboxy-terminal BRCA1 interacting protein
JOURNAL Patent: US 6235263-A 28 22-MAY-2001;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 48.0%; Score 14.4; DB 6; Length 40;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGCAGACTTGTC 26
||||| ||| ||| ||| |||
Db 36 GAATCCTGTTGGCAGAAATGGTCA 13
||||| ||| ||| ||| |||

RESULT 29
LOCUS AX456419 44 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 34 from patent US 6288218.
ACCESSION AR168947
VERSION AR168947.1 GI:17905145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Levinson,D.Adam.

LOCUS AX456419 40 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 277 from Patent WO0216944.
ACCESSION AX456419
VERSION AX456419.1 GI:21715323
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wood,K.V., Wood,M.G., Zhuang,Y. and Paguio,A.
TITLE Synthetic nucleic acid molecule compositions and methods of preparation
JOURNAL Patent: WO 0216944-A 277 28-FEB-2002;
FEATURES Location/Qualifiers
source 1..40
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="An oligonucleotide"

ORIGIN

Query Match 48.0%; Score 14.4; DB 6; Length 40;
Best Local Similarity 93.8%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGCAG 18
||| ||| ||| ||| |||
Db 23 GGCTCCAGGTAGGCAG 38
||| ||| ||| ||| |||

RESULT 30
LOCUS AR143578/c 44 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 34 from patent US 6204371.
ACCESSION AR143578
VERSION AR143578.1 GI:15104864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Levinson,D.Adam.
TITLE Compositions and methods for the treatment and diagnosis of immune disorders
JOURNAL Patent: US 6204371-A 34 20-MAR-2001;
FEATURES Location/Qualifiers
source 1..44
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 48.0%; Score 14.4; DB 6; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 TCCAGGTAGGCAGACTTGTCAGCC 29
||||| ||| ||| ||| |||
Db 40 TGCAGGTGTCAGACTTGGGATCC 17
||||| ||| ||| ||| |||

RESULT 31
LOCUS AR168947/c 44 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 34 from patent US 6288218.
ACCESSION AR168947
VERSION AR168947.1 GI:17905145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Levinson,D.Adam.

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1. 1.1.3
source
/organism="synthetic construct"
/mol_type="genomic DNA"
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ORIGIN

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Query Match      48.0%; Score 14.4; DB 6; Length 45;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGCAGACTTGT 24
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Db 28 GCGGATCCAGGCAGGCGGAACGCGT 5

RESULT 36
AX456402/c
LOCUS AX456402 45 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 260 from Patent WO0216944.
ACCESSION AX456402
VERSION AX456402.1 GI:21715306
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,
TITLE Luisi,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
JOURNAL Gene and sequence variation associated with lipid disorder
Patent: WO 0220847-A 214 14-MAR-2002;
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="An oligonucleotide"

ORIGIN

Query Match      48.0%; Score 14.4; DB 6; Length 45;
Best Local Similarity 93.8%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGCAG 18
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Db 43 GGCTCCAGGTAGGCAG 28

RESULT 37
AX477123
LOCUS AX477123 20 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 214 from Patent WO0220848.
ACCESSION AX477123
VERSION AX477123.1 GI:22216376
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,
TITLE Luisi,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
JOURNAL Gene and sequence variation associated with cancer
Patent: WO 0220848-A 214 14-MAR-2002;
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Primer"

ORIGIN

Query Match      47.3%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.1e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 AGGTAGGCAGACTTGTCTAG 27
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Db 9 AGGTAGGCAGACTTGTCTAG 27

Query Match      47.3%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.1e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGCAGGCAGATTGTGAG 19
    ||||| ||||| ||||| ||||| |||||
Db 1 AGGCAGGCAGATTGTGAG 19

RESULT 38
AX526499
LOCUS AX526499 20 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 214 from Patent WO0220847.
ACCESSION AX526499
VERSION AX526499.1 GI:25171306
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,
TITLE Luisi,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
JOURNAL Gene and sequence variation associated with lipid disorder
Patent: WO 0220847-A 214 14-MAR-2002;
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Primer"

ORIGIN

Query Match      47.3%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.1e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 AGGTAGGCAGACTTGTCTAG 27
    ||||| ||||| ||||| ||||| |||||
Db 1 AGGCAGGCAGATTGTGAG 19

RESULT 39
CQ878078
LOCUS CQ878078 28 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 54 from Patent WO2004081206.
ACCESSION CQ878078
VERSION CQ878078.1 GI:53790792
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Edwards,A., Dharamsi,A., Vedadi,M., Thalakada,R., Arrowsmith,C.,
Ouyang,H., Domagala,M., Virag,C., Beattie,B., Mansoury,K.,
Canadien,V., Richards,D., Ng,I., Nethery,K., Houston,S.,
Buzadzija,K., Tai,W., Kanagarajan,D. and Boora,K.
JOURNAL Patent: WO 2004081206-A 54 23-SEP-2004;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

ORIGIN

Query Match      47.3%; Score 14.2; DB 6; Length 28;
Best Local Similarity 84.2%; Pred. No. 2e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGCAG 19
    ||||| ||||| ||||| ||||| |||||
Db 3 GCGGATCCGCGTAGGCCGA 21

RESULT 40
AR184482
LOCUS AR184482 28 bp DNA linear PAT 20-APR-2002

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DEFINITION Sequence 12 from patent US 6346389.
ACCESSION ARI84482
VERSION ARI84482.1 GI:20230447
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Altieri,D.C.
TITLE Method for selectively modulating the interactions between survivin
and tubulin
JOURNAL Patent: US 6346389-A 12 12-FEB-2002;
FEATURES
 Location/Qualifiers
 1..28
 /organism="unknown"
 /mol_type="unassigned DNA"
ORIGIN
 Query Match 47.3%; Score 14.2; DB 6; Length 28;
 Best Local Similarity 70.4%; Pred. No. 2e+05;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Oy 2 CGGATCCAGGTAGGCAGACTTGTTCAGC 28
Db 2 CGGATCCAGAGAGATGACTTTTAAAC 28

Search completed: November 18, 2005, 17:42:49
Job time : 835.457 secs

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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 206.578 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-2

Perfect score: 30

Sequence: 1 CGGATCCAGTAGCAGACTTGTCAGCCT 30

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
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- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	2	AAQ91122 Beta-card
2	30	100.0	30	9	ACA63112 Human bet
3	30	100.0	30	13	ADR05298 Human bet
C 4	16.6	55.3	37	5	Aaf27237 Pseudomon
5	16.6	55.3	37	4	Aaf82378 Human C-r
6	16.2	54.0	26	6	ABK88923 Human agg
C 7	15.6	52.0	23	8	ABT32007 Rubql for
8	15.6	52.0	41	2	AAQ77830 Human CTL
C 9	15.6	52.0	45	2	AAV81531 Oligonuc
C 10	15.6	52.0	45	3	AAV73048 Transglut
11	15.6	52.0	50	2	AAV81532 Oligonuc
12	15.6	52.0	50	3	AAV73049 Transglut
13	15.4	51.3	29	3	Aaz58442 Primer us
C 14	15.4	51.3	30	6	ABA96284 Human IRG
15	15.4	51.3	33	6	ABK87354 Human G p
16	15.2	50.7	33	2	AAQ45507 Sequence
17	15.2	50.7	42	4	Aaf84270 Poly-3-hy
18	15	50.0	29	3	AAA07726 Human lys
19	14.8	49.3	25	2	AAT04797 T cell re
C 20	14.8	49.3	25	12	ADP13952 Renal cel

21	14.8	49.3	26	2	AAQ15070	Aaql5070 T-cell re
22	14.8	49.3	26	2	AAT10374	Aat10374 T-cell re
C 23	14.8	49.3	31	8	ACD56891	AcD56891 HCV DNAY
C 24	14.8	49.3	31	12	ADI87346	Adi87346 HCV DNAY
25	14.8	49.3	37	2	AAV42608	Aav42608 PCR prime
26	14.6	48.7	24	12	ADH68394	Adh68394 Rosa sp r
27	14.6	48.7	31	2	AAQ05623	AaQ05623 E. coli K
28	14.6	48.7	44	10	ADE94330	AdE94330 Human ABC
C 29	14.4	48.0	25	9	ACI03125	ACi03125 Human mic
30	14.4	48.0	27	3	AA74492	Aa74492 Beet near
31	14.4	48.0	31	2	AA60078	Aa60078 3' untran
32	14.4	48.0	33	2	AA60067	Aa60067 3' untran
33	14.4	48.0	38	6	ACN17176	ACn17176 WNV Inozy
C 34	14.4	48.0	40	2	AA76467	Aa76467 Human BRC
35	14.4	48.0	40	6	ABL99294	AbI99294 Synthetic
C 36	14.4	48.0	44	2	AAT38282	Aat38282 Murine 10
C 37	14.4	48.0	44	3	AA51915	Aa51915 Reverse p
C 38	14.4	48.0	44	4	AA03383	Aa03383 3' primer
C 39	14.4	48.0	44	4	AA92152	Aa92152 Mouse 103
C 40	14.4	48.0	44	4	AAF23475	Aaf23475 3' oligon
C 41	14.4	48.0	44	4	AAI70278	Aai70278 Mouse 103
C 42	14.4	48.0	44	4	AAF82626	Aaf82626 Murine TH
C 43	14.4	48.0	44	6	ABS53332	Ab53332 Mouse 103
C 44	14.4	48.0	44	8	ABQ77055	Abq77055 Murine 10
C 45	14.4	48.0	44	9	ADB37507	Adb37507 Mouse Th-

ALIGNMENTS

RESULT 1
AAQ91122
ID AAQ91122 standard; cDNA; 30 BP.
XX
AC AAQ91122;
XX
DT 19-FEB-1996 (first entry)
XX
DE Beta-cardiac myosin heavy chain PCR primer B.
XX
KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
KW diagnosis; primer; mutation; detection; ss.
XX
OS Synthetic.
PN US429923-A.
XX
PD 04-JUL-1995.
XX
PF 11-DEC-1992; 92US-00989160.
XX
PR 11-DEC-1992; 92US-00989160.
XX
(HARD) HARVARD COLLEGE.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
(GHO-) GEN HOSPITAL SHENYANG MILITARY AREA.
Seidman J, Seidman C, Watkins H, Rosenzweig A;
WPI; 1995-245715/32.
Non-invasive method for diagnosis of hypertrophic cardio-mypathy -
useful for testing asymptomatic individual(s).
Example 1; Col 10; 22pp; English.
AAQ91121-091130 are nested PCR primers used for the amplification and
identification of beta-cardiac myosin heavy-chain RNA. They are used in a
new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
the method involves detecting the presence or absence of specific HC-
associated mutations in the beta-cardiac myosin heavy-chain obtained from
a blood sample. The method may be used to diagnose familial or sporadic
HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. Cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 30 BP; 6 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30
 |||||
 Db 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30

RESULT 2
 ACA63112
 ID ACA63112 standard; DNA; 30 BP.

XX ACA63112;

28-AUG-2003 (first entry)

DE Human beta cardiac myosin heavy chain PCR primer B.

XX Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
 KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
 KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
 KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

XX US2003054343-A1.

XX 20-MAR-2003.

XX 06-JUN-1995; 95US-00469172.

XX 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.
 XX (SEID/) SEIDMAN J.
 XX (WATK/) WATKINS H.
 XX (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;
 XX WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with
 PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
 PT hemophilia, by detecting a mutation in an amplified product of a beta
 PT cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
 CC and FHC) comprises detecting a mutation associated with hypertrophic
 CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy
 CC chain DNA. The mutations associated with SHC/FHC are detected in the
 CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-
 CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
 CC sample). FHC associated point mutation can be classified and used to
 CC determine life expectancy in affected individuals e.g. using a Kaplan-
 CC Meier curve for the classified type of FHC causing point mutation. Also
 CC included are an RNA probe comprising ribonucleotides arranged in a
 CC sequence which is complementary to at least a portion of beta-cardiac
 CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
 CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
 CC chain cDNA containing an FHC-associated mutation

XX Sequence 30 BP; 6 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30
 |||||
 Db 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30

RESULT 3

ADRO5298
 ID ADRO5298 standard; DNA; 30 BP.

XX ADRO5298;

XX 21-OCT-2004 (first entry)

DE Human beta cardiac myosin heavy chain mutation detection primer B.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
 KW familial hypertrophic cardiomyopathy;
 KW sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

XX US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.
 XX (SEID/) SEIDMAN J.
 XX (WATK/) WATKINS H.
 XX (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to
 PT diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
 PT myosin heavy-chain DNA and detecting the mutation in the amplified
 PT product.

XX Claim 18; SEQ ID NO 2; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
 CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
 CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
 CC amplified product, and detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy in the amplified product,
 CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
 CC included are a set of DNA oligonucleotide primers for amplifying beta-
 CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

SQ Sequence 30 BP; 6 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 13; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30
Db 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30

RESULT 4

AAF27237/c
ID AAF27237 standard; DNA; 34 BP.

XX AAF27237;

DT 11-SEP-2003 (revised)
DT 24-APR-2001 (first entry)

XX Pseudomonas aeruginosa strain PAO128 oligonucleotide.

XX Selective cloning; mismatch detection; mismatch binding protein; Muts;
XX mutant gene; strain PAO128; bacterial infection; ss.

OS Pseudomonas aeruginosa; strain PAO128.

XX JP2000308489-A.

XX 07-NOV-2000.

XX 28-APR-1999; 99JP-00121957.

XX 28-APR-1999; 99JP-00121957.

XX (DAUC) DAIICHI PHARM CO LTD.

XX WPI; 2001-127778/14.

XX Detection of minutely mutated DNA useful for detection and treatment of
XX Pseudomonas aeruginosa, and development of antibacterial agents comprises
XX cloning a structurally characterized DNA.

XX Example 6; Fig 6; 13pp; Japanese.

XX The invention relates to a method of cloning a structurally

CC characterised DNA or a flanking DNA containing part of the characterised

CC region by concentrating the DNA of interest using a substance which
CC specifically recognises the structurally characterised region or a
CC fragment thereof, and selectively cloning only the DNA of interest by
CC subtraction treatment. The invention especially relates to a method for
CC cloning or detecting a minutely mutated DNA by concentrating the mutated
CC DNA using a substance (such as a mismatch repair protein) which
CC specifically recognises mismatched DNA, and selectively cloning only the
CC mutant DNA. Such a method of detection may also be used in the diagnosis
CC of disease associated with DNA mutations. The method was exemplified by
CC the cloning and sequencing of DNA from the PAO128 strain of Pseudomonas
CC aeruginosa using an immobilised maltose binding protein (MBP)-Muts fusion
CC protein, and the corresponding DNA from Pseudomonas aeruginosa strain
CC PAO1 (which was designated as the wild-type). The Muts portion of the
CC fusion protein recognised mismatches in PAO1/PAO128 DNA duplexes. The
CC mutant (i.e., PAO128) DNA was thus concentrated, amplified via PCR, and
CC contaminating DNA removed by RDA. A Pseudomonas aeruginosa strain PAO128
CC library was constructed and its genome sequenced. Such a protocol may be
CC used for the detection of Pseudomonas aeruginosa infection, and in the
CC development of antibacterial agents. The present sequence represents a
CC fragment of an unidentified gene from Pseudomonas aeruginosa strain
CC PAO128. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 34 BP; 4 A; 11 C; 13 G; 6 T; 0 U; 0 Other;

Query Match 55.3%; Score 16.6; DB 5; Length 34;
Best Local Similarity 82.6%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 CAGGTAGGCAGACTTGTTCAGCCT 30

Db 27 CAGGCAGGCAGACTTTCGCCGCT 5
|||||
|||||

RESULT 5

AAF82378

ID AAF82378 standard; DNA; 37 BP.

XX AAF82378;

DT 25-JUN-2001 (first entry)

XX Human C-reactive protein 5' primer.

XX Human; C-reactive protein; CRP; chicken embryo lethal orphan virus; CEO;
XX recombinant avian egg; chicken adenovirus expression vector; ACEV;
XX recombinant protein production; vaccine; gene therapy; PCR primer; ss.

OS Homo sapiens.

XX WO200119968-A1.

XX 22-MAR-2001.

XX 15-SEP-2000; 2000WO-US025489.

XX 17-SEP-1999; 99US-0154393P.

XX (CHEM-) CHEMOGEN INC.

XX Grabko VI, Blyden ER;

XX WPI; 2001-328015/34.

XX Use of avian adenovirus for producing recombinant proteins by mixing
XX vector containing avian adenovirus DNA with purified adenovirus DNA,
XX introducing DNA mixture into embryonated avian egg, and harvesting
XX proteins.

XX Example 5; Page 22; 70pp; English.

XX The present sequence was used in the construction of recombinant human C-
XX reactive protein (CRP). It was used in an example illustrating an
CC invention relating to the use of avian adenovirus for producing


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Best Local Similarity 81.8%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CAGGTAGGCAGACTTGTGACCC 29
DB 23 CAATAGGCAGACTTGTGACC 2

RESULT 8
AAQ77830
ID AAQ77830 standard; DNA; 41 BP.
XX AC AAQ77830;
XX DT 25-MAR-2003 (revised)
XX DT 16-JUN-1995 (first entry)
XX DE Human CTLA-1 transcriptional control region PCR primer.
XX KW Human CTLA-1; granzyme B; transcription control region; cytomegalovirus;
XX KW HCMV; immediate early gene IE94 enhancer;
XX KW chloramphenicol acetyl transferase reporter construct; T cell expression;
XX KW T cell activation-induced expression; ss.
XX OS Synthetic.
XX PN WO9422489-A1.
XX PD 13-OCT-1994.
XX PF 04-APR-1994; 94WO-US003659.
XX PR 06-APR-1993; 93US-00044539.
XX PA (TARG-) TARGETED GENETICS CORP.
XX PI Lupton SD, Allen JM, Feldhaus AL;
XX WPI; 1994-332835/41.
XX DR Recombinant polynucleotide encoding stimulatory factor poly:peptide -
XX PT under control of region causing activation-induced expression in T
XX PT lymphocytes to reduce their dependence on helper cells.
XX PS Example 15; Page 33; 79pp; English.
XX CC The human CTLA-1 transcriptional control region was amplified directly
XX CC from human genomic DNA by PCR using oligonucleotides AAQ77829 and
XX CC AAQ77830. The amplified product was operatively linked to a reporter gene
XX CC encoding chloramphenicol acetyl transferase (CAT) in a HyTK plasmid. A
XX CC fragment spanning the HCMV IE94 enhancer was ligated upstream of the CTLA-
XX CC -1-CAT. The plasmid was electroporated into human Jurkat cells. The CTLA-
XX CC 1 transcriptional control region in combination with the CMV enhancer
XX CC mediates activation-induced expression in human T lymphocytes. (Updated
XX CC on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 41 BP; 9 A; 12 C; 13 G; 7 T; 0 U; 0 Other;

Query Match 52.0%; Score 15.6; DB 2; Length 41;
Best Local Similarity 81.8%; Pred. No. 4.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGCAGACTTG 23
DB 8 CGGATCCAGGAGGTCGCCCTG 29

RESULT 9
AAV81531/c
ID AAV81531 standard; DNA; 45 BP.
XX AC AAV81531;
XX XX

Best Local Similarity 81.8%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CAGGTAGGCAGACTTGTGACCC 29
DB 23 CAATAGGCAGACTTGTGACC 2

RESULT 8
AAQ77830
ID AAQ77830 standard; DNA; 41 BP.
XX AC AAQ77830;
XX DT 25-MAR-2003 (revised)
XX DT 16-JUN-1995 (first entry)
XX DE Human CTLA-1 transcriptional control region PCR primer.
XX KW Human CTLA-1; granzyme B; transcription control region; cytomegalovirus;
XX KW HCMV; immediate early gene IE94 enhancer;
XX KW chloramphenicol acetyl transferase reporter construct; T cell expression;
XX KW T cell activation-induced expression; ss.
XX OS Synthetic.
XX PN WO9422489-A1.
XX PD 13-OCT-1994.
XX PF 04-APR-1994; 94WO-US003659.
XX PR 06-APR-1993; 93US-00044539.
XX PA (TARG-) TARGETED GENETICS CORP.
XX PI Lupton SD, Allen JM, Feldhaus AL;
XX WPI; 1994-332835/41.
XX DR Recombinant polynucleotide encoding stimulatory factor poly:peptide -
XX PT under control of region causing activation-induced expression in T
XX PT lymphocytes to reduce their dependence on helper cells.
XX PS Example 15; Page 33; 79pp; English.
XX CC The human CTLA-1 transcriptional control region was amplified directly
XX CC from human genomic DNA by PCR using oligonucleotides AAQ77829 and
XX CC AAQ77830. The amplified product was operatively linked to a reporter gene
XX CC encoding chloramphenicol acetyl transferase (CAT) in a HyTK plasmid. A
XX CC fragment spanning the HCMV IE94 enhancer was ligated upstream of the CTLA-
XX CC -1-CAT. The plasmid was electroporated into human Jurkat cells. The CTLA-
XX CC 1 transcriptional control region in combination with the CMV enhancer
XX CC mediates activation-induced expression in human T lymphocytes. (Updated
XX CC on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 41 BP; 9 A; 12 C; 13 G; 7 T; 0 U; 0 Other;

Query Match 52.0%; Score 15.6; DB 2; Length 41;
Best Local Similarity 81.8%; Pred. No. 4.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGCAGACTTG 23
DB 8 CGGATCCAGGAGGTCGCCCTG 29

RESULT 9
AAV81531/c
ID AAV81531 standard; DNA; 45 BP.
XX AC AAV81531;
XX XX

Best Local Similarity 81.8%; Pred. No. 4.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTCA 26
DB 42 ATCCAGGTAGGCAGACTTGTCA 21

RESULT 10
AAA73048/c
ID AAA73048 standard; DNA; 45 BP.
XX AC AAA73048;
XX DT 24-NOV-2000 (first entry)
XX DE Transglutaminase related oligonucleotide sequence SEQ ID NO:24.
XX KW Transglutaminase; gelled food; jelly; yoghurt; gelled cosmetic; cheese;
XX KW ss.
XX OS Unidentified.
XX PN WO200040706-A1.
XX XX

01-APR-1999 (first entry)
Oligonucleotide used for codon optimisation of transglutaminase gene.
Transglutaminase; microbial; gelled food; jelly; yogurt; cheese;
cosmetic; meat quality; microcapsule production; high thermal stability;
carrier; immobilised enzyme; codon optimised; ss.
Synthetic.
Streptomyces sp.
EP889133-A2.
07-JAN-1999.
02-JUL-1998; 98EP-00112315.
04-JUL-1997; 97JP-00180010.
(AJIN) AJINOMOTO CO INC.
Yokoyama K, Nakamura N, Miwa T, Seguro K;
WPI; 1999-062664/06.
New microbial transglutaminase with N-terminal aspartic acid deleted -
allowing high level recombinant production without added methionine in E.
coli, useful in production of gelled foods, cosmetics etc.
Example 1; Page 34; 56pp; English.
AAV81521-60 were used for construction of a synthetic Streptovorticillium
sp. transglutaminase gene (see AAV81508). The synthetic gene is codon
altered for high expression in Escherichia coli. The specification
describes a new microbial transglutaminase that has the N-terminal
aspartic acid of transglutaminase deleted. Eliminating the N-terminal Asp
from microbial transglutaminase allows efficient removal of the terminal
Met residue added when the protein is expressed in E. coli. The E. coli
methionine aminopeptidase acts well on Met-Ser but only poorly on Met-
Asp, so problems of antigenicity associated with Met-terminated proteins
are avoided. Recombinant transglutaminase is used to produce gelled foods
(jellies, yogurt and cheeses) or cosmetics, to improve the quality of
meat, in the production of materials for microcapsules of high thermal
stability and as a carrier for immobilised enzymes
Sequence 45 BP; 14 A; 10 C; 8 G; 13 T; 0 U; 0 Other;

Query Match 52.0%; Score 15.6; DB 2; Length 45;
Best Local Similarity 81.8%; Pred. No. 4.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTCA 26
DB 42 ATCCAGGTAGGCAGACTTGTCA 21

RESULT 10
AAA73048/c
ID AAA73048 standard; DNA; 45 BP.
XX AC AAA73048;
XX DT 24-NOV-2000 (first entry)
XX DE Transglutaminase related oligonucleotide sequence SEQ ID NO:24.
XX KW Transglutaminase; gelled food; jelly; yoghurt; gelled cosmetic; cheese;
XX KW ss.
XX OS Unidentified.
XX PN WO200040706-A1.
XX XX

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CC (such as recombinant transglutaminase) which can be used in the food
 CC industry for the production of gelled foods such as jellies, yoghurts and
 CC cheeses, and for the production of gelled cosmetics. The present sequence
 CC represents an oligonucleotide which is used in the exemplification from
 CC the present invention

XX SQ Sequence 50 BP; 12 A; 11 C; 11 G; 16 T; 0 U; 0 Other;

Query Match 52.0%; Score 15.6; DB 3; Length 50;

Best Local Similarity 81.8%; Pred. No. 4.4e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5 ATCCAGGTAGGACAGACTTGTCA 26

Db 13 ATCCAGGTAAGCAGATTCATCA 34

RESULT 13

AAZ58442

ID AAZ58442 standard; DNA; 29 BP.

XX AC AAZ58442;

XX DT 23-MAY-2000 (first entry)

XX DE Primer used in pCWbipepER/CI-2A construction.

XX KW Chymotrypsin inhibitor; CI-2A; barley; plasmid pCWbipep;

XX KW endoplasmic reticulum retention signal; CellScreen;

XX KW enzyme activity modulator; enzyme inhibitor; drug discovery;

XX KW peptide library; PCR primer; ss.

XX OS Unidentified.

XX PN WO200005406-A1.

XX PD 03-FEB-2000.

XX PF 16-JUL-1999; 99WO-DK000408.

XX PR 20-JUL-1998; 98DK-00000956.

XX PR 29-JUL-1998; 98US-0094868P.

XX PA (MEBI-) M & E BIOTECH AS.

XX PI Halkier T, Jespersen L, Jensen A;

XX PR WPI; 2000-182719/16.

XX PT Novel screen comprising a pool of vectors with randomly modified

XX PT nucleotide sequences, useful for identifying modulators of enzyme

XX PT activity useful for selecting antibiotic agents.

XX PS Example 1-c; Page 73; 136pp; English.

XX The present sequence is that of a primer used in a PCR amplification
 CC designed to add an endoplasmic reticulum retention signal in frame to the
 CC C-terminus of the chymotrypsin inhibitor 2A (CI-2A) in plasmid
 CC pCWbipepER/CI-2A (see AAZ58442). The invention relates to improvements
 CC in CellScreen technology that encompass screening in prokaryotic as well
 CC as eukaryotic cells, and which can be used to identify and/or prepare
 CC peptides or RNAs capable of modulating the activity in vivo of target
 CC enzymes in eukaryotic cells. Previously unknown interactions between
 CC targets and ligands can be identified. Enzyme inhibitor structures such
 CC as CI-2A are used as scaffolds to display intracellularly potentially
 CC biologically active peptides or RNAs in a stable form. Preparation of a
 CC medicinal product is based on initial identification of targets or
 CC ligands using the methods of the invention

XX SQ Sequence 29 BP; 9 A; 6 C; 11 G; 3 T; 0 U; 0 Other;

Query Match

Best Local Similarity 51.3%; Score 15.4; DB 3; Length 29;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 3 GGATCCAGGTAGGACAGACTTGTCA 27

Db 3 GGATCCATGAAGACAGAGTGGCCAG 27

RESULT 14

ABA96284/c

ID ABA96284 standard; DNA; 30 BP.

XX AC ABA96284;

XX DT 15-MAR-2002 (first entry)

XX DE Human IRG27 PCR primer SEQ ID NO 6.

XX KW Human; IRG27; carcinostatic; cytostatic; anti-viral; cancer; cytokine;
 KW cell growth; differentiation; p53; infection; PCR primer; ss.
 XX OS Homo sapiens.
 XX PN WO200187349-A1.
 XX PD 22-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-JP004155.
 XX PR 19-MAY-2000; 2000JP-00149097.
 XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PI Enjoji T, Tohdoh N, Imamura M;

XX PR WPI; 2002-114218/15.

XX PT Carcinostatic or anti-viral agents comprising a IRG27 polypeptide, useful
 XX PT for the treatment of cancer and viral infection.

XX PS Example 2; Page 94; 104pp; Japanese.

XX The invention relates to carcinostatic, cytostatic or anti-viral agents
 CC comprising an IRG27 polypeptide that is induced by a mutated or modified
 CC cancer controlling gene p53, a cytokine that controls cell growth and/or
 CC by differentiation and is increased in cancer tissue. The gene and IRG27
 CC are useful for treatment and prevention of cancer and viral infection.
 CC The present sequence is that of a PCR primer for amplifying the IRG27
 CC encoding polynucleotide

XX SQ Sequence 30 BP; 8 A; 5 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 6; Length 30;

Best Local Similarity 94.1%; Pred. No. 5.1e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 14 GGACAGACTTGTGCAGCCT 30

Db 22 GGCAAACTTGTGCAGCCT 6

RESULT 15

ABK87354

ID ABK87354 standard; DNA; 33 BP.

XX AC ABK87354;

XX DT 24-SEP-2002 (first entry)

XX DE Human G protein-coupled receptor IGS70 PCR primer IP15,490.

XX KW Human; ss; PCR; G protein-coupled receptor; GPCR; IGS70; CNS; primer;
 KW psychiatric disorder; central nervous system disorder; schizophrenia;
 KW Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;

KW heart failure; angina pectoris; myocardial infarction; kidney disease;
 KW renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;
 KW inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;
 KW asthma; infection; human immunodeficiency virus infection; HIV; diabetes;
 KW osteoporosis; allergy.

OS Homo sapiens.

XX WO200244212-A2.

XX PD 06-JUN-2002.

XX PF 23-NOV-2001; 2001WO-EP013706.

XX PR 30-NOV-2000; 2000EP-00204280.

XX PR 05-DEC-2000; 2000US-0251045P.

XX PA (SOLV) SOLVAY PHARM BV.

XX PI Deleersnijder W, Blockx H, De Moor L;

XX DR WPI; 2002-527703/56.

XX PT Novel G-protein coupled receptor IGS70 polypeptide useful for treating
 PT dysfunctions, disorders or disease related to lung, bone marrow, spinal
 PT cord immune system.

XX PS Example 1; Page 33; 58pp; English.

XX CC The invention relates to a G protein-coupled receptor (GPCR) IGS70
 CC polypeptide including sequences that are 98-99.6% identical. Also
 CC included are the polynucleotide encoding IGS70 (including sequences 98-
 CC 99.6% identical to the polynucleotide or the DNA insert contained in
 CC plasmid CBS 109818), a hybridisation probe derived from the
 CC polynucleotide, a DNA or RNA expression system producing IGS70, a host
 CC comprising the expression system, IGS70 receptor membrane preparation
 CC derived from the cell, an antibody immunospecific for IGS70, IGS70 is
 CC useful for diagnosing a disease or a susceptibility to disease in a
 CC subject related to expression or activity of the IGS70 polypeptide in a
 CC subject by determining the presence or absence of mutation in the
 CC nucleotide sequence encoding IGS70 in the genome of the subject in a
 CC sample derived from the subject. IGS70 is also useful identifying agonist
 CC or antagonist. The IGS70 protein, polynucleotide, antibody and identified
 CC an/agonists are useful for treating psychiatric and central nervous
 CC system (CNS) disorders such as schizophrenia, Alzheimer's disease,
 CC multiple sclerosis, anxiety, cardiovascular diseases such as heart
 CC failure, angina pectoris, myocardial infarction, kidney disease such as
 CC renal failure, gastrointestinal disorders such as irritable bowel
 CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,
 CC inflammation, cancers, asthma, infection (such as bacterial, viral,
 CC fungal, protozoal) especially human immunodeficiency virus infection
 CC (HIV), diabetes, osteoporosis and allergies. The present sequence is a
 CC PCR primer used to isolate the cDNA encoding the human GPCR IGS70

XX SQ Sequence 33 BP; 8 A; 9 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 6; Length 33;
 Best Local Similarity 76.0%; Pred. No. 5.1e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGAGACTTCTCAG 27

Db 3 GGATCCAGCTCTGAAGCTTGTCTCAG 27

RESULT 16

AAQ45507

XX ID AAQ45507 standard; DNA; 33 BP.

XX AC AAQ45507;

XX DT 25-MAR-2003 (revised)

DT 30-NOV-1993 (first entry)

XX DE Sequence of a kappa constant region 3' primer.

XX KW Antibody; C-erbB-2; variable region; therapy; diagnosis; cancer; mammary;
 KW ovary; tumour; PCR; primer; ss.

XX OS Synthetic.

XX XX WO9312220-A1.

XX PD 24-JUN-1993.

XX PF 04-DEC-1992; 92WO-US010437.

XX PR 12-DEC-1991; 91US-00808462.

XX PA (BERL-) BERLEX LAB INC.

XX PI Shawver LK, Liu HC, Parkes DL, Mcbrogan MP, Brandis JW;

XX DR WPI; 1993-214162/26.

XX PT Recombinant and chimeric antibodies to C-ERBB-2 - used as therapeutic and
 PT diagnostic agents for tumours expressing C-ERBB-2.

XX PS Example; Page 69; 106pp; English.

XX CC The human heavy chain gamma-1 constant (C-gamma-1) gene and the human
 CC light chain kappa (C-kappa) gene were cloned from human IGG producing
 CC cell line ARH-77 (ATCC CRL 1621) using PCR. Each amplified C-gamma-1 and
 CC C-kappa gene fragment contd. several hundred base pair flanking sequences
 CC at both the 5' and 3' end. The kappa constant region was amplified from
 CC ARH-77 genomic DNA using PCR. The primers used are found in AAQ45506 (5'
 CC primer) and AAQ45507 (3' primer). The amplified DNA was verified to be
 CC the kappa constant region by Southern blot (AAQ45511 for probe) and
 CC sequence analysis. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 33 BP; 7 A; 10 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 2; Length 33;
 Best Local Similarity 71.4%; Pred. No. 6.3e+03;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGAGACTTGTCTCAGCT 30

Db 4 GGATCCTGACCGTAAGACCTGTCCACCT 31

RESULT 17

AAF84270

ID AAF84270 standard; DNA; 42 BP.

XX AC AAF84270;

XX DT 13-JUN-2001 (first entry)

XX DE Poly-3-hydroxybutyrate synthase gene, phbC, PCR primer rbs-CU.

XX KW Plant; polyester synthase; alkyl 3-hydroxyvalcanoic acid; PCR primer;
 KW phbC; poly-3-hydroxybutyrate synthase; plastid; ss.

XX OS Ralstonia eutropha.

XX XX EP1076095-A1.

XX PD 14-FEB-2001.

XX PF 08-AUG-2000; 2000EP-00117037.

XX PR 09-AUG-1999; 99JP-00225832.

XX PR 09-AUG-1999; 99JP-00225839.

XX PA (RIKE) RIKEN KK.

RESULT 20	ADP13952/c	ADP13952 standard; DNA; 25 BP.
XX	ID	ADP13952 standard; DNA; 25 BP.
XX	AC	ADP13952;
XX	AC	ADP13952;
XX	DT	26-AUG-2004 (first entry)
XX	DE	Renal cell carcinoma differentially expressed gene probe #357.
XX	DE	ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW	KW	peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW	KW	head/neck cancer; differential expression; probe.
XX	OS	Homo sapiens.
XX	OS	Homo sapiens.
XX	PN	WO2004048933-A2.
XX	PN	WO2004048933-A2.
XX	PD	10-JUN-2004.
XX	XX	21-NOV-2003; 2003WO-US037481.
XX	XX	21-NOV-2002; 2002US-0427982P.
PR	PR	23-APR-2003; 2003US-0459782P.
XX	XX	(AMHP) WYETH.
PA	PA	(TWIN/) TWINE N C.
PA	PA	(BURC/) BURCZYNSKI M E.
PA	PA	(TREP/) TREPICCHIO W L.
PA	PA	(DORN/) DORNER A.
PA	PA	(STOV/) STOVER J A.
PA	PA	(SLOW/) SLOMI D K.
XX	XX	Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI	PI	Sioni DK;
XX	XX	WPI; 2004-460799/43.
XX	XX	Diagnosing non-blood disease such as solid tumor, involves comparing
PT	PT	differential expression profile of specific genes in peripheral blood
PT	PT	sample of subject with reference expression profile of specific genes.
XX	XX	Disclosure; SEQ ID NO 688; 350pp; English.
XX	XX	The invention relate to a method of diagnosing (M1) non-blood disease
CC	CC	such as solid tumor by providing peripheral blood sample of human having
CC	CC	non-blood disease, and comparing an expression profile of specific genes
CC	CC	in the peripheral blood sample to reference expression profile of the
CC	CC	genes, where each of the genes is differentially expressed in peripheral
CC	CC	blood mononuclear cells (PBMCs) of patients having the disease as
CC	CC	compared to PBMCs of normal humans. The method is useful for diagnosing
CC	CC	non-blood disease such as solid tumor. The solid tumor is chosen from
CC	CC	renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC	CC	peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC	CC	sample is a whole blood sample (claimed). (M1) is useful for identifying
CC	CC	genes that are differentially expressed in peripheral blood samples
CC	CC	isolated at different stages of progression, development or treatment of
CC	CC	RCC and/or other solid tumors. This sequence corresponds to a probe to
CC	CC	detect a gene that is differentially expressed and detected by the method
CC	CC	of the invention.
XX	XX	Sequence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
XX	XX	Query Match 49.3%; Score 14.8; DB 12; Length 25;
XX	XX	Best Local Similarity 88.9%; Pred. No. 9.2e+03;
XX	XX	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	QY	8 CAGGTAGGCAGACTTGTC 25
DB	DB	25 CAGGAAGGCAGACTTGTC 8

XX	23-FEB-1995;	95WO-EF000670.
PF		
XX	23-FEB-1994;	94EP-00200454.
PR		
XX	(ALKU) AKZO NOBEL NV.	
PA		
XX	Van Der Maaden JM, Rijnders AMM, Graus JPM;	
PI		
XX	WPI; 1995-311502/40.	
DR		
XX	Peptide contained in the variable region of a T-cell receptor beta chain	
PT	- specifically associated with immune disease, esp. rheumatoid arthritis.	
XX		
PS	Example 2; Page 24; 55pp; English.	
XX		
CC	The primers AAT10352-97 were used to PCR amplify the T cell receptor beta	
CC	chain variable regions from T cell culture clones, isolated from the	
CC	synovial joint fluid of 11 patients suffering from rheumatoid arthritis.	
CC	The coding sequences were shown to contain the nucleotide sequence	
CC	AAT07409. The encoded polypeptide can be used as an immunogenic cpd. for	
CC	the detection of or preposition to an immune disease, or for use as a	
CC	vaccine for prevention or treatment of an immune disease	
XX		
SQ	Sequence 26 BP; 9 A; 5 C; 7 G; 5 T; 0 U; 0 Other;	
	Query Match	49.3%; Score 14.8; DB 2; Length 26;
	Best Local Similarity	88.9%; Pred. No. 9,2e+03;
	Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY	9 AGGTAGGCAGACTTGTC A 26	
DB	4 AGGCAGACAGACTTGTC A 21	
RESULT 23		
ACD56891/c		
ID	ACD56891 standard; DNA; 31 BP.	
XX		
AC	ACD56891;	
XX		
DT	23-SEP-2003 (first entry)	
XX		
DE	HCV DNazyme sequence #37.	
XX		
KW	Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;	
KW	RNA stability; RNA expression; RNA synthesis; antisense;	
KW	enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;	
KW	amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;	
KW	HBV reverse transcriptase; Enhancer I region; viral replication;	
KW	degenerative; disease state; HBV infection; HCV infection; cirrhosis;	
KW	liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;	
XX	virucide; antiinflammatory; ss.	
XX		
OS	Hepatitis C virus.	
XX		
PN	WO200281494-A1.	
XX		
PD	17-OCT-2002.	
XX		
PF	26-MAR-2002; 2002WO-US009187.	
XX		
XX	26-MAR-2001; 2001US-00817879.	
PR	08-JUN-2001; 2001US-00877478.	
PR	08-JUN-2001; 2001US-0296876P.	
PR	24-OCT-2001; 2001US-0330509P.	
PR	05-DEC-2001; 2001US-0337055P.	
XX		
XX	(RIBO-) RIBOZYME PHARM INC.	
PA	(BLAT/) BLATT L.	
PA	(MACE/) MACEJAK D.	
PA	(MCSW/) MCSWIGGEN J.	
PA	(MORR/) MORRISSEY D.	

PA (MACE/) MACEJACK D.
 XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
 XX WPI; 2004-031273/03.
 XX Enzymatic nucleic acid molecules which specifically cleave RNA derived
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
 PT especially in combination with type I interferon therapy.
 XX Claim 2; SEQ ID NO 4834; 198pp; English.
 XX The invention relates to an enzymatic nucleic acid molecule which
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
 CC the binding arms of the enzymatic nucleic acid molecule comprises
 CC sequences complementary to any of the defined substrate sequences given
 CC in the specification. The nucleic acid molecule may be administered for
 CC the treatment of HCV infections, especially in combination with type I
 CC interferons. The present sequence represents a HCV DNazyme sequence.
 XX Sequence 31 BP; 7 A; 9 C; 9 G; 6 T; 0 U; 0 Other;
 SQ Query Match 49.3%; Score 14.8; DB 12; Length 31;
 Best Local Similarity 73.1%; Pred. No. 9.4e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 2 CGGATCCAGGTAGCAGACTTGTTCAG 27
 Db 27 CGGATCGTGTAGCTAGCCTTGCCAG 2
 RESULT 25
 AAV42608
 ID AAV42608 standard; DNA; 37 BP.
 AC AAV42608;
 DT 07-OCT-1998 (first entry)
 DE PCR primer used to amplify TCR alpha chain cDNA.
 XX Superantigen; treatment; cancer; tumour-specific antigen;
 KW autoimmune disease related antigen; infection; bacterial; viral;
 KW eukaryotic; autoimmune disease; inhibit; pathological response;
 KW immune response; mouse; T cell receptor; TCR; PCR primer; ss.
 XX Synthetic.
 OS WO9826747-A2.
 PN 25-JUN-1998.
 PD 17-DEC-1997; 97WO-US023637.
 PF 17-DEC-1996; 96US-0033172P.
 PR 17-APR-1997; 97US-0044074P.
 XX (TERM/) TERMAN D S.
 PA Terman DS;
 PI WPI; 1998-362497/31.
 XX Conjugates and polymers containing superantigen and therapeutic antigen -
 PT for treatment of cancer, infection, autoimmune disease and graft
 PT rejection, also treatment by administering lymphocytes treated in vitro
 PT by these antigens.
 XX Example 10; Page 88; 139pp; English.
 FS PCR primers AAV42608-11 were used to amplify the T cell receptor (TCR)
 CC alpha chain cDNA. The products were used to prepare effector T cells with
 CC tumour specificity. The specification describes a method for treatment

CC of cancer which comprises incubating lymphocytes with a tumour-specific
 CC antigen or autoimmune disease related antigen and a superantigen. The
 CC treated cells are then introduced into the patient. The superantigen and
 CC the tumour-specific antigen or autoimmune disease related antigen can be
 CC conjugated together. The products are used to treat cancer (carcinoma,
 CC melanoma, lymphoma etc.), infections (bacterial, viral or eukaryotic) and
 CC autoimmune disease (e.g. idiopathic thrombocytopenic purpura, rheumatoid
 CC arthritis, systemic lupus erythematosus, multiple sclerosis etc.). The
 CC antigens either induce an immune response or inhibit a pathological
 CC response
 XX Sequence 37 BP; 10 A; 8 C; 10 G; 9 T; 0 U; 0 Other;
 SQ Query Match 49.3%; Score 14.8; DB 2; Length 37;
 Best Local Similarity 88.9%; Pred. No. 9.7e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 9 AGGTAGGCAGACTTGTCA 26
 Db 16 AGCAGACAGACTTGTCA 33
 RESULT 26
 ADH68394
 ID ADH68394 standard; DNA; 24 BP.
 XX ADH68394;
 AC 25-MAR-2004 (first entry)
 DT Rosa sp reverse PCR primer for microsatellite marker RMS003.
 DE microsatellite marker; rose genome; PCR; hypervariable region;
 KW genetic mapping; relatedness analysis; hybrid identification; plant;
 KW breeding; primer; ss.
 XX Rosa sp.
 OS WO2003097869-A2.
 PN 27-NOV-2003.
 PD 16-MAY-2003; 2003WO-DE001572.
 PF 17-MAY-2002; 2002DE-01022632.
 PR (CONC-) CON CIPIO GMBH.
 XX Suess K;
 PI WPI; 2004-012541/01.
 DR New oligonucleotides from rose microsatellite markers, useful for genomic
 XX analysis, including identification of varieties and hybrids.
 PT Claim 1; Page 5; 52pp; German.
 FS This invention describes novel oligonucleotides derived from
 CC microsatellite markers and used for the amplification of the rose genome.
 CC The invention also describes a test kit for genetic analysis of cultured
 CC or wild forms of the genus Rosa sp. that contains at least one of the new
 CC oligonucleotide primers and preparing microsatellite markers of Rosa sp.
 CC by PCR amplification of hypervariable genomic regions, using at least one
 CC primer pair, to produce polymorphic fragments which are separated and
 CC amplified. The primer pairs flank the microsatellite locus being
 CC especially on high-resolution agarose or native or denatured,
 CC polyacrylamide gels, or by mass spectrometry. After separation, the
 CC amplicons are detected by staining (ethidium bromide or silver),
 CC radioactive labelling and autoradiography, automated sequencing using
 CC primers labelled with dyes or fluorophores or by mass spectrometry. A
 CC genomic library of 0.5-1.5 kb fragments from the rose variety
 CC 'Lichtblick' was constructed in pUC18 and used to transform Escherichia

CC coli and the cells tested against a high-density array of synthetic
 CC microsatellites. Inserts in plasmids that hybridised were sequenced and
 CC the identified sequences selected for ability to differentiate between a
 CC set of 30 rose varieties. The oligonucleotides are used for genetic
 CC analysis of cultivated and wild types of roses, particularly for genetic
 CC mapping and labelling of mono- or poly-genic traits, selection, analysis
 CC of relatedness, identification of varieties and evaluation of varietal
 CC purity, identification of hybrids and plant breeding. The
 CC oligonucleotides are useful in automated processes, do not require
 CC radioactive detection methods and can differentiate between almost all
 CC commercial rose varieties. ADH68375-ADH68674 represent the PCR primers
 CC used to amplify the rose microsatellite regions described in the method
 CC of the invention.

XX Sequence 24 BP; 10 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 48.7%; Score 14.6; DB 12; Length 24;
 Best Local Similarity 81.0%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTGACCC 29
 DB 2 AGGTAGGCAGAGTGACAGAC 22

RESULT 27

AAAX05623
 ID AAAX05623 standard; DNA; 31 BP.

XX AC AAAX05623;

XX DT 21-APR-1999 (first entry)

XX DE E. coli K12 ilva gene fragment generating primer.

XX KW Transaminase; enzyme; pyruvate; acetolactate synthase; keto acid;
 KW flavouring agent; sweetener; nutritional supplement; pharmaceutical;
 KW L-2-aminobutyrate; ilva gene; PCR primer; ss.

XX OS Synthetic.

XX OS Escherichia coli.

XX PN WO9853088-A1.

XX PD 26-NOV-1998.

XX PF 19-MAY-1998; 98WO-US010169.

XX PR 19-MAY-1997; 97US-00858111.

XX PA (MONS) MONSANTO CO.

XX PI Fotheringham IG;

XX WPI; 1999-070156/06.

XX Preparation of amino acid - which does not react with transaminase.

XX Example 2; Page 20; 57pp; English.

XX The invention relates to preparation of natural and unnatural amino acids
 CC that (a) reacting a first amino acid and a keto acid with transaminase
 CC enzyme to produce an amino acid and pyruvate, and (b) reacting pyruvate
 CC with acetolactate synthase enzyme to produce a compound that does not
 CC react with transaminase enzyme. The amino acids produced in these
 CC processes are useful as flavouring agents, sweeteners, nutritional
 CC supplements, synthetic intermediates in the preparation of
 CC pharmaceuticals. Acetolactate synthase enzyme eliminates the keto acid
 CC produced by the transaminase enzyme reaction, thus preventing the
 CC formation of an equilibrium of the reaction and driving the amino acid
 CC production to completion. The preparations are especially used to produce
 CC L-2-aminobutyrate. Sequences AAAX05623-24 represent PCR primers used for
 CC generating the E. coli K12 ilva gene fragment. This is used in the

CC construction of an expression vector pIF347 comprising the ilva gene
 CC encoding threonine deaminase

XX Sequence 31 BP; 6 A; 13 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 48.7%; Score 14.6; DB 2; Length 31;
 Best Local Similarity 69.0%; Pred. No. 1.2e+04;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGGGATCCAGGTAGGCAGACTTGTGACCC 29
 DB 2 CGGGATCCATCATGCTGACTCGCAACCC 30

RESULT 28

ADE94330

ID ADE94330 standard; DNA; 44 BP.

XX AC ADE94330;

XX DT 12-FEB-2004 (first entry)

XX DE Human ABCA1 C-half PCR primer SEQ ID NO:13.

XX KW ATP-binding cassette subfamily; ABCA subfamily; ABC transporter;
 KW PCR primer; human; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003093468-A2.

XX PD 13-NOV-2003.

XX PF 06-MAY-2003; 2003WO-CA000633.

XX PR 06-MAY-2002; 2002CA-02385110.

XX PR 27-JUN-2002; 2002US-0391644P.

XX (UYER-) UNIV BRITISH COLUMBIA.

XX PI Molday RS, Ahn J, Hauswirth WS;

XX WPI; 2003-903674/82.

XX New nucleic acid composition for expression of a functional member of the
 PT ATP-binding cassette (ABCA) subfamily of ABC transporters in a host cell,
 PT useful in treating a mammal in need of the member of the ABCA subfamily
 PT of ABC transporters.

XX Example 1; SEQ ID NO 13; 55pp; English.

XX The present invention describes a nucleic acid composition (I) for the
 CC expression of a functional member of the ATP-binding cassette (ABCA)
 CC subfamily of ABC transporters in a host cell comprises two or more
 CC different nucleic acid molecules, each of which encodes one or more
 CC domains of an ABC transporter, where the domains are functionally
 CC complementary. Also described: (1) a host cell comprising (1); (2) a
 CC method for expressing a functional member of the ABCA subfamily of ABC
 CC transporters in a host cell; (3) a system for expressing a functional
 CC member of the ABCA subfamily of ABC transporters in a host cell
 CC comprising 2 or more expression vectors; (4) a host cell comprising the
 CC the ABCA subfamily of ABC transporters; (6) a pharmaceutical composition
 CC comprising the nucleic acid or system; and (7) a kit for expressing a
 CC functional member of the ABCA subfamily of ABC transporters in a host
 CC cell. The nucleic acid composition (I) can be used for the expression of
 CC a functional member of the ABCA subfamily of ABC transporters in a host
 CC cell, which is useful in treating a mammal in need of functional member
 CC of the ABCA subfamily of ABC transporters. The present sequence
 CC represents a PCR primer used in the exemplification of the present
 CC invention.

```
SQ Sequence 44 BP; 13 A; 10 C; 15 G; 6 T; 0 U; 0 Other;
Query Match 48.7%; Score 14.6; DB 10; Length 44;
Best Local Similarity 81.0%; Pred. No. 1.2e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGACACTTG 23
Db 24 GAATCCAGAGACAGACTTG 44

RESULT 29
ACI03125/C
ID ACI03125 standard; DNA; 25 BP.
XX AC ACI03125;
XX DT 13-OCT-2003 (first entry)
XX DE Human microarray DNA oligonucleotide SEQ ID NO 3116.
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX Homo sapiens.
XX US2003104410-A1.
XX PD 05-JUN-2003.
XX PF 15-MAR-2002; 2002US-00098263.
XX PR 16-MAR-2001; 2001US-0276759P.
XX PA (APFY-) APFYMATRIX INC.
XX PI Mittmann MP;
XX WPI; 2003-567953/53.
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX Claim 1; SEQ ID NO 3116; 9pp; English.
XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying biallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones
XX for additional subclones containing segments of DNA that have been
XX isolated and previously sequenced. The sequence presented is one of the
XX nucleic acid probes incorporated in the microarray. Note: The sequence
XX data for this patent can also be obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html
XX Sequence 25 BP; 4 A; 8 C; 8 G; 5 T; 0 U; 0 Other;

SQ Sequence 44 BP; 13 A; 10 C; 15 G; 6 T; 0 U; 0 Other;
Query Match 48.0%; Score 14.4; DB 9; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCA 17
Db 20 CGGACCCAGGTAGGCA 5

RESULT 30
AAA74492
ID AAA74492 standard; DNA; 27 BP.
XX AC AAA74492;
XX DT 01-DEC-2000 (first entry)
XX DE Beet necrotic yellow vein virus PCR primer P1.
XX BNYVV-resistance; rhizomania; sugar beet; transgenic plant; PCR primer;
KW ss.
XX Beet necrotic yellow vein virus.
XX OS Beet necrotic yellow vein virus.
XX PN WO200044915-A1.
XX PD 03-AUG-2000.
XX PF 26-JAN-2000; 2000WO-EP000609.
XX PR 27-JAN-1999; 99EP-00200236.
XX PA (SESE-) SES EURO NV SA.
XX PI Richards K, Jonard G, Guillely H, Van Dun CMP;
XX WPI; 2000-505981/45.
XX Conveying resistance to beet necrotic yellow vein virus (BNYVV) to sugar
XX beet (Beta vulgaris) comprises introducing a DNA fragment having a
XX nucleotide sequence which is homologous to the sequence of the genomic
XX RNA 1 of BNYVV.
XX Example 1; Page 12; 31pp; English.
XX Beet necrotic yellow vein virus (BNYVV) causes rhizomania disease in
XX sugar beet plants. The present sequence is a PCR primer for BNYVV. The
XX resulting PCR fragment was cloned and used to convey resistance to BNYVV
XX to a sugar beet plant, to result in production of a transgenic BNYVV-
XX resistant sugar beet plant
XX Sequence 27 BP; 5 A; 9 C; 7 G; 6 T; 0 U; 0 Other;

SQ Sequence 48.0%; Score 14.4; DB 3; Length 27;
Query Match 48.0%; Score 14.4; DB 3; Length 27;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGACACTTGT 24
Db 2 GCGGATCCACCATGGCAGACTTGT 25

RESULT 31
AAAX60078
ID AAAX60078 standard; RNA; 31 BP.
XX AC AAAX60078;
XX DT 17-OCT-2003 (revised)
XX PR 04-AUG-1999 (first entry)
XX 3' untranslated region sequence of a viral genome.
XX
```

KW Protein production; eukaryotic cell; uncapped mRNA;
KW barley yellow dwarf virus PAV serotype; BYDV-PAV; ss.

XX unidentified tobacco necrosis virus.

XX US5910628-A.

XX 08-JUN-1999.

XX 20-MAY-1997; 97US-00858623.

XX 20-MAY-1996; 96US-0017199P.

XX (IOWA) UNIV IOWA STATE RES FOUND INC.

XX Wang S, Miller WA;

XX WPI; 1999-356844/30.

XX Cap-independent in eukaryotic cells.

XX Example 19; Fig 13; 49pp; English.

XX The specification describes a method for producing a protein in a
CC eukaryotic cell, from an uncapped mRNA using sequences derived from the
CC barley yellow dwarf virus PAV serotype (BYDV-PAV). The sequences are
CC useful for increasing the production of a protein translated from an
CC uncapped eukaryotic mRNA. AAX60075-85 represent 3' untranslated regions
CC of viral genomes, and were used in the course of the invention. (Updated
CC on 17-OCT-2003 to standardise OS field)

XX Sequence 31 BP; 9 A; 7 C; 11 G; 0 T; 4 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 2; Length 31;

Best Local Similarity 62.5%; Pred. No. 1.4e+04;

Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGCAGACTTGTGTC 25

||||:||||| :||| :|||

Db 8 CGGAUCCUGGAAACAGGCUUGAC 31

RESULT 32

AAX60067

ID AAX60067 standard; RNA; 33 BP.

XX AAX60067;

XX 17-OCT-2003 (revised)

XX 04-AUG-1999 (first entry)

XX 3' untranslated region sequence of a viral genome.

XX Protein production; eukaryotic cell; uncapped mRNA;

XX barley yellow dwarf virus PAV serotype; BYDV-PAV; ss.

XX unidentified tobacco necrosis virus.

XX US5910628-A.

XX 08-JUN-1999.

XX 20-MAY-1997; 97US-00858623.

XX 20-MAY-1996; 96US-0017199P.

XX (IOWA) UNIV IOWA STATE RES FOUND INC.

XX Wang S, Miller WA;

XX WPI; 1999-356844/30.

XX Cap-independent in eukaryotic cells.

XX Example 5; Fig 4; 49pp; English.

XX The specification describes a method for producing a protein in a
CC eukaryotic cell, from an uncapped mRNA using sequences derived from the
CC barley yellow dwarf virus PAV serotype (BYDV-PAV). The sequences are
CC useful for increasing the production of a protein translated from an
CC uncapped eukaryotic mRNA. AAX60064-74 represent 3' untranslated regions
CC of viral genomes, and were used in the course of the invention. (Updated
CC on 17-OCT-2003 to standardise OS field)

XX Sequence 33 BP; 9 A; 7 C; 13 G; 0 T; 4 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 2; Length 33;

Best Local Similarity 62.5%; Pred. No. 1.4e+04;

Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGCAGACTTGTGTC 25

||||:||||| :||| :|||

Db 9 CGGAUCCUGGAAACAGGCUUGAC 32

RESULT 33

ACN17176

ID ACN17176 standard; RNA; 38 BP.

XX ACN17176;

XX 22-APR-2004 (first entry)

XX WNV Inozyme SEQ ID NO 17179.

XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;

XX Amberzyme; Zinzyne; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 24; SEQ ID NO 17179; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX treating a condition related to WNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, Inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyne. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080


```

PN WO9627603-A1.
XX
XX 12-SEP-1996.
PD
XX 01-MAR-1996; 96WO-US002798.
PF
XX 03-MAR-1995; 95US-00398633.
PR
XX 07-JUN-1995; 95US-00487748.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Levinson DA;
PI
XX WPI; 1996-433404/43.
DR
XX Genes and their products differentially expressed in T helper cells -
PT useful in diagnosis and treatment of immune disorders, e.g. multiple
PT sclerosis, asthma, lepromatous leprosy, etc.
XX
XX Example 11, Page 167; 218pp; English.
PS
XX A 5' primer (AAT38281) and 3' primer (AAT38282) contg. 5' SpeI and 3'
CC BamHI sites were used to amplify the murine 103 gene (see also AAT38272)
CC that is differentially expressed in T helper TH2 cells. Murine TH2-type
CC cell line D10G4 cDNA was used as template. The PCR product was used to
CC replace the IL-10 gene in plasmid pCil-10. The final construct, pCD2-103L
CC -GH, contained the human CD2 enhancer and Pmu promoter and the murine 103
CC gene coding sequence. It was used to produce transgenic mice that
CC expressed the 103 gene product (see also AAT38283-84). Such mice can be
CC used as models of TH2 cell subpopulation-related disorders
XX
XX Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
SQ
Query Match 48.0%; Score 14.4; DB 2; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 6 TCCAGGTAGGCGAGCTTGTGACGC 29
Db 40 TGCAGGTGTGCAGACTTGGGATCC 17
RESULT 37
AAT51915/c
ID AAT51915 standard; DNA; 44 BP.
XX
XX AAT51915;
AC
XX 31-OCT-2000 (first entry)
DT
DE Reverse primer to construct a murine 103 gene transgenic clone.
XX
XX T helper cell; differential expression; 200 gene; immunomodulator;
KW anti-inflammatory; anti-arthritis; antibacterial; immunosuppressive;
KW thymomimetic; anti-thyroid; anti-asthmatic; anti-allergic; antiviral;
KW protozoacide; lymphocyte; modulator; gene therapy; primer; ss.
XX
XX Mus sp.
OS
XX US6084083-A.
PN
XX 04-JUL-2000.
PD
XX 28-MAR-1997; 97US-00829525.
PF
XX 03-MAR-1995; 95US-00398633.
PR
XX 07-JUN-1995; 95US-00487748.
PR
XX 01-MAR-1996; 96US-00609583.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Levinson DA;
PI
XX
XX

```

```

DR WPI; 2000-464385/40.
XX
XX New isolated human 200 gene products or polypeptides, useful for treating
PT and diagnosing immune disorders, especially T helper lymphocyte-related
PT disorders.
XX
XX Example; Col 91; 107pp; English.
XX
XX Genes which are differentially expressed within and among T helper (TH)
CC cells and TH cell subpopulations, e.g. TH0, TH1 and TH2 subpopulations,
CC can be used diagnostically or as targets for therapeutic intervention.
CC The polypeptides are useful for treating and diagnosing of immune
CC disorders, especially T lymphocyte-related disorders. These disorders
CC include chronic inflammatory diseases and disorders (e.g. Crohn's
CC disease, reactive arthritis, Lyme disease, Hashimoto's thyroiditis or
CC Grave's disease), or atopic conditions (e.g. asthma and allergy.
CC including allergic rhinitis or food allergies). Also included are certain
CC pathogen susceptibilities (e.g. leishmaniasis), and viral (e.g. HIV) or
CC bacterial (e.g. tuberculosis or lepromatous leprosy) infections
XX
XX Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
SQ
Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 6 TCCAGGTAGGCGAGCTTGTGACGC 29
Db 40 TGCAGGTGTGCAGACTTGGGATCC 17
RESULT 38
AAT03383/C
ID AAT03383 standard; DNA; 44 BP.
XX
XX AAT03383;
AC
XX 13-JUN-2001 (first entry)
DT
XX 3' primer, to amplify long form of murine 103 gene.
DE
XX
XX 103 gene; immune disorder; T helper lymphocyte 2 related disorder; TH2;
KW ST2; T1; Fit-1; therapy; asthma; allergy; IgE; IL-4; antiviral;
KW immunoglobulin E mediated condition; interleukin-4 mediated condition;
KW Crohn's disease; arthritis; insulin-dependent diabetes; antihelminthic;
KW multiple sclerosis; Hashimoto's thyroiditis; Grave's disease;
KW contact dermatitis; psoriasis; allergic rhinitis; conjunctivitis;
KW glomerular nephritis; systemic lupus erythematosus; eosinophilia;
KW neuroprotective; ophthalmological; antibacterial; immunosuppressive;
KW sarcoidosis; scleroderma; murine; PCR primer; ss.
XX
XX Mus musculus.
OS
XX WO200121641-A1.
PN
XX 29-MAR-2001.
PD
XX 25-SEP-2000; 2000WO-US026555.
PF
XX 24-SEP-1999; 99US-0155862P.
PR
XX 28-APR-2000; 2000US-00560639.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Leiby KR, Kingsbury GA;
PI
XX WPI; 2001-211462/21.
DR
XX New 103 gene products and immunospecific antibodies, useful for the
PT diagnosis and treatment of T helper lymphocyte 2 (like) related immune
PT disorders e.g. asthma, allergy, immunoglobulin E and interleukin-4
PT mediated conditions.
XX

```

PS Example; Page 112; 197pp; English.

CC The invention relates to methods and compositions for treatment and

CC diagnosis of immune disorders, especially T lymphocyte-related disorders.

CC The methods and compositions of the present invention particularly

CC relates to detection and/or modulation of expression and/or activity of

CC 103 gene. This gene is alternatively referred as ST2, T1 and Fit-1 and is

CC differentially expressed in T helper lymphocyte 2 (TH2) cells. Antibodies

CC specific for 103 gene are useful for the treatment and prevention of

CC immune disorders in humans, preferably TH2 related disorders, such as

CC asthma, allergy, immunoglobulin E (IgE) mediated conditions and

CC interleukin-4 (IL-4) mediated conditions. Modulators of 103 gene such as

CC antibodies, ribozymes, antisense oligonucleotides and peptides are useful

CC for the treatment and diagnosis of immune disorders such as Crohn's

CC disease, arthritis, insulin-dependent diabetes, multiple sclerosis,

CC Hashimoto's thyroiditis, Grave's disease, graft rejection, contact

CC dermatitis, psoriasis, allergic rhinitis, conjunctivitis, graft- versus-

CC host disease, glomerular nephritis, sarcoidosis, eosinophilia, systemic

CC lupus erythematosus, scleroderma and helminthic (e.g leishmaniasis),

CC viral and bacterial infections (e.g. tuberculosis and lepromatous

CC leprosy). The present sequence is 3' primer used to amplify long form of

CC murine 103 gene

XX

SQ Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 4; Length 44;

Best Local Similarity 75.0%; Pred. No. 1.5e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTTCAGCC 29

DB 40 TGCAGGTGTCAGACTTGGATCC 17

RESULT 39

AAC92152/c

ID AAC92152 standard; DNA; 44 BP.

XX AAC92152;

AC AAC92152;

XX

DT 20-MAR-2001 (first entry)

XX

DE Mouse 103 gene PCR primer SEQ ID NO:34.

XX

XX Treatment; diagnosis; immune disorder; mast cell related disorder;

KW T-helper lymphocyte-related disorder; ischaemic disorder; identification;

KW vasodilator; cardiac; antidiagonal; angina pectoris;

KW ischaemic renal disease; myocardial ischaemia; myocardial infarction;

KW cortical infarction; ischaemic injury; kidney transplant; PCR primer; ss.

XX

OS Mus musculus.

XX

XX WO200073498-A1.

PN

XX

XX 07-DEC-2000.

PD

XX

XX 31-MAY-2000; 2000WO-US014986.

EF

XX

XX 02-JUN-1999; 99US-00324986.

PR

XX

XX (MILL-) MILLENNIUM PHARM INC.

PA

XX

XX Levinson DA, Lloyd CM, McCarthy SA;

PI

XX

XX WPI; 2001-016510/02.

DR

XX

XX Ameliorating a symptom of an ischemic disorder or injury in a mammal e.g.

PT ischemic renal disease or myocardial ischemia, by administering a 200

PT gene product (S1), a nucleic acid encoding (S1) or an antibody directed

PT against (S1).

XX

XX Example 6; Page 190; 309pp; English.

PS

XX

CC The present invention describes a method for ameliorating a symptom of an

CC ischaemic disorder or injury in a mammal. The method comprises

CC administering a 200 gene product, a nucleic acid encoding (S1) or an

CC antibody directed against (S1). The method is useful for treating a

CC symptom of an ischaemic disorder such as ischaemic renal disease or

CC myocardial ischaemia (such as angina pectoris), myocardial or cortical

CC infarction. The method is also useful for treating a symptom of an

CC ischaemic injury occurring due to transplantation of a kidney. The

CC present sequence represents a PCR primer which is used in the

CC exemplification of the present invention

XX

SQ Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 4; Length 44;

Best Local Similarity 75.0%; Pred. No. 1.5e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTTCAGCC 29

DB 40 TGCAGGTGTCAGACTTGGATCC 17

RESULT 40

AAF23475/c

ID AAF23475 standard; DNA; 44 BP.

XX AAF23475;

AC AAF23475;

XX

DT 21-MAR-2001 (first entry)

XX

XX 3' oligonucleotide used in construction of 103 gene clone.

XX

KW Cysteine protease; immune disorder; T lymphocyte; Crohn's; arthritis;

KW diabetes; multiple sclerosis; viral infection; bacterial; HIV; ds.

XX

XX Unidentified.

OS

XX

XX US6156887-A.

PN

XX

XX 05-DEC-2000.

PD

XX

XX 03-OCT-1997; 97US-00939729.

PF

XX

XX 03-MAR-1995; 95US-00398633.

PR

XX

XX 07-JUN-1995; 95US-00487748.

PR

XX

XX 01-MAR-1996; 96US-00609583.

XX

XX (MILL-) MILLENNIUM PHARM INC.

PA

XX

XX Levinson DA;

PI

XX

XX WPI; 2001-101473/11.

DR

XX

XX Novel polypeptide exhibiting cysteine protease activity, useful for

PT treating and diagnosing immune disorders, especially T lymphocyte-related

PT disorders, e.g. Crohn's disease, multiple sclerosis, graft versus host

PT disease or allergies.

XX

XX Example; Col 93; 107pp; English.

PS

XX

XX The present invention relates to a novel cysteine protease. The protein

CC of the invention is useful for treating and diagnosing immune disorders,

CC especially T lymphocyte-related disorders. In particular, the polypeptide

CC is useful for treating or diagnosing T helper (TH) cell or TH cell

CC subpopulation-related disorders. These disorders include Crohn's disease,

CC reactive arthritis, Lyme disease, insulin-dependent diabetes, organ-

CC specific autoimmunity, multiple sclerosis, Hashimoto's thyroiditis,

CC Grave's disease, contact dermatitis, psoriasis, graft rejection, graft

CC versus host disease, sarcoidosis, atopic (e.g. asthma or allergy),

CC eosinophilia, conjunctivitis, glomerular nephritis, or helminthic (e.g.

CC leishmaniasis), viral (e.g. HIV (human immunodeficiency virus)) or

CC bacterial (e.g. tuberculosis or lepromatous leprosy) infections

XX

Query Match	48.0%;	Score 14.4;	DB 4;	Length 44;
Best Local Similarity	75.0%;	Pred. No. 1.5e+04;		

Best Local Similarity 75.0%; Fied. NO. 1.5e+04;
Matches 18; Conservative 0; Mismatches 6;

100% Local Similarity 75.0%; Freq. NO. 1.3E+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

6 TCCAGGTAGGCAGACTTGTGAGCC 29
| | | | |
40 TGCAGGTGTGCAGACTTGGATCC 17

Search completed: November 18, 2005, 11:52:20
Job time : 209.578 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1434.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-2

Perfect score: 30

Sequence: 1 GCGATCCAGGTAGGACAGCTTGTCAGCCT 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700.residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gssi:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	16	53.3	45	9	CL212784
2	15.2	50.7	45	8	AZ331000
3	14.8	49.3	39	1	AJ428912
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5	14.6	48.7	31	9	EX662359
6	14.6	48.7	46	9	CG784706
7	14.4	48.0	34	1	AA996291
8	14.4	48.0	38	9	CL522268
9	14.4	48.0	46	1	AA836932
10	14.4	48.0	50	1	AU103386
11	14	46.7	49	1	A1312023
12	13.8	46.0	29	8	AZ441837
13	13.8	46.0	31	9	TA21H09P
14	13.8	46.0	40	4	BG431777
15	13.8	46.0	43	8	CC325528
16	13.6	45.3	32	8	AZ303920
17	13.6	45.3	43	9	AL953049
18	13.6	45.3	50	1	AU103363
19	13.4	44.7	33	8	AZ352257
20	13.4	44.7	39	9	CL302526
21	13.4	44.7	50	8	AZ920008
22	13.2	44.0	45	8	BZ764481
23	13.2	44.0	48	5	BU582005
24	13.2	44.0	50	1	AU104377

C	25	13.2	44.0	50	1	AU107676
	26	13.2	44.0	50	9	CR127702
	27	13	43.3	36	9	DR43H15T
	28	13	43.3	39	8	CC057135
C	29	13	43.3	45	8	BH857661
	30	13	43.3	46	1	AA932841
C	31	13	43.3	49	1	AI185949
	32	13	43.3	50	1	AU107828
	33	13	43.3	50	1	AU107829
C	34	13	43.3	50	8	BZ586756
	35	12.8	42.7	27	1	AU260098
	36	12.8	42.7	28	9	AJ622435
C	37	12.8	42.7	37	4	BI080927
	38	12.8	42.7	43	7	H40051
C	39	12.8	42.7	49	9	EX948677
	40	12.8	42.7	50	1	AU102393
C	41	12.8	42.7	50	2	AU104419
	42	12.8	42.7	50	2	AW507256
C	43	12.8	42.7	50	2	AW507292
	44	12.8	42.7	50	9	EX893038
C	45	12.6	42.0	24	8	AZ437757

ALIGNMENTS

RESULT 1
CL212784
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

CL212784
G050F11 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
G050F11, mRNA sequence.
CL212784
CL212784.2 GI:49489438
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,
Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
22810117
12904583
On Jun 30, 2004 this sequence version replaced gi:40729685.
Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
U3CRO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=G050F11', ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'
1' Inhouse Sequence Identifier: 16659
Class: Gene trap.

FEATURES
source

Location/Qualifiers
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/sex="Male"
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/cell_line="ES cells [C57BL/6J x 129SvEvTac] F1"
/clone_lib="GGTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"

ORIGIN

Query Match 53.3%; Score 16; DB 9; Length 45;

AUTHORS
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/, Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)

FEATURES
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1..25
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ORIGIN

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 Best Local Similarity 81.0%; Pred. No. 1.4e+05;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGACGACT 21
 |||||
 Db 5 GCGGATCCAGGTAGGACGACT 25

RESULT 5
 BX662359/c

LOCUS BX662359 31 bp DNA linear GSS 05-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-688E05-023078, genomic survey sequence.

ACCESSION BX662359
VERSION BX662359.1 GI:37618781

KEYWORDS

SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS Li, X., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060

REFERENCE

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321

REFERENCE

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

TITLE BioTechniques 35 (6), 1164-1168 (2003)
JOURNAL 14682050

REFERENCE

PUBMED 4 (bases 1 to 31)
AUTHORS Rosso, M.G., Li, Y., Strizhov, N. and Weishaar, B.
TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T13b4. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the

MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
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 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ517514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 48.7%; Score 14.6; DB 9; Length 31;
 Best Local Similarity 69.0%; Pred. No. 1.4e+05;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGACGACTTCTCAGCCT 30
 |||||
 Db 31 CGGAACCATAAACCAGATTATCAGCGT 3

RESULT 6

LOCUS CG784706

DEFINITION RRR527 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA, mRNA sequence.
 CG784706 46 bp mRNA linear GSS 16-JUN-2004

ACCESSION CG784706

VERSION CG784706.1 GI:38157266

KEYWORDS

SOURCE GSS.
ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 46)

REFERENCE

AUTHORS BayGenomics.
TITLE http://baygenomics.ucsf.edu/
JOURNAL Unpublished (2001)
COMMENT Contact: BayGenomics

Bay Area Functional Genomics Consortium (BayGenomics)
 Email: info@baygenomics.ucsf.edu

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from
 http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL.LINES&KEY=RRR527
 Class: Gene Trap.

FEATURES
 source

1..46
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 ola"
 /db_xref="taxon:10090"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
 /note="Vector: pGT0Lxf"

ORIGIN

Query Match 48.7%; Score 14.6; DB 9; Length 46;
 Best Local Similarity 69.0%; Pred. No. 1.5e+05;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Email: cgabs-r@mail.nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Prepared by: Stratagene, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Cloned distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 589 Std Error: 0.00
 Seq primer: -40ml3 fwd. 5T from Amersham
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1..46
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:142320"
 /sex="mixed"
 /tissue_type="kidney tumor"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="NCI CGAP Kid6"
 /note="Organ: Kidney; Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Pooled kidney tumors. 5' adaptor sequence: 5' GAATTCGCGACGAG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."

ORIGIN

Query Match 48.0%; Score 14.4; DB 1; Length 46;
 Best Local Similarity 75.0%; Pred. No. 1.8e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GATCCAGGTAGGAGACTTGTTCAG 27

DB 33 GAACCTGGGAGCGCAGGTTTCAG 10

RESULT 10

AU103386/c
 LOCUS AU103386 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION CAS11861, mRNA sequence.

ACCESSION AU103386

VERSION AU103386.1 GI:13552907

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese,J.,

Hata.H., Ota.T., Isoqai.T., Tanaka.T., Morishita,S., Okubo,K.,

Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

CONTACT: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and

Sugano,S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

FEATURES

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CAS11861"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 48.0%; Score 14.4; DB 1; Length 50;
 Best Local Similarity 93.8%; Pred. No. 1.8e+05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAG 18

DB 33 GGGTCAGGTAGGCAG 18

RESULT 11

AU1312023/c

LOCUS AU1312023

DEFINITION qp78b08.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone

IMAGE:1929111 3', similar to Tr:Q60980 Q60980 BASIC KRUPPEL-LIKE

FACTOR ; mRNA sequence.

ACCESSION AU1312023

VERSION AU1312023.1 GI:4017628

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

This clone is available royalty-free through LINL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1440 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..49

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1929111"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal lung NBHL19W"

/note="Organ: lung; Vector: p773D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer

[5'-TGTTCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified p773 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. This library was constructed

from the same fetus as the fetal heart library, Soares

fetal heart NBHL19W."

ORIGIN

Query Match 46.7%; Score 14; DB 1; Length 49;

Best Local Similarity 77.3%; Pred. No. 2.7e+05;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTTCAGCCT 30

DB 45 ATGCGCCATACCTTGTTCAGCCT 24

```

RESULT 12
AZ441837/c
LOCUS
DEFINITION
29 bp DNA linear GSS 03-OCT-2000
1M0234007F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0234007 F, genomic survey sequence.

ACCESSION
A2441837
VERSION
A2441837.1 GI:10565950
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0234 row: 0 column: 07
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 29.

FEATURES
Location/Qualifiers
1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0234007"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 46.0%; Score 13.8; DB 8; Length 29;
Best Local Similarity 72.0%; Pred. No. 3e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CGGATCCAGTAGGCAGACTTGCTCA 26
| | | | | | | | | | | | | | | | | |
Db 26 CTGATTTCAGACATTCAGAGTTGTCA 2

RESULT 13
TA21H09P
LOCUS
DEFINITION
31 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 21h09, forward sequence,
genomic survey sequence.

ACCESSION
AL454798
VERSION
AL454798.1 GI:11844296
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 31)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
Location/Qualifiers
1..31
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="21h09"

ORIGIN
Query Match 46.0%; Score 13.8; DB 9; Length 31;
Best Local Similarity 72.0%; Pred. No. 3.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 6 TCCAGGTAGGCAGACTTGTCAGCCT 30
| | | | | | | | | | | | | | | | | |
Db 1 TACTGGAAGCGAGACTTGTCACAT 25

RESULT 14
BG431777/c
LOCUS
DEFINITION
602499583F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613012 5',
mRNA sequence.

ACCESSION
BG431777
VERSION
BG431777.1 GI:13338283
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics Inc.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLC1362 row: f column: 21

High quality sequence stop: 40.

FEATURES

Location/Qualifiers

1..40

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4613012"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_75"

/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgcctggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity 46.0%; Score 13.8; DB 4; Length 40;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY

2 CGGATCCAGGTAGGCAGCTTGTCA 26

DB

34 CGCATCCGGGTAGGCACCAATCCA 10

RESULT 15

CC32528/c

LOCUS

DEFINITION

TEA007 BayGenomics Gene Trap Library pGTILxf Mus musculus cDNA,

mRNA sequence.

ACCESSION

CC32528

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 43)

BayGenomics.

http://baygenomics.ucsf.edu/

Unpublished (2001)

Contact: BayGenomics

Bay Area Functional Genomics Consortium (BayGenomics)

Email: info@baygenomics.ucsf.edu

Sequence tag generated by 5' RACE of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from BayGenomics. Annotation

information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=TEA007

Class: Gene trap.

Location/Qualifiers

1..43

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129 ola"

/db_xref="taxon:10090"

/sex="Male"

/cell_type="Embryonic stem cell"

/clone_lib="BayGenomics Gene Trap Library pGTILxf"

/note="Vector: pGTILxf"

ORIGIN

Query Match

46.0%; Score 13.8; DB 8; Length 43;

Best Local Similarity 88.2%; Pred. No. 3.2e+05;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

6 TCCAGGTAGGCAGCTT 22

DB

39 TCCCGTATGCAGACTT 23

RESULT 16

AZ303920/c

LOCUS

DEFINITION

IM0003F19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0003F19 R, genomic survey sequence.

ACCESSION

AZ303920

VERSION

AZ303920.1

KEYWORDS

GSS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 32)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0003 row: F column: 19

Seg primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

1..32

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0003F19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 [gi4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match

45.3%; Score 13.6; DB 8; Length 32;

Best Local Similarity 80.0%; Pred. No. 3.7e+05; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTT 22
|||||
Db 30 GGACCCAGGTGAGAGACTT 11

RESULT 17
AL953049/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-348B03-016247,
DEFINITION genomic survey sequence.

ACCESSION AL953049
VERSION AL953049.1 GI:24409671

KEYWORDS
SOURCE
ORGANISM

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weissshaar, B.

GABI-Kat SimpleSearch: a flanking sequence tag (EST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829

PUBMED 12874060

REFERENCE

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

Weissshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse Genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE 23117147

PUBMED 14756321

REFERENCE

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and

Weissshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA

JOURNAL mutagenized Arabidopsis thaliana lines

PUBMED 14692050

REFERENCE 4 (bases 1 to 43)

AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weissshaar, B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
F23H6. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

COMMENT

FEATURES
source

1..43

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-348B03-016247"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 45.3%; Score 13.6; DB 9; Length 43;
Best Local Similarity 67.9%; Pred. No. 3.9e+05;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTGCAGC 28

|||||

Db 34 GAGCAATCAGATACGCAGCCCTGTCTATC 7

RESULT 18

AUI03363

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Yutaka Suzuki

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

FEATURES

source

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HBMA0059"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 45.3%; Score 13.6; DB 1; Length 50;

Best Local Similarity 80.0%; Pred. No. 4e+05;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTCTC 25

|||||

Db 18 TCCACACAGGCAGACTTGAC 37

RESULT 19

AZ352257/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AZ352257 33 bp DNA linear GSS 29-SEP-2000
IM0090G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0090G11 R, genomic survey sequence.

AZ352257

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

GSS. Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 33)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0090 row: G column: 11
 Seq primer: CACACAGGAAACAGTATGACC
 Class: plasmid ends
 High quality sequence stop: 33.

FEATURES

source
 1. .33
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0090G11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number: inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.7%; Score 13.4; DB 8; Length 33;
 Best Local Similarity 73.9%; Pred. No. 4.6e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 TCCAGGTAGGCAGACTTGTGCAGC 28
 ||||| ||||| ||||| |||||
 Db 28 TCCAGGGAGACAGACTCTCGCAGC 6

RESULT 20

CL302526
 LOCUS G061A09 GQTC Gene Trap Library GV07C05 Mus musculus cDNA clone
 DEFINITION G061A09, mRNA sequence.
 ACCESSION CL302526
 VERSION CL302526.2 GI:49489458
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 39)
 AUTHORS Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,

TITLE

JOURNAL MEDLINE
 PUBMED
 COMMENT

Arnold, H.H., Schmutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
 A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
 22810117
 12904583
 On Jun 30, 2004 this sequence version replaced gi:42743355.
 Contact: GGTC
 German Genetrap Consortium (GGTC)
 Email: info@genetrap.de
 U3CEO gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
 'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=G061A09'. ES cell line harboring insertion mutation of target gene is available at:
 'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm 1' Inhouse Sequence Identifier: 18060
 Class: Gene Trap.

FEATURES

Location/Qualifiers
 1. .39
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 Sv"
 /db_xref="taxon:10090"
 /clone="G061A09"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /cell_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"
 /clone_lib="GGTC Gene Trap Library GV07C05"
 /note="Vector: U3CEO"

ORIGIN

Query Match 44.7%; Score 13.4; DB 9; Length 39;
 Best Local Similarity 65.4%; Pred. No. 4.7e+05;
 Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTGCAGCCT 30
 ||||| ||||| ||||| |||||
 Db 13 ATCCAGGTATGCAGANNNTCAGGCT 38

RESULT 21

AZ920008/c
 LOCUS 1006017F11.y1 1006 - RescueMu Grid G Zea mays genomic, genomic survey sequence.
 DEFINITION

ACCESSION AZ920008
 VERSION AZ920008.1 GI:13390291
 KEYWORDS GSS.
 SOURCE Zea mays

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 50)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon
 Walbot, V.
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 1006017 row: 37
 Class: transposon-tagged.
 Location/Qualifiers
 1. .50
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"

FEATURES

source

/tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1006 - RescueMu Grid G"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 44.7%; Score 13.4; DB 8; Length 50;
 Best Local Similarity 73.9%; Pred. No. 4.8e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CCAGGTAGGCAGACTTGTCCAGCC 29
 ||||| ||||| ||||| ||||| |||||
 Db 47 CCAGCCACCCAGCCTTGTCCGCC 25

RESULT 22

BZ764481

LOCUS

DEFINITION SALX 124922.26.85.x Arabidopsis thaliana DNA T2NA insertion lines
 Arabidopsis thaliana genomic clone SALX_124922.26.85.x, genomic survey sequence.

ACCESSION BZ764481

VERSION BZ764481.1 GI:28937034

KEYWORDS GSS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.

1 (bases 1 to 45)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel.: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckergsalk.edu

This is single pass sequence recovered from the left border of T2NA. This sequence lies within 300 bases of the 5' end of At2g20721 and 300 bases of the 3' end of At2g20723.

Class: T2NA tagged.

FEATURES

source

1..45

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK 124922.26.85.x"

/clone_lib="Arabidopsis thaliana T2NA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more T2NA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/t2na_protocols.html"

ORIGIN

Query Match 44.0%; Score 13.2; DB 8; Length 45;
 Best Local Similarity 69.2%; Pred. No. 5.8e+05;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTCCAGCCT 30

||| ||||| ||||| ||||| |||||

Db 1 AACAAATGTAGGCAGAAATTGAATCCT 26

RESULT 23

BZ582005/c

LOCUS

DEFINITION BZ582005 48 bp mRNA linear EST 18-SEP-2002
 Oryctolagus cuniculus adult subtractive hybridization library
 Oryctolagus cuniculus cDNA, mRNA sequence.

ACCESSION BZ582005.1 GI:23186905

VERSION EST.

KEYWORDS Oryctolagus cuniculus (rabbit)

SOURCE Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 48)

Zhang,B., Wang,Z. and Zhu,P.

Cloning and identification of injury-related gene(s) in the process

of fetal rabbit skin healing

Unpublished (2002)

Contact: Zhang Bo

Department 4

Research Institute of surgery

Changjiangzhi 10, Chongqing, P.R.China., 400042

Tel: 86-23-68757444

Fax: 86-23-68819750

Email: john.power1201@hotmail.com.

Location/Qualifiers

1..48

/organism="Oryctolagus cuniculus"

/mol_type="mRNA"

/db_xref="taxon:9986"

/sex="female"

/tissue_type="skin"

/dev_stage="adult"

/lab_host="E.coli HB101"

/clone_lib="Oryctolagus cuniculus adult subtractive

hybridization library"

/note="Vector: pUCm-T; inserts-subtractive hybridization

and PCR products"

ORIGIN

Query Match 44.0%; Score 13.2; DB 5; Length 48;
 Best Local Similarity 69.2%; Pred. No. 5.8e+05;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGCAGACTTGTCCAGC 28

||||| ||||| ||||| ||||| |||||

Db 42 GGATCCAGACTTCCAGTCTTTCGAGC 17

RESULT 24

AUI04377

LOCUS

DEFINITION AUI04377 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HEP21718, mRNA sequence.

ACCESSION AUI04377

VERSION AUI04377.1 GI:13553898

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL
MEDLINE
PUBMED
COMMENT

21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source

Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP21718"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 5.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGATCCAGTAGGACAGCTTGTGCAG 28
|||||
DB 11 GGAGCCAGGTCGTATAGCGCCAGC 36

RESULT 25
LOCUS

AU107676 50 bp mRNA linear EST 28-JAN-2004
AU107676 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP21286, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AU107676.1 GI:13557197
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL
MEDLINE
PUBMED
COMMENT

21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source

Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP21286"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 5.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGACAGACTTGTCTCAG 27
|||||
DB 32 CGCAACCGGTAGTCGGCTTCTCAG 7

RESULT 26
LOCUS

CR127702 50 bp DNA linear GSS 06-JUL-2004
CR127702 Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP408a08, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CR127702.1 GI:49875154
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Rogers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,

REFERENCE
AUTHORS

Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>

TITLE
JOURNAL

Location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP408a08"
/clone_lib="MHPP"

FEATURES
source

ORIGIN

Query Match 44.0%; Score 13.2; DB 9; Length 50;
Best Local Similarity 69.2%; Pred. No. 5.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGACAGACTTGTCTCAG 27
|||||
DB 5 CGGATCAAGAAACAGACTTCAAAG 30

RESULT 27
LOCUS

DR43H15T 36 bp DNA linear GSS 22-NOV-2002
DR43H15T Danio rerio genomic clone DKEY-43H15, genomic survey sequence.

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL981997.1 GI:25184424
GSS.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 36)
Humphray,S.J., Huckle,E. and Hunt,S.E.
Direct Submission

REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphray@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 43H15. 43H15 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

COMMENT

Location/Qualifiers
1..36
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"

FEATURES
source


```

/clone="DKEY-43H15"
/tissue_type="Testis"
/note="Vector pIndigoBAC-53c"

ORIGIN
Query Match      43.3%; Score 13; DB 9; Length 36;
Best Local Similarity 76.2%; Pred. No. 6.8e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TCCAGGTAGGCAGACTTGTCTCA 26
Db 14 TGCAGGCATGCAAGCTTGTCTCA 34

RESULT 28
CC057135
LOCUS
DEFINITION SALK_111730.14.10.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_111730.14.10.n, genomic
survey sequence.
GSS.
Arabisopsis thaliana (thale cress)
Arabisopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 39)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of AC5948010.
Class: TDNA tagged.
Location/Qualifiers
1..39
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="SALK_111730.14.10.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES
source
1..39
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="SALK_111730.14.10.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      43.3%; Score 13; DB 8; Length 39;
Best Local Similarity 76.2%; Pred. No. 6.9e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGCAGACT 21
Db 18 GCCAATACAGGAGGAGAGT 38

RESULT 29
BH857661/c
LOCUS
DEFINITION SALK_016405.53.70.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_016405.53.70.x, genomic
survey sequence.
GSS.
Arabisopsis thaliana (thale cress)
Arabisopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 45)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At1g10190.
Class: TDNA tagged.
Location/Qualifiers
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_016405.53.70.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      43.3%; Score 13; DB 8; Length 45;
Best Local Similarity 76.2%; Pred. No. 7e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 9 AGGTAGGCAGACTTGTCTAGCC 29
Db 31 AAGTAGACATACACTTATTAGCC 11

RESULT 30
AA932841
LOCUS
DEFINITION O057a07.s1 NCI_CGAP Lu5 Homo sapiens cDNA clone IMAGE:1570260 3'
similar to SW:ASH1_HUMAN P50553 ACHAETE-SCUTE HOMOLOG 1. i, mRNA
sequence.
AA932841
VERSION AA932841.1 GI:3086806
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

```


Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation by: Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert length: 1206 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

```
1. .46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1570260"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP LuS"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
```

ORIGIN

```
Query Match 43.3%; Score 13; DB 1; Length 46;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTC 25
Db 23 ATCCATCTTGGCAGACTCTTC 43

RESULT 31
A1185949/c
LOCUS
DEFINITION
A1185949 49 bp mRNA linear EST 29-OCT-1998
IMAGE:1740390 3' similar to S:RL2B_HUMAN P29316 60S RIBOSOMAL
PROTEIN L23A. ; mRNA sequence.

ACCESSION A1185949
VERSION A1185949.1 GI:3736587
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 360 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
```

FEATURES

source

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1. .49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```

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/clone="IMAGE:1740390"
/dev stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung_NDHL19W"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NDHL19W."
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ORIGIN

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Query Match 43.3%; Score 13; DB 1; Length 49;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 7 CCAGGTAGGCAGACTTGTCAG 27
Db 39 CCAGAGGCGCAGTGTGTAAG 19

RESULT 32
A1107828
LOCUS
DEFINITION
A1107828 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAE00112, mRNA sequence.

ACCESSION A1107828
VERSION A1107828.1 GI:13557350
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
145-156 (1997)
```

FEATURES

source

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1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAE00112"
/clone_lib="Sugano Homo sapiens cDNA library"
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ORIGIN

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Query Match 43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGCAGACT 21
Db 23 GCGGATCGGGAAGCCGACT 43
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RESULT	33
AUI07829	
LOCUS	50 bp mRNA linear EST 28-JAN-2004
DEFINITION	Sugano Homo sapiens cDNA library Homo sapiens cDNA clone ZR61043, mRNA sequence.
ACCESSION	AUI07829
VERSION	AUI07829.1 GI:13557351
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 50)
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano.S.
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE	21270072
PUBMED	11375929
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2).

Y. Ito, S. Murakami, K. Minakawa, Tokyo 106-8039, Japan
Email: yszuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

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FEATURES
source
1.50
Location/Qualifiers
/organism="Homo sapiens"
/mol type="mRNA"

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ORIGIN
Query Match          43.3%;   Score 13;   DB 1;   Length 50;
Best Local Similarity 76.2%;   Pred. No. 7.1e+05;
/db_xref=taxon:9606"
/clone="ZRV61043"
/clone_lib="Sugano Homo sapiens cDNA library"

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	Matches	16;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps
Qy	1	CGCGATCCAGGTAGGCAGACT	21						
Db	26	CGCGATCGGGAGCCGGACT	46						

RESULT_34	BZ586756	50 bp	DNA	linear	GSS 17-DEC-2002
LOCUS	BZ586756/c	3590_1_20_1_G08.2EL_Y_1	3590 - RescueMu	Grid M Zea	mays genomic,
DEFINITION		genomic survey sequence.			
ACCESSION	BZ586756				
VERSION	BZ586756.1	GI:27221817			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 50)	Walbot, V.	Maize genomic sequences found using engineered RescueMu transposon	Unpublished (2001)	Contact: Walbot V
clade; Panicoidae; Andropogoneae; Zea.				Department of Biological Sciences Stanford University

855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

```

Best Local Similarity 70.8%; Pred. No. 8e+05; 7; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GATCCAGGTAGGCGACTTGTCTAG 27
Db 1 GATCCAGGAAGAAGCCTTATTAG 24

RESULT 36
AJ622435 28 bp DNA linear GSS 28-JAN-2004
LOCUS Drosophila melanogaster flanking sequence of RS P element insertion
DEFINITION P[RS]5-HA-2412, clone library P[RS5], genomic survey sequence.
ACCESSION AJ622435
VERSION 1 GI:41366647
KEYWORDS GSS; genome survey sequence.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1
AUTHORS Ryder, E.J., Ashburner, M., Bagunya, J., Blows, P., Bucheton, A.,
Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N.,
Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P.,
Mechler, B., O'Kane, C., Pflugfelder, G., Rasmuson-Lestander, A.,
Reuter, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and
Russell, S.
TITLE Mapping of RS P element insertions in Drosophila melanogaster for
the DrosDel second generation deficiency kit
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 28)
AUTHORS Ryder, E.J.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2004) Ryder E.J., Department of Genetics,
University Of Cambridge, Downing Street, CB23EH, UNITED KINGDOM
COMMENT The insertion point of the P element is before base 1 of the
sequence. Further information about this P element insertion line
can be found at http://www.flyseq.org.uk and
http://www.drosdel.org.uk.
FEATURES
source
1..28
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="2L"
/clone="P[RS5]5-HA-2412"
/clone_lib="P[RS5]"
/note="read=5' end"
misc_feature 1..28
/note="P element insertion in the 3' to 5' orientation"
ORIGIN
Query Match 42.7%; Score 12.8; DB 9; Length 28;
Best Local Similarity 87.5%; Pred. No. 8e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 15 GCAGACTTGTGACGCT 30
Db 3 GCAGACTTGTCCGACT 18

RESULT 37
BI080927/c 37 bp mRNA linear EST 20-JUN-2001
LOCUS 602878838F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5010561 5',
DEFINITION mRNA sequence.
ACCESSION BI080927
VERSION 1 GI:14499257
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing By: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1058 row: k column: 10
High quality sequence stop: 37.
FEATURES
Location/Qualifiers
1..37
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5010561"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH108"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
ORIGIN
Query Match 42.7%; Score 12.8; DB 4; Length 37;
Best Local Similarity 70.8%; Pred. No. 8.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 6 TCCAGGTAGGCGACTTGTCTAGCC 29
Db 25 TCCAGGTCTCTCCGCATGTCAGCC 2

RESULT 38
H40051/c 43 bp mRNA linear EST 31-JUL-1995
LOCUS Y144d10.r1 Soares breast 3NDH8st Homo sapiens cDNA clone
DEFINITION IMAGE:161107 5' similar to SP:S29539 S29539 BASIC PROTEIN, 23K - ;,
mRNA sequence.
ACCESSION H40051
VERSION 1 GI:916103
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Riffin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
CONTACT: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 910
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL

```

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 910 Std Error: 0.00
Seq primer: M13Rev
High quality sequence stop: 1.

FEATURES

Location/Qualifiers
1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:575217"
/db_xref="taxon:9606"
/clone="IMAGE:161107"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NBH8et"
/note="Organ: breast; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 42.7%; Score 12.8; DB 7; Length 43;
Best Local Similarity 87.5%; Pred. No. 8.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CCAGGTAGGCAGACTT 22
|||||
Db 41 CCAGATAGGCAGACTT 26

RESULT 39

BX948677/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-792A06-025017, genomic survey sequence.

ACCESSION
BX948677.1 GI:42598363

VERSION
GSS.

KEYWORDS
Arabidopsis thaliana (thale cress)

SOURCE

ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

1
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P., and Weisshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

JOURNAL

Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE

22755829

PUBMED

12874060

REFERENCE

2
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.

TITLE

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL

Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE

23117147

PUBMED

14756321

REFERENCE

3
Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weisshaar,B.

TITLE

High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL

PUBMED

14682050

REFERENCE

4 (bases 1 to 49)

AUTHORS

Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.

TITLE

Direct Submision

JOURNAL

Submitted (31-MAR-2004)

Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T20F20. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

Location/Qualifiers

1. .49

source

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-792A06-025017"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 42.7%; Score 12.8; DB 9; Length 49;

Best Local Similarity 70.8%; Pred. No. 8.7e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTTGTCA 26

|||||

Db 31 GGTACAGATATGCATGTTGTCA 8

RESULT 40

AU102393/c

LOCUS

DEFINITION

Sugano Homo sapiens cDNA library Homo sapiens cDNA clone COLF4942, mRNA sequence.

ACCESSION

AU102393

VERSION

AU102393.1 GI:13551913

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

REFERENCE

AUTHORS

Suzuki,Y., Tsura,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

21270072

MEDLINE

11375929

PUBMED

11375929

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Location/Qualifiers

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source      1..50
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="COLP4942"
            /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match : 42.7%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 8.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      4 GATCCAGGTAGGCAGACTTGTTCAG 27
      |||||
Db      33 GAACCTGGAAGGCAGAGGCTTCAG 10

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Search completed: November 18, 2005, 21:12:37
 Job time : 1437.98 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 58.289 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-2

Perfect score: 30

Sequence: 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1	US-07-989-160-2
2	16	53.3	25	4	US-09-396-196G-80578
3	15.6	52.0	41	2	US-08-244-548-14
4	15.6	52.0	41	4	US-09-213-993-14
5	15.6	52.0	45	3	US-09-109-063-26
6	15.6	52.0	45	4	US-09-448-310-26
7	15.6	52.0	45	4	US-09-884-948-26
8	15.6	52.0	45	4	US-09-892-864A-25
9	15.6	52.0	50	3	US-09-109-063-27
10	15.6	52.0	50	4	US-09-448-310-27
11	15.6	52.0	50	4	US-09-884-948-27
12	15.6	52.0	50	4	US-09-892-864A-26
13	15.2	50.7	42	4	US-09-635-132-10
14	15	50.0	29	4	US-09-786-025A-5
15	14.8	49.3	25	3	US-08-963-121C-20
16	14.8	49.3	25	4	US-09-543-513-20
17	14.8	49.3	25	4	US-09-396-196G-6441
18	14.8	49.3	25	5	PCT-US95-04803-21
19	14.8	49.3	37	3	US-08-992-877-68
20	14.6	48.7	25	4	US-09-396-196G-15342
21	14.6	48.7	25	4	US-09-396-196G-18196
22	14.6	48.7	31	3	US-08-858-111-14
23	14.4	48.0	31	2	US-08-858-623A-19
24	14.4	48.0	33	2	US-08-858-623A-8
25	14.4	48.0	40	3	US-08-975-703-28
26	14.4	48.0	40	3	US-09-515-884-28
27	14.4	48.0	44	3	US-08-829-525-34

C 28	14.4	48.0	44	3	US-08-609-583A-34	Sequence 34, Appl
C 29	14.4	48.0	44	3	US-08-937-399-34	Sequence 34, Appl
C 30	14.4	48.0	44	3	US-09-560-639-27	Sequence 27, Appl
C 31	14.4	48.0	44	3	US-09-310-367-34	Sequence 34, Appl
C 32	14.4	48.0	44	3	US-09-032-337-34	Sequence 34, Appl
C 33	14.4	48.0	44	4	US-09-464-231-34	Sequence 34, Appl
C 34	14.2	47.3	25	4	US-09-396-196G-107784	Sequence 107784,
C 35	14.2	47.3	28	3	US-09-283-144-12	Sequence 12, Appl
C 36	14.2	47.3	30	1	US-08-123-702-42	Sequence 42, Appl
C 37	14.2	47.3	39	3	US-08-936-632B-41	Sequence 41, Appl
C 38	14.2	47.3	39	3	US-08-582-333A-92	Sequence 92, Appl
C 39	14.2	47.3	47	4	US-09-671-317-767	Sequence 767, App
C 40	14	46.7	23	3	US-09-209-668-22	Sequence 22, Appl
C 41	14	46.7	25	4	US-09-396-196G-4728	Sequence 4728, Ap
C 42	14	46.7	25	4	US-09-396-196G-59663	Sequence 59663, A
C 43	14	46.7	25	4	US-09-396-196G-80579	Sequence 80579, A
C 44	14	46.7	31	3	US-08-973-965-11	Sequence 11, Appl
C 45	14	46.7	33	4	US-09-530-095B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-07-989-160-2
; Sequence 2, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-07-989-160-2

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30
|||||

Db 1 GCGGATCCAGGTAGGCAGACTTGTGCAGCCT 30

RESULT 2

US-09-396-196G-80578/c

; Sequence 80578, Application US/09396196G

; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396.196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 80578

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-80578

Query Match 53.3%; Score 16; DB 4; Length 25;

Best Local Similarity 79.2%; Pred. No. 5.4e+02;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGCAGACTTGT 24

Db 24 GTGGATCCAGTCAGCCAGACGTGT 1

RESULT 3

US-08-244-548-14

; Sequence 14, Application US/08244548

; Patent No. 5874556

GENERAL INFORMATION:

; APPLICANT: LUPTON, STEPHEN D.

; APPLICANT: ALLEN, JAMES M.

; TITLE OF INVENTION: HYBRID GENES FOR USE IN THE PRODUCTION

; OF TH-INDEPENDENT CYTOTOXIC T CELLS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison & Foerster

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/244.548

FILING DATE: 06-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: DYLAN, TYLER M.

REGISTRATION NUMBER: 37,612

REFERENCE/DOCKET NUMBER: 22627-20005.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-213-993-14

Query Match 52.0%; Score 15.6; DB 4; Length 41;

Best Local Similarity 81.8%; Pred. No. 9.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTG 23

Db 8 CGGATCCAGGAAGGCTGCCCTG 29

RESULT 4

US-09-213-993-14

; Sequence 14, Application US/09213993

; Patent No. 6593124

GENERAL INFORMATION:

; APPLICANT: LUPTON, STEPHEN D.

; APPLICANT: ALLEN, JAMES M.

; APPLICANT: Felchhaus, Andrew L.

; TITLE OF INVENTION: HYBRID GENES FOR USE IN THE PRODUCTION

; OF TH-INDEPENDENT CYTOTOXIC T CELLS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison & Foerster

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/213.993

FILING DATE: 16-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/244.548

FILING DATE: 6-JUN-1994

APPLICATION NUMBER: PCT/US94/03659

FILING DATE: 4-APR-1994

APPLICATION NUMBER: US 08/044.539

FILING DATE: 6-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: POLIZZI, CATHERINE M.

REGISTRATION NUMBER: 40,130

REFERENCE/DOCKET NUMBER: 22627-20005.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5651

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-213-993-14

Query Match 52.0%; Score 15.6; DB 4; Length 41;

Best Local Similarity 81.8%; Pred. No. 9.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTG 23

Db 8 CGGATCCAGGAAGGCTGCCCTG 29


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RESULT 5
US-09-109-063-26/c
; Sequence 26, Application US/09109063
; Patent No. 6013498
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/109,063
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: JP 180010/1997
; EARLIER FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-109-063-26
Query Match      52.0%; Score 15.6; DB 3; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TC A 21

RESULT 6
US-09-448-310-26/c
; Sequence 26, Application US/09448310
; Patent No. 6538122
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/448,310
; CURRENT FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/109,063
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-448-310-26
Query Match      52.0%; Score 15.6; DB 4; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TC A 21

RESULT 7
US-09-884-948-26/c
; Sequence 26, Application US/09884948
; Patent No. 6821763
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-884-948-26
Query Match      52.0%; Score 15.6; DB 4; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TC A 21

RESULT 8
US-09-892-864A-25/c
; Sequence 25, Application US/09892864A
; Patent No. 6833258
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: ONO, Kunio
; APPLICANT: EJIMA, Daisuke
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUAMINASE
; FILE REFERENCE: 209524USOCNT
; CURRENT APPLICATION NUMBER: US/09/892,864A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/JP99/07250
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: JP 10-373131
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-892-864A-25
Query Match      52.0%; Score 15.6; DB 4; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TC A 21

RESULT 9
US-09-109-063-27
; Sequence 27, Application US/09109063
; Patent No. 6013498
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-109-063-27
Query Match      52.0%; Score 15.6; DB 4; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TC A 21
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; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/109,063
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: JP 180010/1997
; EARLIER FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-109-063-27

Query Match          52.0%; Score 15.6; DB 3; Length 50;
Best Local Similarity 81.8%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTC A 26
Db 13 ATCCAGGTAAGCAGATTTCATCA 34

RESULT 10
US-09-448-310-27
; Sequence 27, Application US/09448310
; Patent No. 6538122
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/448,310
; CURRENT FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/109,063
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-448-310-27

Query Match          52.0%; Score 15.6; DB 4; Length 50;
Best Local Similarity 81.8%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTC A 26
Db 13 ATCCAGGTAAGCAGATTTCATCA 34

RESULT 11
US-09-884-948-27
; Sequence 27, Application US/09884948
; Patent No. 6821763
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310

```

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; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-884-948-27

Query Match          52.0%; Score 15.6; DB 4; Length 50;
Best Local Similarity 81.8%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTC A 26
Db 13 ATCCAGGTAAGCAGATTTCATCA 34

RESULT 12
US-09-892-864A-26
; Sequence 26, Application US/09892864A
; Patent No. 6833258
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: ONO, Kunio
; APPLICANT: EJIMA, Daisuke
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUUTAMINASE
; FILE REFERENCE: 209524USOCONT
; CURRENT APPLICATION NUMBER: US/09/892,864A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/JP99/07250
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: JP 10-373131
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-892-864A-26

Query Match          52.0%; Score 15.6; DB 4; Length 50;
Best Local Similarity 81.8%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTC A 26
Db 13 ATCCAGGTAAGCAGATTTCATCA 34

RESULT 13
US-09-635-132-10
; Sequence 10, Application US/09635132
; Patent No. 6620601
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, ISAMU
; APPLICANT: NAKASHITA, HIDEO
; APPLICANT: YOSHIOKA, KEIKO
; APPLICANT: DOI, YOSHIHARU
; TITLE OF INVENTION: METHODS FOR TRANSFORMATION OF PLANTS, TRANSFORMED
; FILE REFERENCE: 081356/0148
; CURRENT APPLICATION NUMBER: US/09/635,132
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: JP 11-225832
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: JP 11-225839
; PRIOR FILING DATE: 1999-08-09

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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-635-132-10

Query Match      50.7%; Score 15.2; DB 4; Length 42;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy  2  CGGATCCAGGTAGGCGAGACTTGTCTAGCC 29
      |||||
Db   3  CGGATCCAGGAGGGAATCATGGCGACC 30

RESULT 14
US-09-786-025A-5
; Sequence 5, Application US/09786025A
; Patent No. 6660512
; GENERAL INFORMATION:
; APPLICANT: Yu, Long
; APPLICANT: Fu, Qiang
; APPLICANT: Zhao, Yong
; APPLICANT: Bi, Anding
; TITLE OF INVENTION: A NOVEL HUMAN LYSOZYME GENE, ITS ENCODED
; FILE REFERENCE: A34052-PCT-USA
; CURRENT APPLICATION NUMBER: US/09/786,025A
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: CN98111044.4
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-09-786-025A-5

Query Match      50.0%; Score 15; DB 4; Length 29;
Best Local Similarity 78.3%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  GCGGATCCAGGTAGGCGAGACTTG 23
      |||||
Db   3  GCGGATCCATGAGGCGATCCGTG 25

RESULT 15
US-08-963-121C-20
; Sequence 20, Application US/08963121C
; Patent No. 6084087
; GENERAL INFORMATION:
; APPLICANT: Friedman, Steven M
; APPLICANT: Crow, Mary K
; APPLICANT: Yi, Y.
; APPLICANT: Tumang, Joseph
; APPLICANT: Sun, Guang-Rong
; TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,121C
; FILING DATE: October 28, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/427,009
; FILING DATE: April, 24, 1995
; APPLICATION NUMBER: 08/229,285
; FILING DATE: April 18, 1994
; APPLICATION NUMBER: 07/766,751, Patent No. 6084087 5,480,895
; FILING DATE: September 27, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 5983/17499-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: TCra 3'antisense
US-08-963-121C-20

Query Match      49.3%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  9  AGGTAGGACAGACTTGTCAC 26
      |||||
Db   4  AGGTGACAGACTTGTCAC 21

RESULT 16
US-09-543-513-20
; Sequence 20, Application US/09543513
; Patent No. 6303750
; GENERAL INFORMATION:
; APPLICANT: Friedman, Steven M
; APPLICANT: Crow, Mary K
; APPLICANT: Yi, Y.
; APPLICANT: Tumang, Joseph
; APPLICANT: Sun, Guang-Rong
; TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,513
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/963,121
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 5983/17499-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: TCra 3'antisense
;
US-09-543-513-20
Query Match 49.3%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 AGGTAGGCAGACTTGTC A 26
Db 4 AGGTCGACAGACTTGTC A 21

RESULT 17
US-09-396-196G-6441/c
; Sequence 6441, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6441
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
;
US-09-396-196G-6441
Query Match 49.3%; Score 14.8; DB 4; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTT 22
Db 18 ATCCAGGCAGGCAGCCTT 1

RESULT 18
PCT-US95-04803-21
; Sequence 21, Application PC/TUS9504803
; GENERAL INFORMATION:
; APPLICANT: New York Society For the ruptured and
```

```
; APPLICANT: Crippled Maintaining The Hospital for
; APPLICANT: Special Surgery
; APPLICANT: INVENTORS: Friedman, Steven M
; APPLICANT: Crow, Mary K
; APPLICANT: Yi, Y.
; APPLICANT: Tumang, Joseph
; APPLICANT: Sun, Guang-Rong
; TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04803
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 5983/09449
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: TCra 3'antisense
;
PCT-US95-04803-21
Query Match 49.3%; Score 14.8; DB 5; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 AGGTAGGCAGACTTGTC A 26
Db 4 AGGTCGACAGACTTGTC A 21

RESULT 19
US-08-992-877-68
; Sequence 68, Application US/08992877
; Patent No. 6340461
; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: SUPERANTIGEN USED METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF INFECTIOUS DISEASE
; FILE REFERENCE: superantigen
; CURRENT APPLICATION NUMBER: US/08/992,877
; CURRENT FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/044,074
; PRIOR FILING DATE: 1997-04-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 68
; LENGTH: 37
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Query Match 48.7%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;

RESULT 23
US-08-858-623A-19
Sequence 19, Application US/08858623A
Patent No. 5910628
GENERAL INFORMATION:
APPLICANT: Miller, W.A., and Wang, S.
TITLE OF INVENTION: Cap-Independent Translation Sequences
TITLE OF INVENTION: Derived From Barley Yellow Dwarf Virus
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: United States of America

```
;
;
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,623A
; FILING DATE: May 20, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,199
; FILING DATE: May 20, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: genomic RNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Tobacco Necrosis Virus Strain A
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; OTHER INFORMATION: GenBank Accession No. 5910628 X58455
; PUBLICATION INFORMATION:
; US-08-858-623A-19

Query Match 48.0%; Score 14.4; DB 2; Length 31;
Best Local Similarity 62.5%; Pred. No. 3.1e+03;
Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGACGACTTGTC 25
Db 8 CGGAUCCUGGAGAAACAGGCUUGAC 31

RESULT 24
US-08-858-623A-8
; Sequence 8, Application US/08858623A
; Patent No. 5910628
; GENERAL INFORMATION:
; APPLICANT: Miller, W.A., and Wang, S.
; TITLE OF INVENTION: Cap-Independent Translation Sequences
; TITLE OF INVENTION: Derived From Barley Yellow Dwarf Virus
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,623A
; FILING DATE: May 20, 1997
```

```
;
;
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,199
; FILING DATE: May 20, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: genomic RNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Tobacco Necrosis Virus Strain A
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; OTHER INFORMATION: GenBank Accession No. 5910628 X58455
; PUBLICATION INFORMATION:
; US-08-858-623A-8

Query Match 48.0%; Score 14.4; DB 2; Length 33;
Best Local Similarity 62.5%; Pred. No. 3.1e+03;
Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGACGACTTGTC 25
Db 9 CGGAUCCUGGAGAAACAGGCUUGAC 32

RESULT 25
US-08-975-703-28/C
; Sequence 28, Application US/08975703
; Patent No. 6030832
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Bartel, Paul L.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,703
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2318-0174
```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
US-08-975-703-28

Query Match 48.0%; Score 14.4; DB 3; Length 40;

Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTTGTC A 26
DB 36 GAATCCTGTTGGCAGAAATGGTCA 13

RESULT 26

US-09-515-884-28/c
Sequence 28, Application US/09515884
Patent No. 6235263
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
Bartel, Paul L.
Teng, David H.-P.
Tavtiglian, Sean V.

TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting Protein
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East Tower
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,884
FILING DATE: 29-Feb-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/975,703

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Stephen A.

REGISTRATION NUMBER: 38,609

REFERENCE/DOCKET NUMBER: 2318-0174

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-624-1589

TELEFAX: 202-783-6031

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-515-884-28

Query Match 48.0%; Score 14.4; DB 3; Length 40;

Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTTGTC A 26
DB 36 GAATCCTGTTGGCAGAAATGGTCA 13

RESULT 27

US-08-829-525-34/c
Sequence 34, Application US/08829525
Patent No. 6084083
GENERAL INFORMATION:

APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,525
FILING DATE: 28-MAR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/609,583

FILING DATE: 01-MAR-1996

APPLICATION NUMBER: US 08/487,748

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/398,633

FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-081

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-829-525-34

Query Match 48.0%; Score 14.4; DB 3; Length 44;

Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTCAGCC 29
DB 40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 28

US-08-609-583A-34/c

Sequence 34, Application US/08609583A

Patent No. 6204371

GENERAL INFORMATION:

APPLICANT: Levinson, Douglas A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

```
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,583A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-609-583A-34

Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
| | | | | | | | | | | | | | | |
Db 40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 29
US-08-937-399-34/c
; Sequence 34, Application US/08937399
; Patent No. 6288218
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,399
; FILING DATE:
```

```
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-937-399-34

Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
| | | | | | | | | | | | | | | |
Db 40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 30
US-09-560-639-27/c
; Sequence 27, Application US/09560639
; Patent No. 6323334
; GENERAL INFORMATION:
; APPLICANT: Kingsbury, G.
; APPLICANT: Leiby, K.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 7853-158
; CURRENT APPLICATION NUMBER: US/09/560,639
; CURRENT FILING DATE: 2000-04-28
; EARLIER APPLICATION NUMBER: 60/155,862
; EARLIER FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3' oligonucleotide
; US-09-560-639-27

Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
| | | | | | | | | | | | | | | |
Db 40 TCCAGGTGTCAGACTTGGGATCC 17

RESULT 31
US-09-310-367-34/c
; Sequence 34, Application US/09310367
; Patent No. 641417
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
```


;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
;; NUMBER OF SEQUENCES: 38
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036/2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/310,367
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/829,525
;; FILING DATE: 28-MAR-1997
;; APPLICATION NUMBER: US/08/609,583
;; FILING DATE: 01-MAR-1996
;; APPLICATION NUMBER: US/08/487,748
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US/08/398,633
;; FILING DATE: 03-MAR-1995
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-081
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-790-9090
;; TELEFAX: 212-869-8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 44 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
US-09-310-367-34
Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
DB 40 TGCAGGTGTCAGACTTGGGATCC 17
RESULT 32
US-09-032-337-34/c
; Sequence 34, Application US/09032337
; Patent No. 6455685
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/032,337
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/609,583
;; FILING DATE: 01-MAR-1996
;; APPLICATION NUMBER: US/08/487,748
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US/08/398,633
;; FILING DATE: 03-MAR-1995
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-016
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-790-9090
;; TELEFAX: 212-869-8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 44 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
US-09-032-337-34
Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
DB 40 TGCAGGTGTCAGACTTGGGATCC 17
RESULT 33
US-09-464-231-34/c
; Sequence 34, Application US/09464231
; Patent No. 6562343
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/464,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US/08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/398,633
; FILING DATE: 03-MAR-1995
; NAME: Coruzzi, Laura A.

;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-048
;; TELEPHONE: 212-790-9090
;; TELEFAX: 212-869-8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 44 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-09-464-231-34

Query Match 48.0%; Score 14.4; DB 4; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGCACC 29
DB 40 TCCAGGTGTGCAGACTTGGGATCC 17

RESULT 34
US-09-396-196G-107784/c
; Sequence 107784, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107784

Query Match 47.3%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACT 21
DB 20 GGATCCAGGTAGGCAGAGT 2

RESULT 35
US-09-283-144-12
; Sequence 12, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21880
; EARLIER FILING DATE: 1997-11-20

;; EARLIER APPLICATION NUMBER: US 60/031,435
;; EARLIER FILING DATE: 1996-11-20
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 12
;; LENGTH: 28
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Primer for
;; OTHER INFORMATION: cloning Survivin construct
US-09-283-144-12

Query Match 47.3%; Score 14.2; DB 3; Length 28;
Best Local Similarity 70.4%; Pred. No. 3.7e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGCAGACTTGTCCAGC 28
DB 2 CGGATCCAGAGAGATGACTTTTAAAC 28

RESULT 36
US-08-123-702-42
; Sequence 42, Application US/08123702
; Patent No. 5604131
; GENERAL INFORMATION:
; APPLICANT: Wadsworth, Samuel
; APPLICANT: Snyder, Benjamin
; APPLICANT: Reddy, Vermuri, B.
; APPLICANT: Wei, Chamer
; TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770
; Patent No. 5604131
; TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.125
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,702
; FILING DATE: 17-SEPT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: TSI121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8795
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-123-702-42

Query Match 47.3%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 3.8e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 GATCCAGGTAGGCAGACTTGTCCAGCCT 30

Db 4 GGTGGAGTAGTAAACTTGCTGCAT 30
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RESULT 37
US-08-936-632B-41
; Sequence 41, Application US/08936632B
; Patent No. 6159705
; GENERAL INFORMATION:
; APPLICANT: Truehart, Joshua
; APPLICANT: Paul, Jeremy I.
; APPLICANT: Fuernkranz, Hans
; APPLICANT: Nathans, Debra
; APPLICANT: Holmes, Scott
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; IDENTIFYING RECEPTOR EFFECTORS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,632B
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/718,910
; FILING DATE: 24 SEPTEMBER 1996
; APPLICATION NUMBER: US 08/851,469
; FILING DATE: 05 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: DECONTI, GIULIO A., JR.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: CPI-031CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-936-632B-41
Query Match 47.3%; Score 14.2; DB 3; Length 39;
Best Local Similarity 84.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 12 TAGGCAGACTTGTCAGCCT 30
| | | | | | | | | | | | | | | | | | | | | |
Db 9 TTGGCTGACTTGTCGCCT 27
| | | | | | | | | | | | | | | | | | | | | |
RESULT 38
US-08-582-333A-92
; Sequence 92, Application US/08582333A
; Patent No. 6255059
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J. M.
; TITLE OF INVENTION: Methods and Compositions for
; IDENTIFYING RECEPTOR EFFECTORS
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,333A
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine J. Kara
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: CPI-012CP5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-4214
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-582-333A-92
Query Match 47.3%; Score 14.2; DB 3; Length 39;
Best Local Similarity 84.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 12 TAGGCAGACTTGTCAGCCT 30
| | | | | | | | | | | | | | | | | | | | | |
Db 9 TTGGCTGACTTGTCGCCT 27
| | | | | | | | | | | | | | | | | | | | | |
RESULT 39
US-09-671-317-767/c
; Sequence 767, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62-US3-CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.Pm
; SEQ ID NO 767
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 12-603-191 : polymorphic base T or C
US-09-671-317-767

Query Match 47.3%; Score 14.2; DB 4; Length 47;
Best Local Similarity 76.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGACAGACTTGTG 25
|||||:|||||
Db 30 ATCCAAATAGCCAAATTGTG 10

RESULT 40
US-09-209-668-22
; Sequence 22, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-209-668-22

Query Match 46.7%; Score 14; DB 3; Length 23;
Best Local Similarity 77.3%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGACACTT 22
|||||
Db 2 GCGGATCCGCTACTCAGAGTT 23

Search completed: November 18, 2005, 11:21:57
Job time : 58.289 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 403.232 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-2

Perfect score: 30

Sequence: 1 GCGGATCCAGGTAGGACACTTGTCAGCCT 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	8	US-08-469-172-2
2	30	100.0	30	20	US-10-788-779-2
c 3	18.4	61.3	25	26	US-11-036-317-64086
4	16.8	56.0	25	22	US-10-719-900-107278
5	16.8	56.0	25	26	US-11-036-317-28585

c	6	16.8	56.0	25	26	US-11-036-317-411291	Sequence 411291,
	7	16.8	56.0	25	26	US-11-036-317-635455	Sequence 635455,
	8	16.8	56.0	37	26	US-11-004-843-25	Sequence 25, Appl
	9	16.6	55.3	25	26	US-11-036-317-621574	Sequence 621574,
	10	16.6	55.3	25	26	US-11-036-317-772379	Sequence 772379,
	11	16.6	55.3	25	26	US-11-036-317-839968	Sequence 839968,
	12	16.2	54.0	25	22	US-10-719-900-160368	Sequence 160368,
	13	16.2	54.0	25	22	US-10-956-157-127072	Sequence 127072,
	14	16.2	54.0	25	24	US-10-719-956-427846	Sequence 427846,
	15	16	53.3	25	22	US-10-719-900-851373	Sequence 851373,
	16	16	53.3	25	22	US-10-719-900-906412	Sequence 906412,
	17	16	53.3	25	22	US-10-809-189-80578	Sequence 80578, A
	18	16	53.3	25	24	US-10-719-956-83060	Sequence 83060, A
	19	16	53.3	25	24	US-10-719-956-167727	Sequence 167727,
	20	15.8	52.7	25	22	US-10-719-900-190832	Sequence 190832,
	21	15.8	52.7	25	22	US-10-719-900-243203	Sequence 243203,
	22	15.8	52.7	25	26	US-11-036-317-475065	Sequence 475065,
	23	15.6	52.0	23	22	US-10-481-113-72	Sequence 72, Appl
	24	15.6	52.0	25	22	US-10-719-900-156288	Sequence 156288,
	25	15.6	52.0	25	24	US-10-719-956-172680	Sequence 172680,
	26	15.6	52.0	25	24	US-10-719-956-634810	Sequence 634810,
	27	15.6	52.0	25	26	US-11-036-317-90978	Sequence 90978, A
	28	15.6	52.0	25	26	US-11-036-317-588184	Sequence 588184,
	29	15.6	52.0	25	26	US-11-036-317-791168	Sequence 791168,
	30	15.6	52.0	25	26	US-11-060-756-254016	Sequence 254016,
	31	15.6	52.0	45	9	US-09-892-861A-25	Sequence 25, Appl
	32	15.6	52.0	45	9	US-09-996-561-26	Sequence 26, Appl
	33	15.6	52.0	45	9	US-09-884-948-26	Sequence 26, Appl
	34	15.6	52.0	45	9	US-09-892-864A-26	Sequence 26, Appl
	35	15.6	52.0	50	9	US-09-996-561-27	Sequence 27, Appl
	36	15.6	52.0	50	9	US-09-884-948-27	Sequence 27, Appl
	37	15.6	52.0	50	9	US-10-719-900-258355	Sequence 258355,
	38	15.4	51.3	25	22	US-10-719-956-303122	Sequence 303122,
	39	15.4	51.3	25	24	US-10-719-956-463637	Sequence 463637,
	40	15.4	51.3	25	24	US-10-719-956-606347	Sequence 606347,
	41	15.4	51.3	25	24	US-10-719-900-107277	Sequence 107277,
	42	15.2	50.7	25	22	US-10-719-900-539634	Sequence 539634,
	43	15.2	50.7	25	22	US-10-719-900-580775	Sequence 580775,
	44	15.2	50.7	25	22	US-10-719-900-217141	Sequence 217141,
	45	15.2	50.7	25	26	US-11-036-317-217141	Sequence 217141,

ALIGNMENTS

RESULT 1
US-08-469-172-2
; Sequence 2, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-469-172-2

Query Match      100.0%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30
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Db 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30

RESULT 2
US-10-788-779-2
; Sequence 2, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-10-788-779-2

;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-788-779-2

Query Match      100.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30
   |||||
Db 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30

RESULT 3
US-11-036-317-64086/c
; Sequence 64086, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 64086
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-64086

Query Match      61.3%; Score 18.4; DB 26; Length 25;
Best Local Similarity 95.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTTCAGC 28
   |||||
Db 21 AGGTAGGCAGACTTGTTCAGC 2

RESULT 4
US-10-719-900-107278
; Sequence 107278, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 107278
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-107278

Query Match      56.0%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTT 22
   |||||
Db 5 GGTTCATGTAGGCAGACTT 24
```

```
RESULT 5
US-11-036-317-28585
; Sequence 28585, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 28585
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-28585

Query Match          56.0%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GTAGGCAGACTTGTTCAGCCT 30
   ||||| ||||| |||||
Db 1 GAAGGCAGCCTTGTTCAGCCT 20

RESULT 6
US-11-036-317-411291/c
; Sequence 411291, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-411291

Query Match          56.0%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GTAGGCAGACTTGTTCAGCCT 30
   ||||| ||||| |||||
Db 1 GAAGGCAGCCTTGTTCAGCCT 20

RESULT 7
US-11-036-317-635455
; Sequence 635455, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-635455

Query Match          56.0%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTCT 24
   ||||| ||||| |||||
Db 21 AGCCAGGTAGCCAGACTTCT 2
```

```
RESULT 8
US-11-004-843-25
; Sequence 25, Application US/11004843
; Publication No. US20050239173A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, INC.
; TITLE OF INVENTION: PRODUCTION OF AMINO SUGARS
; FILE REFERENCE: 023829/0393
; CURRENT APPLICATION NUMBER: US/11/004,843
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 11/004,843
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 60/527,309
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 25
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-004-843-25

Query Match          56.0%; Score 16.8; DB 26; Length 37;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTTCAGC 28
   ||||| ||||| ||||| |||||
Db 2 GCGGATCCAGAATGTCTACACAGTCAGC 29

RESULT 9
US-11-036-317-621574
; Sequence 621574, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 621574
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-621574

Query Match          55.3%; Score 16.6; DB 26; Length 25;
```

```

Best Local Similarity 82.6%; Pred.No. 2.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGCAGC 28
    |||||  |||||  |||||  |||||
DB 3 TCCAGGATGTCAGATTTGTGCAGC 25

RESULT 10
US-11-036-317-772379
; Sequence 772379, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 772379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-772379

Query Match 55.3%; Score 16.6; DB 26; Length 25;
Best Local Similarity 82.6%; Pred.No. 2.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGCAGC 28
    |||||  |||||  |||||  |||||
DB 1 TCCAGGATGTCAGATTTGTGCAGC 23

RESULT 11
US-11-036-317-839968
; Sequence 839968, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 839968
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-839968

Query Match 55.3%; Score 16.6; DB 26; Length 25;
Best Local Similarity 82.6%; Pred.No. 2.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGCAGC 28
    |||||  |||||  |||||  |||||
DB 2 TCCAGGATGTCAGATTTGTGCAGC 24

RESULT 12
US-10-719-900-160368/c
; Sequence 160368, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

```



```
Query Match          54.0%; Score 16.2; DB 24; Length 25;
Best Local Similarity 85.7%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 0; Gaps 0; Indels 3;

QY 9 AGCTAGGCAGACTTGTTCAGCC 29
Db 3 AGCTCTGCAGACTTGTTCAGCC 23

RESULT 15
US-10-719-900-851373/c
; Sequence 851373, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 851373
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-851373

Query Match          53.3%; Score 16; DB 22; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

QY 3 GCATCCAGTAGGCAGACTTGTCA 26
Db 24 GGAACACAGGAGTGCACACTTCTCA 1

RESULT 16
US-10-719-900-906412
; Sequence 906412, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 906412
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-906412

Query Match          53.3%; Score 16; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCAGACTTGTTCAGCCT 30
Db 4 GCAGACTTGTTCAGCCT 19

RESULT 17
US-10-809-189-80578/c
; Sequence 80578, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80578
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-80578

Query Match          53.3%; Score 16; DB 22; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

QY 1 GCGGATCCAGTAGGCAGACTTGT 24
Db 24 GTGGATCCAGTCAGCCAGACGTGT 1

RESULT 18
US-10-719-956-83060
; Sequence 83060, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 83060
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-83060

Query Match          53.3%; Score 16; DB 24; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

QY 7 CCAGGTAGGCAGACTTGTTCAGCCT 30
Db 2 CCAGGGATGCAGAAATTCAGTCT 25

RESULT 19
US-10-719-956-167727/c
; Sequence 167727, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 167727
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-167727

Query Match      53.3%; Score 16; DB 24; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 CCAGGTAGGCAGACTTGTTCAGCCT 30
   ||||| ||||| ||||| ||||| ||
Db 24 CCAGGTAGGCAGCCTTAGTCAAACT 1

RESULT 20
US-10-719-900-190832
; Sequence 190832, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 190832
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-190832

Query Match      52.7%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACT 21
   ||||| ||||| ||||| |||||
Db 2 GGATCCAGGCAGCCAGACT 20

RESULT 21
US-10-719-900-243203/c
; Sequence 243203, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 243203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-243203

Query Match      52.7%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 TAGGCAGACTTGTTCAGCCT 30
   ||||| ||||| ||||| |||||
Db 24 TAGACAGACTTGGCAGCCT 6

RESULT 22
US-11-036-317-475065
; Sequence 475065, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 475065
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-475065

Query Match      52.7%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGA 19
   ||||| ||||| ||||| |||||
Db 3 GCGCATCCAGGTAGGCACA 21

RESULT 23
US-10-481-113-72/c
; Sequence 72, Application US/10481113
; Publication No. US20050032156A1
; GENERAL INFORMATION:
; APPLICANT: Sessions, Allen
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen P.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PHOSPHATE TRANSPORTER GENE
; FILE REFERENCE: Case 60145USPCT
; CURRENT APPLICATION NUMBER: US/10/481,113
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/332,064
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/361,819
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/06968
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 72
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-481-113-72

Query Match      52.0%; Score 15.6; DB 22; Length 23;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CAGGTAGGCAGACTTGTTCAGCC 29
   ||||| ||||| ||||| |||||
Db 23 CAATAGGCAGACTTGTGACC 2
```

```
RESULT 24
US-10-719-900-156288/c
; Sequence 156288, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 156288
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-156288

Query Match          52.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTGACGCT 30
||||| ||||| ||||| ||||| |||||
Db 24 AGGTGGGAGTCTCTGTCACCT 3

RESULT 25
US-10-719-956-172680/c
; Sequence 172680, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 172680
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-172680

Query Match          52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTGACGCT 30
||||| ||||| ||||| ||||| |||||
Db 24 AAGTGGGAGACTTGACACTCT 3

RESULT 26
US-10-719-956-634810/c
; Sequence 634810, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 634810
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-634810

Query Match          52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CAGGTAGGCAGACTTGTGACGC 29
||||| ||||| ||||| ||||| |||||
Db 23 CAGGTAAGAAGAGTTGTGAGCC 2

RESULT 27
US-11-036-317-90978
; Sequence 90978, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90978
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-90978

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CCAGGTAGGCAGACTTGTGAGC 28
||||| ||||| ||||| ||||| |||||
Db 1 CCAGGATGTCAGATTGTGAGC 22

RESULT 28
US-11-036-317-588184
; Sequence 588184, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 588184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-588184

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CCAGGTAGGCAGACTTGTGAGC 28
||||| ||||| ||||| ||||| |||||
Db 1 CCAGGATGTCAGATTGTGAGC 22
```

```
RESULT 29
US-11-036-317-791168
; Sequence 791168, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 791168
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-791168

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6  TCCAGGTAGGCAGACTTGTGCAG 27
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Db      4  TCCAGGTAGCAGATTGTGCAG 25

RESULT 30
US-11-036-317-791169
; Sequence 791169, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 791169
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-791169

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6  TCCAGGTAGGCAGACTTGTGCAG 27
      ||||| ||||| ||||| |||||
Db      4  TCCAGGTAGTCAGATTGTGCAG 25

RESULT 31
US-11-060-756-254016/c
; Sequence 254016, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TARGET: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
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; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 254016
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-254016

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      9  AGGTAGGCAGACTTGTGCAGCCT 30
      ||||| ||||| ||||| |||||
Db      24  AGGGAGGTAGACTCGTTAGCCT 3

RESULT 32
US-09-892-864A-25/c
; Sequence 25, Application US/09892864A
; Patent No. US20020090675A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: ENO, Kunio
; APPLICANT: EJIMA, Daisuke
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUAMINASE
; FILE REFERENCE: 209524USOCONT
; CURRENT APPLICATION NUMBER: US/09/892,864A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/JP99/07250
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: JP 10-373131
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-892-864A-25

Query Match          52.0%; Score 15.6; DB 9; Length 45;
Best Local Similarity 81.8%; Pred. No. 7.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5  ATCCAGGTAGGCAGACTTGTCA 26
      ||||| ||||| ||||| |||||
Db      42  ATCCAGGTAGCAGATTTCATCA 21

RESULT 33
US-09-996-561-26/c
; Sequence 26, Application US/09996561
; Patent No. US20020151703A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/996,561
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/449,310
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/109,063
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
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; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-996-561-26

Query Match 52.0%; Score 15.6; DB 9; Length 45;
Best Local Similarity 81.8%; Pred. No. 7.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTCA 26
|||||
Db 42 ATCCAGGTAAGCAGATTCATCA 21

RESULT 34
US-09-884-948-26/c
; Sequence 26, Application US/09884948
; Patent No. US20020173021A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310
; PRIOR FILING DATE: 1999-11-24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-884-948-26

Query Match 52.0%; Score 15.6; DB 9; Length 45;
Best Local Similarity 81.8%; Pred. No. 7.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTCA 26
|||||
Db 42 ATCCAGGTAAGCAGATTCATCA 21

RESULT 35
US-09-892-864A-26
; Sequence 26, Application US/09892864A
; Patent No. US20020090675A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: ONO, Kunio
; APPLICANT: EJIMA, Daisuke
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUTAMINASE
; FILE REFERENCE: 209524USOCONT
; CURRENT APPLICATION NUMBER: US/09/892,864A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/JP99/07250
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: JP 10-373131
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic DNA
US-09-892-864A-26

Query Match 52.0%; Score 15.6; DB 9; Length 50;
Best Local Similarity 81.8%; Pred. No. 7.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTCA 26
|||||
Db 13 ATCCAGGTAAGCAGATTCATCA 34

RESULT 36
US-09-996-561-27
; Sequence 27, Application US/09996561
; Patent No. US20020151703A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/996,561
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/448,310
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/109,063
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-996-561-27

Query Match 52.0%; Score 15.6; DB 9; Length 50;
Best Local Similarity 81.8%; Pred. No. 7.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTCA 26
|||||
Db 13 ATCCAGGTAAGCAGATTCATCA 34

RESULT 37
US-09-884-948-27
; Sequence 27, Application US/09884948
; Patent No. US20020173021A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-884-948-27

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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 665.886 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-3

Perfect score: 24

Sequence: 1 ATGCCAACCCCTGCTCTGGAGGCCT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	112896	I12896 Sequence 3
2	16	66.7	40	10	F272557S01 Rattus no
3	15.8	65.8	41	6	AX515479 Sequence
4	15.8	65.8	41	6	AX521027 Sequence
5	15	62.5	25	6	CQ864052 Sequence
6	14.8	61.7	47	6	AR284760 Sequence
7	14.6	60.8	30	6	AX316342 Sequence
8	14.6	60.8	30	6	AX431254 Sequence
9	14.6	60.8	30	6	AX671506 Sequence
10	14.6	60.8	40	6	AX456311 Sequence
11	14.6	60.8	47	6	AR291259 Sequence
12	14.4	60.0	17	6	BD254805 Regulation
13	14.4	60.0	20	6	BD250383 Enzyme. 7
14	14.4	60.0	20	6	AX038772 Sequence
15	14.4	60.0	50	6	CQ003936 Sequence
16	14.4	60.0	50	6	CQ008720 Sequence
17	14	58.3	24	6	AB4037 Sequence 24
18	14	58.3	24	6	BD072714 Gene conv
19	14	58.3	25	6	AX651215 Sequence

C 20	14	58.3	25	6	AX651216	Sequence
C 21	14	58.3	36	6	CQ840251	Sequence
C 22	14	58.3	40	6	CQ857597	Sequence
C 23	14	58.3	40	6	CQ857598	Sequence
C 24	14	58.3	41	6	AX518421	Sequence
C 25	13.8	57.5	50	6	AX157284	Sequence
C 26	13.6	56.7	24	6	AR175455	Sequence
C 27	13.6	56.7	24	6	AR442928	Sequence
C 28	13.6	56.7	24	6	AR494164	Sequence
C 29	13.6	56.7	24	6	AX934355	Sequence
C 30	13.6	56.7	25	6	AX651213	Sequence
C 31	13.6	56.7	25	6	AX651214	Sequence
C 32	13.6	56.7	34	6	BD170870	Human apo
C 33	13.6	56.7	36	6	BD095049	Antibody
C 34	13.6	56.7	50	6	BD172240	Secreted
C 35	13.6	56.7	50	6	BD172559	Secreted
C 36	13.6	56.7	50	6	BD172878	Secreted
C 37	13.6	56.7	50	6	BD173197	Secreted
C 38	13.6	56.7	50	6	BD175231	Secretory
C 39	13.6	56.7	50	6	AR410609	Sequence
C 40	13.6	56.7	50	6	AR438973	Sequence
C 41	13.6	56.7	50	6	AR472993	Sequence
C 42	13.6	56.7	50	6	AR526979	Sequence
C 43	13.6	56.7	50	6	AR566012	Sequence
C 44	13.6	56.7	50	6	AX076918	Sequence
C 45	13.6	56.7	50	6	AX098266	Sequence

ALIGNMENTS

RESULT 1
LOCUS I12896 I12896 24 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 3 from patent US 5429923.
ACCESSION I12896
VERSION I12896.1 GI:910873
KEYWORDS mutations
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 3 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred.No.0.37;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAGGCCT 24
|||||
Db 1 ATGCCAACCCCTGCTCTGGAGGCCT 24

RESULT 2
LOCUS F272557S01 40 bp DNA linear ROD 15-FEB-2001
DEFINITION Rattus norvegicus liver-specific organic anion transporter 1 (rlst-1) gene, exon 1.
ACCESSION AF272557
VERSION AF272557.2 GI:12831759
KEYWORDS
SEGMENT 1 of 15
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RESULT 4
AX521027/c
LOCUS           AX521027       41 bp    DNA
DEFINITION      Sequence 7225 from Patent WO02052044.
ACCESSION       AX521027
VERSION         AX521027.1 GI:23571753
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1  Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
   Detection of genetic polymorphisms
   Patent: WO 02052044-A 7225 04-JUL-2002;
   Riken (JP)
FEATURES
     source             1..41
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
ORIGIN
Query Match          65.8%; Score 15.8; DB 6; Length 41;
Best Local Similarity 81.0%; Pred.No. 6.5e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      4  CMAACCTGCTCTGGAGGCCT 24
        |||||:|||||
Db       25  CCAAYCCTACTCTGTGGGCCT 5

RESULT 5
CQ864052/c
LOCUS           CQ864052       25 bp    DNA
DEFINITION      Sequence 2685 from Patent WO2004072265.
ACCESSION       CQ864052
VERSION         CQ864052.1 GI:51985041
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1  Burczynski,M., Twine,N., Dörner,A.J. and Trepicchio,W.L.
   METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /I
   Patent: WO 2004072265-A 2685 26-AUG-2004;
   Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
   Dörner, Andrew J. (US); Trepicchio, William L. (US)
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     source             1..25
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
ORIGIN
Query Match          62.5%; Score 15; DB 6; Length 25;
Best Local Similarity 78.3%; Pred.No. 1.7e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2  TGCCAACCTGCTCTGGAGGCCT 24
        |||||:|||||
Db       25  TGTCACCTGCTCTGGGTACCT 3

RESULT 6
AR284760
LOCUS           AR284760       47 bp    DNA
DEFINITION      Sequence 812 from patent US 6528260.
ACCESSION       AR284760
VERSION         AR284760.1 GI:29721664
KEYWORDS

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Qy 3 GCCAACCTGCTCTGGAGCC 23
Db 16 GGCATTCTGATCTGGAGCC 36

RESULT 11
LOCUS AR291259 47 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2994 from patent US 6537751.
ACCESSION AR291259
VERSION AR291259.1 GI:31678543
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 2994 25-MAR-2003;
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source location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 60.8%; Score 14.6; DB 6; Length 47;
Best Local Similarity 73.9%; Pred. No. 2.7e+04;
Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAGCC 23
Db 11 ATGCCAAGGCTGCTTGATCCC 33

RESULT 12
LOCUS BD254805 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254805
VERSION BD254805.1 GI:33064575
KEYWORDS JP 2002541795-A/2598.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2598 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2598
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source location/Qualifiers
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FT Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"

FEATURES
source

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ORIGIN
/db_xref="taxon:32644"

Query Match 60.0%; Score 14.4; DB 6; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCCTGCTCTGGAGCC 22
Db 1 ACCCGCTCTGGAGCC 16

RESULT 13
LOCUS BD250383 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Enzyme.
ACCESSION BD250383
VERSION BD250383.1 GI:33060153
KEYWORDS JP 2002541794-A/28.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Talas,U.G., Dunlop,J. and Kelsell,D.P.
TITLE Enzyme
JOURNAL Patent: JP 2002541794-A 28 10-DEC-2002;
COMMENT QUEEN MARY AND WESTFIELD COLLEGE
OS Artificial Sequence
PN JP 2002541794-A/28
PD 10-DEC-2002
PF 12-APR-2000 JP 2000611653
PR 13-APR-1999 GB 9908458.4
PI ULVI GERST TALAS,JOHN DUNLOP, DAVID PETER KELSELL PC
C12N15/09,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/ PC
50,C12Q1/68,
CC C1201/68,G01N33/573,G01N33/574//C12P21/08,C12N15/00,C12N5/00
CC Primer
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 60.0%; Score 14.4; DB 6; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AACCTGCTCTGGAGG 21
Db 5 ACCCGCTCTGGAGG 20

RESULT 14
LOCUS AX038772 20 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 28 from Patent WO0061728.
ACCESSION AX038772
VERSION AX038772.1 GI:11228117
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Dunlop,J., Kelsell,D.P. and Gerst-Talas,U.
TITLE Enzyme
JOURNAL Patent: WO 0061728-A 28 19-OCT-2000;
DUNLOP JOHN (ES) ; KELSELL DAVID PETER (GB) ; GERST TALAS ULVI (GB)
; QUEEN MARY & WESTFIELD COLLEGE (GB)
; Location/Qualifiers

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match
Best Local Similarity 60.0%; Score 14.4; DB 6; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AACCTGCTCTGGAGG 21
    |||||
Db 5 ACCCTGCTCTGGAGG 20

RESULT 15
LOCUS CQ003936 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 2576 from Patent WO0147944.
ACCESSION CQ003936
VERSION CQ003936.1 GI:41010568
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Shimkets,R.A. and Leach,M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE methods of use thereof
JOURNAL Patent: WO 0147944-A 2576 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26"
Accession number CG43985274"

ORIGIN
Query Match
Best Local Similarity 60.0%; Score 14.4; DB 6; Length 50;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCCAACCTGCTCTG 17
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Db 22 TGCCAGCCCTGCTCTG 37

RESULT 16
CQ008720/c
LOCUS CQ008720 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 7360 from Patent WO0147944.
ACCESSION CQ008720
VERSION CQ008720.1 GI:41015434
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Shimkets,R.A. and Leach,M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE methods of use thereof
JOURNAL Patent: WO 0147944-A 7360 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/db_xref="taxon:9606"
25..26
/note="Nucleotide deleted between bases 25 and 26"
Accession number CG43966585"

ORIGIN
Query Match
Best Local Similarity 60.0%; Score 14.4; DB 6; Length 50;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGCTT 24
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Db 39 ATGCTGACCTTGGGCTGGAGGCTT 16

RESULT 17
LOCUS A84037 24 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 24 from Patent WO9846772.
ACCESSION A84037
VERSION A84037.1 GI:6733178
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 24)
AUTHORS Bovenberg,R.A. and Seltlen,G.C.
TITLE GENE CONVERSION AS A TOOL FOR THE CONSTRUCTION OF RECOMBINANT
INDUSTRIAL FILAMENTOUS FUNGI
JOURNAL Patent: WO 9846772-A 24 22-OCT-1998;
BOVENBERG ROELOF ARY LANS (NL); GIST BROCADES BV (NL)
FEATURES
source
Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match
Best Local Similarity 58.3%; Score 14; DB 6; Length 24;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GCCAACCTGCTCTGGAGGCTT 24
    |||||
Db 1 GCCTACTCTGTTCTGGAGAGCT 22

RESULT 18
LOCUS BD072714 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Gene conversion as a tool for the construction of recombinant
industrial organisms.
ACCESSION BD072714
VERSION BD072714.1 GI:22618317
KEYWORDS JP 2001518798-A/24.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 24)
AUTHORS Seltlen,G.C.M., Swinkels,B.W. and Bovenberg,R.A.L.
TITLE Gene conversion as a tool for the construction of recombinant
industrial organisms
JOURNAL Patent: JP 2001518798-A 24 16-OCT-2001;
DSM NV
COMMENT OS Unidentified
PN JP 2001518798-A/24
PD 16-OCT-2001
PF 09-APR-1998 JP 1998543456
PR 11-APR-1997 EP 97201091.2
PI GERARDUS CORNELIS MARIA SELTEN,BART WILLEM SWINKELS, PI
ROELOF ARY LANS BOVENBERG
PC C12N15/80,C12N15/65,C12N15/52,C12N1/15
CC Strandedness: Single;
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CC      Topology: Linear;
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FH      Key      Location/Qualifiers
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            /organism='Unidentified'.
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     source        1..24
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 24;
Best Local Similarity 77.3%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  GCCAACCCCTGCTCGGAGGCT 24
         ||| ||| ||| ||| ||| ||| |||
Db      1  GCCTACTCTGTTCTGGAGAGCT 22

RESULT 19
AX651215/c
LOCUS      AX651215                25 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION Sequence 3055 from Patent EP1273660.
ACCESSION  AX651215
VERSION     AX651215.1 GI:29154033
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
     AUTHORS   Gu, Y.
     TITLE     Human sodium-hydrogen exchanger like protein 1
     JOURNAL   Patent: EP 1273660-A 3055 08-JAN-2003;
     Acomica, Inc. (US)
FEATURES             Location/Qualifiers
     source        1..25
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN

Query Match      58.3%; Score 14; DB 6; Length 25;
Best Local Similarity 77.3%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  ATGCCAACCCCTGCTCGGAGGC 22
         ||| ||| ||| ||| ||| ||| |||
Db      25  ACGCCAACCTCTGATCTGAAGCC 4

RESULT 20
AX651216/c
LOCUS      AX651216                25 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION Sequence 3056 from Patent EP1273660.
ACCESSION  AX651216
VERSION     AX651216.1 GI:29154034
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
     AUTHORS   Gu, Y.
     TITLE     Human sodium-hydrogen exchanger like protein 1
     JOURNAL   Patent: EP 1273660-A 3056 08-JAN-2003;
     Acomica, Inc. (US)
FEATURES             Location/Qualifiers
     source        1..25
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"

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ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 25;
Best Local Similarity 77.3%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  ATGCCAACCCCTGCTCGGAGGC 22
         ||| ||| ||| ||| ||| ||| |||
Db      24  ACGCCAACCTCTGATCTGAAGCC 3

RESULT 21
CQ840251/c
LOCUS      CQ840251                36 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 18 from Patent WO2004056863.
ACCESSION  CQ840251
VERSION     CQ840251.1 GI:50838027
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE   1
     AUTHORS   Fagan, R.J., Phelps, C.B., Rodrigues, T.M., Power, C. and de Tiani, M.
     TITLE     Splice variant of human placental growth hormone
     JOURNAL   Patent: WO 2004056863-A 18 08-JUL-2004;
     ARES TRADING S.A. (CH)
FEATURES             Location/Qualifiers
     source        1..36
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer INSP105- exon4R"
ORIGIN

Query Match      58.3%; Score 14; DB 6; Length 36;
Best Local Similarity 77.3%; Pred. No. 5.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  ATGCCAACCCCTGCTCGGAGGC 22
         ||| ||| ||| ||| ||| ||| |||
Db      34  ATCCAAACGCTGATGTGGAGGC 13

RESULT 22
CQ857597
LOCUS      CQ857597                40 bp      DNA      linear      PAT 31-AUG-2004
DEFINITION Sequence 7 from Patent WO2004070060.
ACCESSION  CQ857597
VERSION     CQ857597.1 GI:51951747
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE   1
     AUTHORS   Cimadevilla, J.C. and Villahermosa, J.M.
     TITLE     Nucleic acid probes for the detection of small exons and methods of
            designing the same
     JOURNAL   Patent: WO 2004070060-A 7 19-AUG-2004;
            GENOMICA S.A.U. (ES)
FEATURES             Location/Qualifiers
     source        1..40
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="oligonucleotide probe"
ORIGIN

Query Match      58.3%; Score 14; DB 6; Length 40;
Best Local Similarity 77.3%; Pred. No. 5.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  ATGCCAACCCCTGCTCGGAGGC 22

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REFERENCE 1 (bases 1 to 24)
AUTHORS Serrero,G.
TITLE 88kDa tumorigenic growth factor and antagonists
JOURNAL Patent: US 6670193-A 15 30-DEC-2003;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 24;
Best Local Similarity 80.0%; Pred. No. 8.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CCAACCCCTGCTCTGGAGGCC 23
Db 5 CCAGCCCTGCTGTTAAGGCC 24

RESULT 28
AR494164
LOCUS AR494164 24 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 15 from patent US 6720159.
ACCESSION AR494164
VERSION AR494164.1 GI:47267029
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Serrero,G.
TITLE 88kDa tumorigenic growth factor and antagonists
JOURNAL Patent: US 6720159-A 15 13-APR-2004;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 24;
Best Local Similarity 80.0%; Pred. No. 8.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CCAACCCCTGCTCTGGAGGCC 23
Db 5 CCAGCCCTGCTGTTAAGGCC 24

RESULT 29
AX934355
LOCUS AX934355 24 bp DNA linear PAT 22-DEC-2003
DEFINITION Sequence 15 from Patent EP1356824.
ACCESSION AX934355
VERSION AX934355.1 GI:40313199
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Serrero,G.
TITLE 88kDa tumorigenic growth factor and antagonists
JOURNAL Patent: EP 1356824-A 15 29-OCT-2003;
FEATURES Location/Qualifiers
source 1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:3264"
/note="mammalian-Antisense oligonucleotide to human GP88"

ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 24;
Best Local Similarity 80.0%; Pred. No. 8.9e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CCAACCCCTGCTCTGGAGGCC 23
Db 5 CCAGCCCTGCTGTTAAGGCC 24

RESULT 30
AX651213/c
LOCUS AX651213 25 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3053 from Patent EP1273660.
ACCESSION AX651213
VERSION AX651213.1 GI:29154031
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 3053 08-JAN-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 8.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 GCCAACCCCTGCTCTGGAGGC 22
Db 25 GCCAACTCTGATCTGAAGCC 6

RESULT 31
AX651214/c
LOCUS AX651214 25 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3054 from Patent EP1273660.
ACCESSION AX651214
VERSION AX651214.1 GI:29154032
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 3054 08-JAN-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 8.9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 GCCAACCCCTGCTCTGGAGGC 22
Db 24 GCCAACTCTGATCTGAAGCC 5

RESULT 32
BD170870/c

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LOCUS       BD170870               34 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION   Human apoptosis-associated gene and human apoptosis-associated
              protein produced by the gene.
ACCESSION    BD170870
VERSION      BD170870.1  GI:27876682
KEYWORDS     WO 02057444-A/25.
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 34)
AUTHORS      Kondo,S. and Akiyama,N.
TITLE        Human apoptosis-associated gene and human apoptosis-associated
              protein produced by the gene
JOURNAL      SHINAE KONDO,NOBUTAKE AKIYAMA
              Patent: WO 02057444-A 25 25-JUL-2002;
COMMENT      SHINAE KONDO,NOBUTAKE AKIYAMA
              OS Artificial Sequence
              PN WO 02057444-A/25
              PD 25-JUL-2002
              PF 22-JAN-2002 WO 2002JP000413
              PR 22-JAN-2001 JP 01P 013217,11-MAY-2001 JP 01P 141490 PI
              SHINAE KONDO,NOBUTAKE AKIYAMA
              PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,A61K38/00,A61K48/00, PC
              A61P35/00,A61P43/00,G01N33/15,G01N33/50/C12P21/08 CC
              Description of Artificial Sequence: Synthesized CC
oligonucleotide
FH Key      Location/Qualifiers
FT source   1..34
FT          /organism='Artificial Sequence'.

FEATURES
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    Query Match      56.7%; Score 13.6; DB 6; Length 34;
    Best Local Similarity 80.0%; Pred. No. 8.9e+04;
    Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ORIGIN
      4  CCAACCTGCTCTGGAGGCC 23
      32  CCAGCCCTGGTGAGGAGGCC 13

RESULT 33
BD095049
LOCUS       BD095049               36 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION   Antibody against dendritic cell (DC) membrane molecule, Siglec-9,
              and DC detection method and DC separation method using it.
ACCESSION    BD095049
VERSION      BD095049.1  GI:22640637
KEYWORDS     JP 2001352977-A/2.
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 36)
AUTHORS      Watarai,H. and Yamaguchi,Y.
TITLE        Antibody against dendritic cell (DC) membrane molecule, Siglec-9,
              and DC detection method and DC separation method using it
JOURNAL      Patent: JP 2001352977-A 2 25-DEC-2001;
              KIRIN BREWERY CO LTD
COMMENT      PN JP 2001352977-A/2
              PD 25-DEC-2001
              PF 12-JUN-2000 JP 2000176187
              PI HIROSHI WATARAI,YASUNORI YAMAGUCHI
              PC C12N15/02,C07K16/18,C12N15/09,C12P21/08,C12Q1/02,G01N33/53, PC
              G01N33/53,
              CC G01N33/577/C12Q1/68,C12N15/00,C12N15/00
              CC Description of Artificial Sequence: a sense primer specific
              for 5'-leader
              CC sequence of Siglec-9 gene

LOCUS       BD172240/c            50 bp      DNA      linear      PAT 18-FEB-2003
DEFINITION   Secreted and transmembrane polypeptides and nucleic acids encoding
              the same.
ACCESSION    BD172240
VERSION      BD172240.1  GI:28413538
KEYWORDS     JP 200223786-A/13.
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
              Yuan,J.
TITLE        Secreted and transmembrane polypeptides and nucleic acids encoding
              the same
JOURNAL      Patent: JP 200223786-A 13 13-AUG-2002;
              GENENTECH INC
COMMENT      OS Artificial Sequence
              PN JP 200223786-A/13
              PD 13-AUG-2002
              PF 18-DEC-2001 JP 2001385135
              PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
              17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR
              17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR
              17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR
              18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR
              17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR
              21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR
              24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR
              24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR
              27-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR
              28-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR
              28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR
              28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR
              29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR
              29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR
              29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR
              29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR
              31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR
              07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR
              17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR
              21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR
              24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR
              24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
              24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
              WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
              JIAN ZHENG,
              PI JEAN YUAN
              PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
              C12N5/10,
              PC C12P21/02//C12P21/08,C12P21/02,C12R1:19), (C12P21/02,C12R1:91), PC

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(C12P21/02,C12R1:645),C12N15/00,C12N5/00
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FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGCCAACCCCTGCTCTGGAG 20
Db 22 ATGCCACAGCTGCTGTGGAG 3
RESULT 35
BD172559/c
LOCUS BD172559 50 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
ACCESSION BD172559.1 GI:28413861
VERSION BD172559.1
KEYWORDS JP 2002238586-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238586-A 13 27-AUG-2002;
COMMENT GENENTECH INC
OS Artificial Sequence
PN JP 2002238586-A/13
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385205
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/063327,27-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR
28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR
29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR
31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR
17-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR
17-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR
24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066840 PI
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
C12N5/10,

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PC C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),
PC (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),(C12P21/02,C12R1:645), PC
(C12P21/02,C12R1:19),(C12P21/08,C12R1:91),C12N15/00,C12N5/00, PC
(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic FH Key
FT Location/Qualifiers
FT source 1..50
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGCCAACCCCTGCTCTGGAG 20
Db 22 ATGCCACAGCTGCTGTGGAG 3
RESULT 36
BD172878/c
LOCUS BD172878 50 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
ACCESSION BD172878
VERSION BD172878.1 GI:28414184
KEYWORDS JP 2002238587-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238587-A 13 27-AUG-2002;
COMMENT GENENTECH INC
OS Artificial Sequence
PN JP 2002238587-A/13
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385248
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR
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18-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR
17-OCT-1997 US 60/059266,15-OCT-1997 US 60/062125 PR
21-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR
24-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/063327,27-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR
28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR
29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR
29-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR
17-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR
17-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR
21-NOV-1997 US 60/066770,24-NOV-1997 US 60/066840 PI
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

```


JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC
C12P21/02, C12P21/08/(C12P21/02, C12R1:91), (C12P21/02, C12R1:19), PC
(C12P21/02, C12R1:645), C12N15/00, C12N5/00, C12N15/00 CC
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Location/Qualifiers
FT source 1.50 /organism='Artificial Sequence'.
FT Location/Qualifiers
FEATURES
source
1.50
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/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04; 4; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ATGCCAACCTCTCTGGAG 20
||||| ||||| |||||
Db 22 ATGCCACAGCTCTGTGGAG 3

RESULT 37

BD173197/c
LOCUS
DEFINITION
Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
ACCESSION
BD173197
VERSION
BD173197.1 GI:28414506
KEYWORDS
JP 2002238588-A/13.
SOURCE
synthetic construct
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 50)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: JP 2002238588-A 13 27-AUG-2002;
GENENTECH INC
COMMENT
OS Artificial Sequence
PN JP 2002238588-A/13
PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385315
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/063127 PR
24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR
27-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063542 PR
29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR
29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR
31-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR
17-NOV-1997 US 60/064809, 12-NOV-1997 US 60/064248 PR
21-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065186 PR
24-NOV-1997 US 60/066120, 21-NOV-1997 US 60/065693 PR
24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066364 PR
24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02/(C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),
C12N5/10, C12R1:91), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC
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Location/Qualifiers
FT source 1.50 /organism='Artificial Sequence'.
FT Location/Qualifiers
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source
1.50
/organism='synthetic construct'
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/db_xref='taxon:32630'

ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04; 4; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ATGCCAACCTCTCTGGAG 20
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Db 22 ATGCCACAGCTCTGTGGAG 3

RESULT 38

BD175231/c
LOCUS
DEFINITION
Secretory and transmembrane polypeptide and nucleic acid encoding
the same.
ACCESSION
BD175231
VERSION
BD175231.1 GI:29120927
KEYWORDS
JP 2002253280-A/13.
SOURCE
synthetic construct
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 50)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
Secretory and transmembrane polypeptide and nucleic acid encoding
the same
JOURNAL
Patent: JP 2002253280-A 13 10-SEP-2002;
GENENTECH INC
COMMENT
OS Artificial Sequence
PN JP 2002253280-A/13
PD 10-SEP-2002

PF 18-DEC-2001 JP 2001385319
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
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17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR
27-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR
28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR
29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR
29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR
31-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR
17-NOV-1997 US 60/064809, 12-NOV-1997 US 60/064248 PR
21-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065186 PR
24-NOV-1997 US 60/066120, 21-NOV-1997 US 60/065693 PR
24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066364 PR
24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770;24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453;25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC
A61P25/00,
PC A61P25/16,A61P25/28,A61P31/12,A61P35/00,C07K14/47,C07K16/18,
PC C07K19/00,
PC C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,
PC A61P43/00,
PC C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,
PC C12R1:91),
PC C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91) CC
Description of Artificial Sequence: Synthetic FH Key

Location/Qualifiers
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/organism='Artificial Sequence'.
FT Location/Qualifiers
1..50
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

FEATURES
source

ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 39
AR410609/C
LOCUS AR410609 50 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6635468.
ACCESSION AR410609
VERSION AR410609.1 GI:40162109
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J.,
Kl javin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tamas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6635468-A 16 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..50
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ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 40
AR438973/C
LOCUS AR438973 50 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 16 from patent US 6664376.
ACCESSION AR438973

VERSION AR438973.1 GI:42664822

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)
AUTHORS Unclassified.

Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J.,
Kl javin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tamas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6664376-A 16 16-DEC-2003;
FEATURES Location/Qualifiers
source 1..50
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/mol_type='genomic DNA'

ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

Search completed: November 18, 2005, 17:42:51
Job time : 667.986 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 165.262 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-3

Perfect score: 24

Sequence: 1 ATGCCAACCTCTCTGGAGCCT 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
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9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
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12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	24	100.0	24	2	AaQ91123
2	24	100.0	24	9	ACA63113
3	24	100.0	24	13	ADR05299
4	16.8	70.0	50	12	ADP10021
5	16.2	67.5	41	6	AB250443
6	16.2	67.5	41	6	AB244893
7	15.6	65.0	45	12	ADM97503
8	15.6	65.0	45	12	ADM97521
9	15.6	65.0	45	12	ADM97483
10	15	62.5	25	13	ADM5334
11	14.6	60.8	30	6	ABL60842
12	14.6	60.8	30	6	ABL16712
13	14.6	60.8	30	8	ABL52021
14	14.6	60.8	40	6	ABL99201
15	14.4	60.0	17	3	AAF02607
16	14.4	60.0	20	3	ACAC2092
17	14.4	60.0	50	4	AAL29368
18	14.4	60.0	50	4	AAL34152
19	14.2	59.2	20	12	ADG86318
20	14.2	59.2	20	12	ADG86349

C 21	14.2	59.2	25	12	ADP17501	Adp17501 Renal cel
22	14	58.3	24	2	AAV68288	AAV68288 Penicilli
C 23	14	58.3	25	10	ADC06568	Adc06568 Human Na/
C 24	14	58.3	25	10	ADC08569	Adc08569 Human Na/
C 25	14	58.3	35	2	AAQ70259	Aaq70259 T. gondii
C 26	14	58.3	36	12	ADP71324	Adp71324 Human INS
27	14	58.3	40	13	ADQ99501	Adq99501 Flanked e
28	14	58.3	40	13	ADQ99500	Adq99500 Flanked e
29	14	58.3	42	6	AB249539	Abz49539 Human glu
30	14	58.3	42	6	AB245912	Abz45912 Human glu
C 31	13.8	57.5	20	9	ACH66436	Ach66436 Sense PCR
32	13.8	57.5	20	10	ABZ84928	Abz84928 Human Oli
33	13.8	57.5	20	11	ABD21158	Abd21158 Human tra
34	13.8	57.5	20	12	ADO31281	Ado31281 Human XT-
C 35	13.8	57.5	25	2	AAQ05223	Aaq05223 Murine IC
36	13.8	57.5	33	6	ABS55668	Abz55668 cAMP depe
C 37	13.8	57.5	41	6	ABK11967	Abk11966 Human TIM
C 38	13.8	57.5	41	6	ABK11967	Abk11967 Human TIM
39	13.8	57.5	50	4	AAI73671	Aai73671 Human sil
C 40	13.6	56.7	20	12	ADP22838	Adp22838 Human BUB
41	13.6	56.7	20	12	ADP22760	Adp22760 Human BUB
42	13.6	56.7	22	2	AAT35560	Aat35560 Beta-HCG
43	13.6	56.7	22	3	AAA39224	Aaa39224 Beta-HCG
C 44	13.6	56.7	22	6	ABK88718	Abk88718 Human YB-
45	13.6	56.7	24	2	AAV82832	Aav82832 Human GP8

ALIGNMENTS

RESULT 1

AAQ91123

ID AAQ91123 standard; CDNA; 24 BP.

XX

AC AAQ91123;

XX

DT 19-FEB-1996 (first entry)

XX

DE Beta-cardiac myosin heavy chain PCR primer A'.

XX

KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;

XX

OS Synthetic.

XX

PN USS429923-A.

XX

PD 04-JUL-1995.

XX

PF 11-DEC-1992; 92US-00989160.

XX

PR 11-DEC-1992; 92US-00989160.

XX

PA (HARD) HARVARD COLLEGE.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA (GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.

XX

PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX

DR WPI; 1995-245715/32.

XX

PT Non-invasive method for diagnosis of hypertrophic cardio-myopathy -

XX

PS useful for testing asymptomatic individual(s).

XX

PS Example 1; Col 10; 22pp; English.

XX

AAQ91121-091130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria

XX
 SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTGCTCTGGAGGCCT 24
 |||||
 Db 1 ATGCCAACCCCTGCTCTGGAGGCCT 24

RESULT 2
 ACA63113
 ID ACA63113 standard; DNA; 24 BP.
 XX
 AC ACA63113;
 XX
 DT 28-AUG-2003 (first entry)
 XX
 DE Human beta cardiac myosin heavy chain PCR primer A'.
 XX
 KW Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
 KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
 KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
 KW phenylketonuria; cystic fibrosis.

XX
 OS Homo sapiens.
 XX
 PN US2003054343-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 06-JUN-1995; 95US-00469172.
 XX
 PR 11-DEC-1992; 92US-00989160.
 XX
 PA (SEID/) SEIDMAN C.
 PA (SEID/) SEIDMAN J.
 PA (WATK/) WATKINS H.
 PA (ROSE/) ROSENZWEIG A.

PI Seidman C, Seidman J, Watkins H, Rosenzweig A;
 XX
 DR WPI; 2003-512374/48.
 XX

PT Detecting a presence or absence of a mutation associated with
 PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
 PT hemophilia, by detecting a mutation in an amplified product of a beta
 PT cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

PS The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
 CC and FHC) comprises detecting a mutation associated with hypertrophic
 CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy
 CC chain DNA. The mutations associated with SHC/FHC are detected in the
 CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-
 CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
 CC sample). FHC associated point mutation can be classified and used to
 CC determine life expectancy in affected individuals e.g. using a Kaplan-
 CC Meier curve for the classified type of FHC causing point mutation. Also
 CC included are an RNA probe comprising ribonucleotides arranged in a
 CC sequence which is complementary to at least a portion of beta-cardiac
 CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
 CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a nested PCR primer used to amplify a region of the beta cardiac
 CC myosin heavy chain cDNA containing an FHC-associated mutation

XX Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTGCTCTGGAGGCCT 24
 |||||
 Db 1 ATGCCAACCCCTGCTCTGGAGGCCT 24

RESULT 3
 ADR05299
 ID ADR05299 standard; DNA; 24 BP.
 XX
 AC ADR05299;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human beta cardiac myosin heavy chain mutation detection primer A'.
 XX
 KW Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
 KW familial hypertrophic cardiomyopathy;
 KW sporadic hypertrophic cardiomyopathy.

OS Homo sapiens.

XX US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

PI Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2004-592586/57.

XX Claim 18; SEQ ID NO 3; 22pp; English.

PS The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
 CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy
 CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
 CC amplified product, and detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy in the amplified product,
 CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
 CC included are a set of DNA oligonucleotide primers for amplifying beta-
 CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
 CC oligonucleotide primers being useful for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
 CC cardiomyopathy-associated mutation) and a kit for facilitating the
 CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
 CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
 CC heavy chain DNA, where the RNA probe is capable of detecting a
 CC hypertrophic cardiomyopathy-associated mutation, a second container
 CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
 CC instructions for using the components of the kit to detect the presence
 CC or absence of a hypertrophic cardiomyopathy-associated mutation in
 CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
 CC detecting the presence or absence of a mutation associated with
 CC hypertrophic cardiomyopathy for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
 CC having hypertrophic cardiomyopathy relies on the presence of typical
 CC clinical symptoms and the demonstration of unexplained ventricular
 CC hypertrophy. The present invention is non-invasive and based, at least in
 CC part, on the discovery that hypertrophic cardiomyopathy is caused by
 CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
 CC reveals that there are no extensive studies involving a large number of
 CC families which established that this particular disease or disorder was
 CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
 CC The present sequence is a PCR primer used to amplify a region of the beta
 CC cardiac myosin heavy chain having a disease-related point mutation.
 CC
 SQ . Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 13; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGCT 24
 DB 1 ATGCCAACCTGCTCTGGAGGCT 24

RESULT 4
 ADP10021/c
 ID ADP10021 standard; DNA; 50 BP.
 XX
 AC ADP10021;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE 50-mer oligonucleotide marker probe of the invention #30.
 XX
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-0011831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX
 DR WPI; 2004-400724/37.
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX

PS Claim 2; SEQ ID NO 30; 1762pp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC 50 mer oligonucleotide marker for diagnosis and monitoring of allograft
 CC rejection and other disorders.
 XX

SQ Sequence 50 BP; 9 A; 13 C; 18 G; 10 T; 0 U; 0 Other;

Query Match 70.0%; Score 16.8; DB 12; Length 50;
 Best Local Similarity 90.0%; Pred. No. 9.8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCC 23
 DB 37 CCACCCCTCTCTGGAGGCC 18

RESULT 5
 ABZ50443/c
 ID ABZ50443 standard; DNA; 41 BP.

XX AC ABZ50443;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human cytochrome P450 CYP4F3 gene polymorphic site, #7225.
 XX
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
 KW polymorphic site; drug evaluation; drug screening; genotyping;
 KW genetic profiling; therapeutic customisation; adverse reaction;
 KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT variation replace(21,A)
 FT /*tag= a
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 XX

PN WO200252044-A2.

XX

PD 04-JUL-2002.

XX

PF 27-DEC-2001; 2001WO-JP011592.

XX

PR 27-DEC-2000; 2000JP-00399443.

XX

PR 02-MAY-2001; 2001JP-00135256.

XX

PR 27-AUG-2001; 2001JP-00256862.

XX

PA (RIKE) RIKEN KK.

XX

PI Nakamura Y, Sekine A, Iida A, Saito S;
 XX
 DR WPI; 2002-583571/62.
 XX
 PT Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.
 XX
 PS Claim 23; Page 213; 2785pp; English.
 XX

CC Sequences AB243217-ABZ50887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from AB243217-ABZ50887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphism data, particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolising enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy

SQ Sequence 41 BP; 12 A; 6 C; 16 G; 7 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 41;
 Best Local Similarity 85.7%; Pred. No. 1.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCCT 24
 DB 25 CCAACCTACTCTGTGGCCT 5

RESULT 6
 ID AB244893/C
 XX AB244893 standard; DNA; 41 BP.
 AC AB244893;
 XX

DT 26-JUN-2003 (first entry)

XX Human cytochrome P450 CYP4F3 gene polymorphic site, #1677.

XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
 KW polymorphic site; drug evaluation; drug screening; genotyping;
 KW genetic profiling; therapeutic customisation; adverse reaction;
 KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH replace(21,A)
 FT /*tag= a
 FT /standard_name= "Single nucleotide polymorphism (SNP)"

XX WO200252044-A2.

XX 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX

PR 27-DEC-2000; 2000JP-00399443.
 PR 02-MAY-2001; 2001JP-00135256.
 PR 27-AUG-2001; 2001JP-00256862.
 PA (RIKE) RIKEN KK.
 XX
 XX Nakamura Y, Sekine A, Iida A, Saito S;
 XX WPI; 2002-583571/62.
 DR

XX Identifying individuals having a polymorphism, useful for determining the
 XX effectiveness or side effect of a drug or treatment protocol, comprises
 XX detecting at least one polymorphism in the drug metabolizing enzyme
 XX nucleic acid.

XX Claim 23; Page 92; 2785pp; English.

XX Sequences AB243217-ABZ50887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from AB243217-ABZ50887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphism data, particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolising enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy

XX Sequence 41 BP; 12 A; 6 C; 16 G; 7 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 41;
 Best Local Similarity 85.7%; Pred. No. 1.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCCT 24
 DB 25 CCAACCTACTCTGTGGCCT 5

RESULT 7
 ADM97503/C
 ID ADM97503 standard; DNA; 45 BP.
 XX

AC ADM97503;

XX 01-JUL-2004 (first entry)

XX CD1d-IgG-B2M complex F(ab'2) fragment PCR primer SEQ ID NO: 26.

XX CD1d complex; cytostatic; antiinflammatory; cancer; autoimmune disease;

KW inflammatory disease; immunosuppressive; antimicrobial; neuroprotective;
 KW antidiabetic; antiarthritic; antirheumatic; ophthalmological;
 KW gastrointestinal; nephrotropic; dermatological; hepatotropic;
 KW beta2-microglobulin; ss; primer; PCR.

XX Unidentified.

XX WO2004029206-A2.

XX PD 08-APR-2004.

XX PF 26-SEP-2003; 2003WO-US030238.

XX PR 27-SEP-2002; 2002EP-00405838.

XX PA (VACC-) VACCINEX INC.

PA (ROBE/) ROBERT B.

PA (DOND/) DONDA A.

PA (CESS/) CESSON V.

PA (MACH/) MACH J.

XX PI Robert B, Donda A, Cesson V, Mach J, Zauderer M;

XX DR WPI; 2004-316095/29.

XX New compound comprising CDId complexes and an antibody specific for a
 PT cell surface marker, useful for preventing or treating tumors and
 PT autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
 PT diabetes or psoriasis.

XX Example 10; Page 85; 152pp; English.

XX The present invention relates to a compound comprising one or more CDId
 CC complexes and an antibody or its fragment specific for a cell surface
 CC marker. The CDId complexes comprise a CDId and a beta2-microglobulin
 CC molecule, and are linked to the antibody or its fragment. The composition
 CC and methods are useful for preventing or treating tumors and
 CC autoimmune/inflammatory or infectious diseases, such as multiple
 CC sclerosis, type I diabetes, ankylosing spondylitis, acute anterior
 CC uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease,
 CC Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic
 CC arthritis, rheumatoid arthritis, systemic lupus erythematosus, systemic
 CC sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary
 CC cirrhosis, ulcerative colitis or autoimmune hepatitis. The present
 CC sequence is a PCR primer used in the exemplification of the invention.

XX SQ Sequence 45 BP; 5 A; 15 C; 17 G; 8 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 12; Length 45;

Best Local Similarity 81.8%; Pred. No. 3.3e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTGCTCGAGGC 22

||||| ||||| ||||| ||||| |||||

Db 40 ATGCCAACCCGTGCCAGGAGGC 19

RESULT 8

ADM97521/c

ID ADM97521 standard; DNA; 45 BP.

XX AC ADM97521;

XX DT 01-JUL-2004 (first entry)

XX DE CDId-IgG complex F(ab'2) fragment PCR primer SEQ ID NO: 44.

XX CDId complex; cytostatic; antiinflammatory; cancer; autoimmune disease;
 KW inflammatory disease; immunosuppressive; antimicrobial; neuroprotective;
 KW antidiabetic; antiarthritic; antirheumatic; ophthalmological;
 KW gastrointestinal; nephrotropic; dermatological; hepatotropic;
 KW beta2-microglobulin; ss; primer; PCR.

XX

OS Unidentified.

XX WO2004029206-A2.

XX PD 08-APR-2004.

XX PF 26-SEP-2003; 2003WO-US030238.

XX PR 27-SEP-2002; 2002EP-00405838.

XX PA (VACC-) VACCINEX INC.

PA (ROBE/) ROBERT B.

PA (DOND/) DONDA A.

PA (CESS/) CESSON V.

PA (MACH/) MACH J.

XX PI Robert B, Donda A, Cesson V, Mach J, Zauderer M;

XX DR WPI; 2004-316095/29.

XX New compound comprising CDId complexes and an antibody specific for a
 PT cell surface marker, useful for preventing or treating tumors and
 PT autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
 PT diabetes or psoriasis.

XX Example 15; Page 95; 152pp; English.

XX The present invention relates to a compound comprising one or more CDId
 CC complexes and an antibody or its fragment specific for a cell surface
 CC marker. The CDId complexes comprise a CDId and a beta2-microglobulin
 CC molecule, and are linked to the antibody or its fragment. The composition
 CC and methods are useful for preventing or treating tumors and
 CC autoimmune/inflammatory or infectious diseases, such as multiple
 CC sclerosis, type I diabetes, ankylosing spondylitis, acute anterior
 CC uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease,
 CC Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic
 CC arthritis, rheumatoid arthritis, systemic lupus erythematosus, systemic
 CC sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary
 CC cirrhosis, ulcerative colitis or autoimmune hepatitis. The present
 CC sequence is a PCR primer used in the exemplification of the invention.

XX SQ Sequence 45 BP; 5 A; 15 C; 17 G; 8 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 12; Length 45;

Best Local Similarity 81.8%; Pred. No. 3.3e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTGCTCGAGGC 22

||||| ||||| ||||| ||||| |||||

Db 40 ATGCCAACCCGTGCCAGGAGGC 19

RESULT 9

ADM97483/c

ID ADM97483 standard; DNA; 45 BP.

XX AC ADM97483;

XX DT 01-JUL-2004 (first entry)

XX DE CDId-IgG-avidin complex F(ab'2) fragment PCR primer SEQ ID NO: 6.

XX CDId complex; cytostatic; antiinflammatory; cancer; autoimmune disease;
 KW inflammatory disease; immunosuppressive; antimicrobial; neuroprotective;
 KW antidiabetic; antiarthritic; antirheumatic; ophthalmological;
 KW gastrointestinal; nephrotropic; dermatological; hepatotropic;
 KW beta2-microglobulin; ss; primer; PCR.

OS Unidentified.

XX WO2004029206-A2.

XX PD 08-APR-2004.

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XX PF 26-SEP-2003; 2003WO-US030238.
XX PR 27-SEP-2002; 2002EP-00405838.
XX PA (VACC-) VACCINEX INC.
XX PA (ROBE/) ROBERT B.
XX PA (DOND/) DONDA A.
XX PA (CESS/) CESSON V.
XX PA (MACH/) MACH J.
XX
XX PI Robert B, Donda A, Cesson V, Mach J, Zauderer M;
XX WIPI; 2004-316095/29.
XX
XX New compound comprising CD1d complexes and an antibody specific for a
XX cell surface marker, useful for preventing or treating tumors and
XX autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
XX diabetes or psoriasis.
XX
XX Example 4; Page 74; 152pp; English.
XX
XX The present invention relates to a compound comprising one or more CD1d
XX complexes and an antibody or its fragment specific for a cell surface
XX marker. The CD1d complexes comprise a CD1d and a beta2-microglobulin
XX molecule, and are linked to the antibody or its fragment. The composition
XX and methods are useful for preventing or treating tumors and
XX autoimmune/inflammatory or infectious diseases, such as multiple
XX sclerosis, type I diabetes, ankylosing spondylitis, acute anterior
XX uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease,
XX Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic
XX arthritis, rheumatoid arthritis, systemic lupus erythematosus, systemic
XX sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary
XX cirrhosis, ulcerative colitis or autoimmune hepatitis. The present
XX sequence is a PCR primer used in the exemplification of the invention.
XX
XX Sequence 45 BP; 5 A; 15 C; 17 G; 8 T; 0 U; 0 Other;
SQ
Query Match 65.0%; Score 15.6; DB 12; Length 45;
Best Local Similarity 81.8%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 ATGCCAACCCCTGCTGGAGGC 22
DB 40 ATGCCAACCCGTGCCAGGAGC 19
RESULT 10
ADR55334/c
ID ADR55334 standard; DNA; 25 BP.
XX AC
XX ADR55334;
XX
XX 18-NOV-2004 (first entry)
XX
XX Drug therapy altered expressed gene #2685.
XX
XX drug activity monitoring; expression profile; gene expression;
XX peripheral blood sample; peripheral blood mononuclear cell; drug therapy;
XX CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;
XX mTOR; ds.
XX
XX Homo sapiens.
XX
XX WO2004072265-A2.
XX
XX 26-AUG-2004.
XX
XX 11-FEB-2004; 2004WO-US004118.
XX
XX 11-FEB-2003; 2003US-0446133P.
XX
XX 03-APR-2003; 2003US-0459782P.
XX
XX 23-JAN-2004; 2004US-0538246P.
XX
XX (AMHP ) WYETH.
XX PA (BURC/) BURCZYNSKI M.
XX PA (TWIN/) TWINE N.
XX PA (DORN/) DORNER A J.
XX PA (TREP/) TREPICCHIO W L.
XX
XX Burczynski M, Twine N, Dornier AJ, Trepicchio WL;
XX WIPI; 2004-642301/62.
XX
XX Monitoring drug activities in vivo comprises comparing an expression
XX profile of a gene in a peripheral blood sample of a patient before and
XX after drug therapy.
XX
XX Disclosure; SEQ ID NO 2685; 136pp; English.
XX
XX The invention relates to a method of monitoring drug activities in vivo
XX by comparing an expression profile of at least one gene in a peripheral
XX blood sample of a patient to a reference expression profile of the at
XX least one gene, where the at least one gene is differentially expressed
XX in peripheral blood mononuclear cells (PBMCs) of patients who have a non-
XX blood disease and are subjected to a drug therapy as compared to PBMCs
XX isolated from the patient before the drug therapy, and where the patient
XX has the non-blood disease and is being treated by the drug therapy. The
XX method, kit, and nucleic acid array are useful for monitoring drug
XX activities in vivo. The drug is especially CCI-779, an ester analogue of
XX the immunosuppressant rapamycin which is a potent inhibitor of the
XX mammalian target of rapamycin (mTOR). This sequence represents a gene
XX expressed in PBMC altered by the drug therapy. (Note: this sequence does
XX no form part of the printed specification but was obtained in electronic
XX format from WIPO at ftp.wipo.int/pub/published_pct_sequences/).
XX
XX Sequence 25 BP; 7 A; 7 C; 9 G; 2 T; 0 U; 0 Other;
SQ
Query Match 62.5%; Score 15; DB 13; Length 25;
Best Local Similarity 78.3%; Pred. No. 6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 2 TGCCAACCCCTGCTGGAGGCCT 24
DB 25 TGTCCACCCCTGCTGGTACCT 3
RESULT 11
ABL60842/c
ID ABL60842 standard; DNA; 30 BP.
XX AC
XX ABL60842;
XX
XX 10-SEP-2002 (first entry)
XX
XX Murine CIS DNA fragment amplifying reverse primer.
XX
XX Leptin; receptor; cytokine signalling 3; SOCS3; CIS; Vav; anabolic;
XX cytokine-inducible SH2-containing protein; anorectic; vulnery;
XX cyostatic; PCR; primer; ss.
XX
XX Mus sp.
XX
XX WO200240543-A1.
XX
XX 23-MAY-2002.
XX
XX 29-OCT-2001; 2001WO-EP012569.
XX
XX 14-NOV-2000; 2000EP-00204001.
XX
XX 15-NOV-2000; 2000US-0248970P.
XX
XX (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Eyckerman S, Tavernier J, Zabeau L;

```


DR WPI; 2002-500206/53.
 XX New functional fragment of leptin receptor, involved in suppressor of
 PT cytokine signaling 3, cytokine-inducible SH2-containing protein and/or
 PT Vav signaling, useful for modulating ligand induced signaling.
 XX Example; Page 9; 35pp; English.
 XX The invention relates to functional fragments of a leptin receptor,
 CC involved in suppressor of cytokine signalling 3 (SOCS3), cytokine-
 CC inducible SH2-containing protein (CIS) and/or Vav signalling. The leptin
 CC receptor functional fragments are useful for modulating ligand (e.g.
 CC leptin) induced signalling, and to screen compounds that interfere with
 CC the binding of the functional fragment with a signalling molecule e.g.
 CC Vav, SOCS3 or CIS. Modulators of leptin may be useful in food intake
 CC disorders and regulation of weight, angiogenesis, wound healing and
 CC susceptibility to digestive cancers. The present sequence represents a
 CC PCR primer for amplifying the murine CIS DNA fragment
 XX
 SQ Sequence 30 BP; 7 A; 5 C; 11 G; 7 T; 0 U; 0 Other;
 Query Match 60.8%; Score 14.6; DB 6; Length 30;
 Best Local Similarity 81.0%; Pred. No. 9.1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TGCCAAACCTGCTCTGGAGGC 22
 Db 21 TTCCAACCTCTGATCTAGAGGC 1
 RESULT 12
 ID ABK16712/c
 XX ABK16712 standard; DNA; 30 BP.
 AC ABK16712;
 XX
 DT 26-MAR-2002 (first entry)
 DE CIS primer MBU-O-678.
 XX Recombinant transmembrane receptor; PCR primer; ss.
 KW Mus sp.
 OS Synthetic.
 XX WO200190188-A2.
 PN 29-NOV-2001.
 XX 22-MAY-2001; 2001WO-BP005916.
 PF 22-MAY-2000; 2000EP-00201771.
 PR (VLAAs-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 PA Eyckerman S, Van Ostade X, Vandekerckhove J, Verhee A;
 PI Tavernier J;
 PI WPI; 2002-097646/13.
 XX New recombinant transmembrane receptor, useful for detecting compound-
 PT compound binding, comprises extracellular ligand binding domain and
 PT cytoplasmic domain containing heterologous bait polypeptide.
 XX Example 9; Page 41; 74pp; English.
 PS The invention describes a novel recombinant transmembrane receptor
 CC comprising an extracellular ligand binding domain and a cytoplasmic
 CC domain that contains a heterologous bait polypeptide. The receptor is
 CC activated by binding of a ligand to the ligand binding domain and by
 CC binding of a prey polypeptide to the heterologous bait peptide. The
 CC receptor or the prey polypeptide is useful for detection of compound-
 CC compound binding, where the binding is modification state dependant and

CC the modification is phosphorylation, acetylation, acylation, methylation,
 CC ubiquitination or glycosylation. The binding is mediated by three or
 CC more partners, where one or more of the partners is not or not completely
 CC of proteinaceous nature. This sequence is one of 47 PCR primers (see
 CC ABK16683-ABK16729) associated with the construction of the recombinant
 CC transmembrane receptor, described in the method of the invention
 XX
 SQ Sequence 30 BP; 7 A; 5 C; 11 G; 7 T; 0 U; 0 Other;
 Query Match 60.8%; Score 14.6; DB 6; Length 30;
 Best Local Similarity 81.0%; Pred. No. 9.1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TGCCAAACCTGCTCTGGAGGC 22
 Db 21 TTCCAACCTCTGATCTAGAGGC 1
 RESULT 13
 ID AAL52021/c
 XX AAL52021 standard; DNA; 30 BP.
 AC AAL52021;
 XX
 DT 10-MAY-2003 (first entry)
 DE Recombinant receptor-related construction PCR primer #18.
 XX PCR; primer; ss; recombinant receptor; ligand binding domain;
 KW heterologous bait polypeptide; protein-protein interaction; screening.
 XX Unidentified.
 XX WO2003004643-A2.
 PN 16-JAN-2003.
 PD 02-JUL-2002; 2002WO-EP007419.
 PF 03-JUL-2001; 2001EP-00202569.
 PR (VLAAs-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 PA Eyckerman S, Tavernier J, Vandekerckhove J;
 PI WPI; 2003-210363/20.
 XX New recombinant receptor comprising a ligand binding domain and a domain
 PT that comprises a heterologous bait polypeptide, useful for screening
 PT compounds that disrupt compound-compound binding.
 XX Example 3; Page 25; 45pp; English.
 PS The invention comprises a recombinant receptor which contains a ligand
 CC binding domain and a heterologous bait polypeptide. The activation of the
 CC receptor is inhibited by the binding of a prey polypeptide to the
 CC heterologous bait polypeptide. The recombinant receptor is useful for
 CC screening compounds that disrupt compound-compound binding - especially
 CC protein-protein interactions that are essential to any biological
 CC process. The present DNA sequence represents a PCR primer that is used in
 CC the exemplification of the invention
 XX
 SQ Sequence 30 BP; 7 A; 5 C; 11 G; 7 T; 0 U; 0 Other;
 Query Match 60.8%; Score 14.6; DB 8; Length 30;
 Best Local Similarity 81.0%; Pred. No. 9.1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TGCCAAACCTGCTCTGGAGGC 22
 Db 21 TTCCAACCTCTGATCTAGAGGC 1

```

RESULT 14
ABL9201
ID ABL99201 standard; DNA; 40 BP.
XX
XX AC
XX ABL99201;
XX
DT 28-JUN-2002 (first entry)
XX
DE Green/red click beetle luciferase preparing oligo SEQ ID NO:169.
XX
DE Luciferase; synthetic nucleic acid; transcriptional characteristic;
XX transcripition; codon usage; PCR; primer; ss.
XX
OS Coleoptera.
OS Synthetic.
XX
XX WO200216944-A2.
XX
XX 28-FEB-2002.
XX
XX 24-AUG-2001; 2001WO-US026566.
XX
XX 24-AUG-2000; 2000US-00645706.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Wood KV, Wood MG, Zhuang Y, Paguio A;
XX WPI; 2002-304140/34.
XX
XX Preparing a synthetic nucleic acid molecule with reduced inappropriate
XX transcriptional characteristics when expressed in a cell, for e.g making
XX fusion proteins, by altering a wild type or another synthetic nucleic
XX acid sequence.
XX
XX Example 1; Fig 6; 294pp; English.
XX
XX The present invention relates to the preparation of synthetic nucleic
XX acid molecules which have altered transcriptional regulatory sequences
XX compared to the wild-type. These sequences are then transcribed with less
XX frequency compared to the wild-type. In particular, the invention relates
XX to altered luciferase sequences. This can be used to detect weak promoter
XX activity, to express fusion proteins, to detect and/or measure levels of
XX gene expression, subcellular localisation or targeting, in life science
XX research, agrogenetics, gene therapy, developmental science and
XX pharmaceutical development. The present sequence is an oligonucleotide
XX described in the exemplification of the invention
XX
XX Sequence 40 BP; 4 A; 10 C; 16 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 60.8%; Score 14.6; DB 6; Length 40;
XX Best Local Similarity 81.0%; Pred. No. 9.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 3 GCCAACCTGCTCTGGAGGCC 23
XX 16 GCATTCCTGATCTGGAGGCC 36
XX
XX Db
XX
XX RESULT 15
AAF02607
ID AAF02607 standard; DNA; 17 BP.
XX
XX AC
XX AAF02607;
XX
XX 16-FEB-2001 (first entry)
XX
XX Hammerhead ribozyme substrate #902.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
XX

RESULT 16
AAC62092
ID AAC62092 standard; DNA; 20 BP.
XX
XX AC
XX AAC62092;
XX
XX 06-MAR-2001 (first entry)
XX
XX Reverse primer used to amplify a human elastase I gene exon 8.
XX
XX Human; elastase I; chromosome 12q13; mutant; serine protease; eczema;
XX hyperproliferative skin condition; psoriasis; lupus erythematosis;
XX erythema; cancer; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO2000061728-A2.
XX
XX 19-OCT-2000.
XX
XX 12-APR-2000; 2000WO-GB001389.
XX
XX 13-APR-1999; 99GB-00008458.
XX
XX (QUEB-) QUEEN MARY & WESTFIELD COLLEGE.
XX
XX Gerst-Talas U, Dunlop J, Kelsell DP;
XX
XX WPI; 2000-679482/66.
XX
XX Recombinant polynucleotide encoding human elastase I mutant useful for
XX determining the predisposition of a subject to cancer or

```

PT hyperproliferative skin condition such as psoriasis, eczema,
XX erythematosis.

PS Disclosure; Page 20; 35pp; English.

CC PCR primers AAC62091-92 were used to amplify a human elastase I gene
CC fragment. The elastase I gene maps to chromosome 12q13. Elastase is a
CC serine protease, and is localised in the basal layer of the mammalian
CC skin. The specification describes a mutant elastase I, with a frame shift
CC mutation in any one of the codons 207-225. The mutation results in the
CC disruption of the carboxy terminal of the protein, and possibly affects
CC substrate binding. An allele encoding a mutant elastase I can be detected
CC to determine the predisposition of a subject to a hyperproliferative skin
CC condition (e.g. psoriasis, eczema, lupus erythematosus and erythema) or
CC cancer

SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 3; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.1e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AACCTGCTCTGGAGG 21

DB 5 ACCCTGCTCTGGAGG 20

RESULT 17

AAL29368

ID AAL29368 standard; DNA; 50 BP.

XX AC

XX AAL29368;

XX DT

XX 24-JAN-2002 (first entry)

XX DE

XX Human SNP oligonucleotide #2576.

XX KW

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; histone; kinase; colony stimulating factor;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

XX OS

XX Homo sapiens.

XX PN

XX WO200147944-A2.

XX PD

XX 05-JUL-2001.

XX PF

XX 28-DEC-2000; 2000WO-US035498.

XX PR

XX 28-DEC-1999; 99US-0173419P.

XX PR

XX 27-DEC-2000; 2000US-00173419.

XX PA

XX (CURA-) CURAGEN CORP.

XX PI

XX Shimkets RA, Leach M;

XX DR

XX WPI; 2001-465210/50.

XX PT

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.

XX PS

XX Claim 1; Page 2121; 4143pp; English.

XX CC

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related

CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms

SQ Sequence 50 BP; 6 A; 21 C; 15 G; 8 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 4; Length 50;

Best Local Similarity 93.8%; Pred. No. 1.2e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCCAACCCCTGCTCTG 17

DB 22 TGCCAGCCCTGCTCTG 37

RESULT 18

AAL34152/C

ID AAL34152 standard; DNA; 50 BP.

XX AC

XX AAL34152;

XX DT

XX 24-JAN-2002 (first entry)

XX DE

XX Human SNP oligonucleotide #7360.

XX KW

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; histone; kinase; colony stimulating factor;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

XX OS

XX Homo sapiens.

XX PN

XX WO200147944-A2.

XX PD

XX 05-JUL-2001.

XX PF

XX 28-DEC-2000; 2000WO-US035498.

XX PR

XX 28-DEC-1999; 99US-0173419P.

XX PR

XX 27-DEC-2000; 2000US-00173419.

XX PA

XX (CURA-) CURAGEN CORP.

XX PI

XX Shimkets RA, Leach M;

XX DR

XX WPI; 2001-465210/50.

XX PT

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.

XX PS

XX Claim 1; Page 3504; 4143pp; English.

XX CC

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of the proteins listed above.
 CC Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms

XX SQ Sequence 50 BP; 10 A; 21 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 4; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1.2e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ATGCCAACCTGCTCTGGAGGCT 24

Db 39 ATGCTGACCTGGCTGGAGGCTT 16

RESULT 19

ADG86318

ID ADG86318 standard; DNA; 20 BP.

XX AC ADG86318;

XX DT 11-MAR-2004 (first entry)

XX DE Human SMRT chimeric phosphorothioate oligonucleotide SEQ ID NO:32.

XX KW SMRT; silencing mediator for retinoid and thyroid hormone action;
 KW SMRT inhibitor; cytostatic; antiinflammatory; antiarthritic;
 KW antirheumatic; antisense therapy; inflammatory disorder;
 KW rheumatoid arthritis; hyperproliferative disorder; cancer; leukaemia;
 KW breast cancer; human; phosphorothioate; ss; chimeric.

XX OS Chimeric.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "phosphorothioate linkages, and all cytidine

FT residues are 5-methylcytidines"

FT modified_base 1..5

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2'-O-methoxyethyls"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-O-methoxyethyls"

XX WO2003106645-A2.

XX PD 24-DEC-2003.

XX PF 17-JUN-2003; 2003WO-US018923.

XX PR 17-JUN-2002; 2002US-00174014.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Freier SM, Dobie KW;

XX DR WPI; 2004-082184/08.

XX Novel antisense compound targeted to nucleic acid encoding SMRT
 XX PT (silencing mediator for retinoid and thyroid hormone action), useful for
 XX PT treating animal having disease associated with SMRT such as cancer,

PT rheumatoid arthritis.

XX Example 15; SEQ ID NO 32; 260pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding SMRT (silencing mediator for
 CC retinoid and thyroid hormone action), where (I) specifically hybridises
 CC with the nucleic acid molecule encoding SMRT and inhibits expression of a
 CC SMRT. (I) specifically hybridises with at least 8-nucleobase portion of a
 CC preferred target region on nucleic acid molecule encoding SMRT. Also
 CC described is a composition (II) comprising (I) and a carrier or diluent.
 CC (I) and (II) have cytostatic, antiinflammatory, antiarthritic and
 CC antirheumatic activities, and can be used in antisense therapy, and as
 CC SMRT expression inhibitors. (I) is useful for inhibiting the expression
 CC of SMRT in cells or tissues. (I) is also useful for treating an animal
 CC having a disease or condition associated with SMRT, e.g., inflammatory
 CC disorder such as rheumatoid arthritis; or a hyperproliferative disorder
 CC such as cancer chosen from leukaemia and breast cancer, by inhibiting the
 CC expression of SMRT. (I) is useful for diagnostics, therapeutics,
 CC prophylaxis and as research reagents and kits. The present sequence
 CC represents a chimeric phosphorothioate antisense oligonucleotide which
 CC inhibits human SMRT, which is used in an example from the present
 CC invention. N.B. The present sequence is designated as SEQ ID NO:30 in
 CC example 15 but corresponds to SEQ ID NO:32 in the Sequence Listing.

XX SQ Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 12; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.3e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 GCCAACCTGCTCTGGAGG 21

Db 2 GCCCACCTGCTCTGCATG 20

RESULT 20

ADG86349/c

ID ADG86349 standard; DNA; 20 BP.

XX AC ADG86349;

XX DT 11-MAR-2004 (first entry)

XX DE Human SMRT target region SEQ ID NO:63.

XX KW SMRT; silencing mediator for retinoid and thyroid hormone action;
 KW SMRT inhibitor; cytostatic; antiinflammatory; antiarthritic;
 KW antirheumatic; antisense therapy; inflammatory disorder;
 KW rheumatoid arthritis; hyperproliferative disorder; cancer; leukaemia;
 KW breast cancer; human; ss; target.

XX OS Synthetic.

XX OS Homo sapiens.

XX WO2003106645-A2.

XX PD 24-DEC-2003.

XX PF 17-JUN-2003; 2003WO-US018923.

XX PR 17-JUN-2002; 2002US-00174014.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Freier SM, Dobie KW;

XX DR WPI; 2004-082184/08.

XX Novel antisense compound targeted to nucleic acid encoding SMRT
 XX PT (silencing mediator for retinoid and thyroid hormone action), useful for
 XX PT treating animal having disease associated with SMRT such as cancer,
 XX PT rheumatoid arthritis.

```
XX PS Example 15; SEQ ID NO 63; 260pp; English.
XX CC The present invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule encoding SMRT (silencing mediator for
CC retinoid and thyroid hormone action), where (I) specifically hybridises
CC with the nucleic acid molecule encoding SMRT and inhibits expression of a
CC SMRT. (I) specifically hybridises with at least 8-nucleobase portion of a
CC preferred target region on nucleic acid molecule encoding SMRT. Also
CC described is a composition (II) comprising (I) and a carrier or diluent.
CC (I) and (II) have cytostatic, antiinflammatory, antiarthritic and
CC antirheumatic activities, and can be used in antisense therapy, and as
CC SMRT expression inhibitors. (I) is useful for inhibiting the expression
CC of SMRT in cells or tissues. (I) is also useful for treating an animal
CC having a disease or condition associated with SMRT, e.g., inflammatory
CC disorder such as rheumatoid arthritis; or a hyperproliferative disorder
CC such as cancer chosen from leukaemia and breast cancer, by inhibiting the
CC expression of SMRT. (I) is useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. The present sequence
CC represents a human SMRT target region sequence, which is used in an
CC example from the present invention. N.B. The present sequence is
CC designated as SEQ ID NO:61 in example 15 but corresponds to SEQ ID NO:63
CC in the Sequence listing.
XX CC
XX SQ Sequence 20 BP; 4 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
      Query Match      59.2%; Score 14.2; DB 12; Length 20;
      Best Local Similarity 84.2%; Pred. No. 1.3e+04;
      Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCCAACCTGCTCTGAGG 21
Db 19 GCCACCTGCTCTGCATG 1
      |||||
RESULT 21
ADP17501/c
ID ADP17501 standard; DNA; 25 BP.
XX AC ADP17501;
XX CC
XX DT 26-AUG-2004 (first entry)
XX DE Renal cell carcinoma differentially expressed gene probe #3906.
XX KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX OS Homo sapiens.
XX PN WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.
XX PR 21-NOV-2002; 2002US-0427982P.
XX PR 03-APR-2003; 2003US-0459782P.
XX PA (AMHP ) WYETH.
XX PA (TWIN/) TWINE N C.
XX PA (BURC/) BURCZYNSKI M E.
XX PA (TREP/) TREPICCHIO W L.
XX PA (DORN/) DORNER A.
XX PA (STOV/) STOVER J A.
XX PA (SLON/) SLONI D K.
XX PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
XX PI Sloni DK;
XX DR WPI; 2004-460799/43.
XX CC
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```
PT Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX PS Disclosure; SEQ ID NO 4237; 350pp; English.
XX CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX CC
XX SQ Sequence 25 BP; 6 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
      Query Match      59.2%; Score 14.2; DB 12; Length 25;
      Best Local Similarity 84.2%; Pred. No. 1.4e+04;
      Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGCCAACCTGCTCTGGA 19
Db 19 ATGCCATCTCAGCTCTGGA 1
      |||||
RESULT 22
AAV68288
ID AAV68288 standard; DNA; 24 BP.
XX AC AAV68288;
XX CC
XX DT 01-MAR-1999 (first entry)
XX DE Penicillium chrysogenum primer 24.
XX KW ss; PCR; amplification; primer; filamentous fungus; recombinant DNA;
KW DNA domain; fermentation.
XX OS Synthetic.
XX OS Penicillium chrysogenum.
XX PN WO9846772-A2.
XX PD 22-OCT-1998.
XX PF 09-APR-1998; 98WO-EP002070.
XX PR 11-APR-1997; 97EP-00201091.
XX PA (KONN ) GIST-BROCADES BV.
XX PI Selten GCM, Swinkels BW, Bovenberg RAL;
XX PI WPI; 1998-609917/51.
XX DR Recombinant filamentous fungus produced by gene conversion - has DNA
XX PT integrated into two or more mostly homologous DNA domains of its
XX PT chromosomes, used in the fermentation industry.
XX CC Example; Page 33; 171pp; English.
XX CC The primers AAV68265-V68314 are used in examples of the construction of
XX CC new filamentous fungus with a recombinant DNA molecule integrated into at
XX CC least 2 substantially homologous DNA domains of its chromosome(s), and
```

CC where the DNA domains are not the ribosomal DNA repeats. The recombinant
CC fungus is used in the fermentation industry, and the DNA domains can be
CC further multiplied with integrated recombinant DNA through gene
CC conversion or amplification. The new fungi provide greater versatility
CC compared with available systems, because the fungus is not confined to
CC the use of deficient selectable marker genes for transformation, and is
CC not confined to the use of only ribosomal DNA as target sequences for
CC integration. Also, the fungi provide greater genetic stability of the
CC integrated multiple copies compared with conventional recombinant fungi
CC in which recombinant DNA are randomly integrated in tandem arrays. The
CC genotype of the fungi can be completely defined, facilitating regulatory
CC approval, and the phenotype will be more predictable
XX
XX Sequence 24 BP; 3 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
SQ

Query Match 58.3%; Score 14; DB 2; Length 24;
Best Local Similarity 77.3%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GCCAACCTGCTCTGGAGCCT 24
DB 1 GCCTACTCTGTTCTGGAGAGCT 22

RESULT 23
ADC06568/c
ID ADC06568 standard; DNA; 25 BP.
XX
AC ADC06568;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Na/H exchanger-like protein 1 gene oligonucleotide #3015.
XX
KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
KW NHELP1; passive replacement therapy; vaccine; diagnosis.
XX
OS Homo sapiens.
XX
PN EP1273660-A2.
XX
PD 08-JAN-2003.
XX
PF 25-JAN-2002; 2002EP-00001160.
XX
PR 30-JAN-2001; 2001WO-US000666.
PR 23-MAY-2001; 2001US-00864761.
PR 21-DEC-2001; 2001US-0343331P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y;
XX
DR WPI; 2003-302724/30.
XX
PT New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as a
PT passive replacement therapy or as a vaccine for treating or preventing
PT disorders associated with aberrant expression or activity of human
PT NHELP1.
XX
PS Example 2; SEQ ID NO 3055; 468pp; English.
XX

The invention relates to a nucleic acid molecule which encodes a Na+/H+
CC exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide, an antibody against the protein or its antigen-binding
CC fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide and an agonist are particularly useful for manufacturing a
CC medicament for treating or preventing a disorder associated with
CC decreased expression or activity of human NHELP1. The antibody or its
CC antigen-binding fragment, and an antagonist, are useful for manufacturing
CC a medicament for treating or preventing a disorder associated with
CC increased expression or activity of human NHELP1. The NHELP1 nucleic acid
CC molecule is useful as passive replacement therapy, as a vaccine, or in
CC or protein is useful as passive replacement therapy, as a vaccine, or in

CC diagnostic methods. This sequence corresponds to a 256-mer
CC oligonucleotide spanning the sequence of the human NHELP1 gene
CC (ADC03514).
XX
SQ Sequence 25 BP; 4 A; 5 C; 8 G; 8 T; 0 U; 0 Other;
XX

Query Match 58.3%; Score 14; DB 10; Length 25;
Best Local Similarity 77.3%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGC 22
DB 25 ACGCCAACTCTGATCTGAAGCC 4

RESULT 24
ADC06569/c
ID ADC06569 standard; DNA; 25 BP.
XX
AC ADC06569;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Na/H exchanger-like protein 1 gene oligonucleotide #3016.
XX
KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
KW NHELP1; passive replacement therapy; vaccine; diagnosis.
XX
OS Homo sapiens.
XX
PN EP1273660-A2.
XX
PD 08-JAN-2003.
XX
PF 25-JAN-2002; 2002EP-00001160.
XX
PR 30-JAN-2001; 2001WO-US000666.
PR 23-MAY-2001; 2001US-00864761.
PR 21-DEC-2001; 2001US-0343331P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y;
XX
DR WPI; 2003-302724/30.
XX
PT New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as a
PT passive replacement therapy or as a vaccine for treating or preventing
PT disorders associated with aberrant expression or activity of human
PT NHELP1.
XX
PS Example 2; SEQ ID NO 3056; 468pp; English.
XX

The invention relates to a nucleic acid molecule which encodes a Na+/H+
CC exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide, an antibody against the protein or its antigen-binding
CC fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide and an agonist are particularly useful for manufacturing a
CC medicament for treating or preventing a disorder associated with
CC decreased expression or activity of human NHELP1. The antibody or its
CC antigen-binding fragment, and an antagonist, are useful for manufacturing
CC a medicament for treating or preventing a disorder associated with
CC increased expression or activity of human NHELP1. The NHELP1 nucleic acid
CC molecule is useful as passive replacement therapy, as a vaccine, or in
CC or protein is useful as passive replacement therapy, as a vaccine, or in

QV 1 ATGCCAACCTGCTCTGGAGGC 22
 Db 24 ACGCCAACTCTGATCTGAAGCC 3

RESULT 25
 ID AAQ70259/c
 AC AAQ70259;
 XX AAQ70259;
 DT 25-MAR-2003 (revised)
 DT 15-MAR-1995 (first entry)
 XX
 DE T. gondii P30.291 PCR primer.
 XX
 KW Toxoplasma gondii; toxoplasmosis; P30; P30.291; nP30.873; trachyzoite;
 KW surface antigen; vaccine; alpha-virus; vector; PCR;
 KW polymerase chain reaction; amplification; primer; secretion; ss.
 XX
 OS Synthetic.
 XX
 PN WO9417813-A1.
 XX
 PD 18-AUG-1994.
 XX
 PD 08-FEB-1994; 94WO-US001398.
 XX
 PD 08-FEB-1993; 93US-00015414.
 XX
 PA (PARA-) PARAVAX INC.
 XX
 PI Grieve RB, Xiong C;
 XX
 XX WPI; 1994-279381/34.
 XX
 XX Use of packaging defective alpha-virus expression vectors - for prodn. of
 PT protective cpds. for protecting animals from disease, partic.
 PT toxoplasmosis.
 XX
 PS Example; Page 81; 128pp; English.
 XX

A sequence is provided (AAQ70254) that contains the entire coding region for the T. gondii tachyzoite major surface antigen P30 (AARS7065). DNA fragment nP30.873 encoding T. gondii antigen P30.291 was obtained by PCR amplification of a clone encoding the P30 gene using the primers given in AAQ70259-60. P30.291 comprises amino acids 46-336 of P30, but is functionally equivalent to the natural protein. Deletion of the N-terminal hydrophobic region of P30 allows improved secretion from producer cells, for use in toxoplasmosis vaccine production. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 35 BP; 6 A; 13 C; 10 G; 6 T; 0 U; 0 Other;
 Query Match 58.3%; Score 14; DB 2; Length 35;
 Best Local Similarity 77.3%; Pred No. 1.7e-04;
 . Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QV 1 ATGCCAACCTGCTCTGGAGGC 22
 Db 25 ATGCCATCCCGGCTAGAGTC 4

RESULT 26
 ADP71324/c
 ID ADP71324 standard; DNA; 36 BP.
 XX
 AC ADP71324;
 XX
 DT 23-SEP-2004 (first entry)
 DT
 XX Human INSP105 PCR primer INSP105-exon4R.

XX human; INSP105; growth hormone; antiinflammatory; cytostatic;
 KW neuroprotective; virucide; osteopathic; antibacterial; fungicide;
 KW anorectic; nephrotropic; cardiant; reproductive disorder;
 KW pregnancy disorder; gestational trophoblastic disease;
 KW developmental disorder; Silver-Russell syndrome; growth disorder;
 KW growth hormone deficiency; Cushing's disease; endocrine disorder;
 KW cell proliferative disorder; neoplasm; carcinoma; tumour; melanoma;
 KW adenocarcinoma; choriocarcinoma; osteosarcoma; angiogenesis;
 KW myeloproliferative disorder; autoimmune disorder; inflammatory disorder;
 KW cardiovascular disorder; neurological disorder; pain; metabolic disorder;
 KW diabetes mellitus; osteoporosis; obesity; cachexia; AIDS; renal disease;
 KW lung injury; ageing; infection; PCR; primer; ss; chromosome 17.
 XX
 OS Homo sapiens.
 XX
 PN WO2004056863-A2.
 XX
 PD 08-JUL-2004.
 XX
 PD 19-DEC-2003; 2003WO-GB005594.
 XX
 PD 20-DEC-2002; 2002GB-00029850.
 XX
 PA (ARES-) ARES TRADING SA.
 XX
 PI Fagan RJ, Phelps CB, Rodrigues TM, Power C, De Tiani M;
 XX WPI; 2004-500284/47.
 XX

New INSP105 polypeptides, useful in preparing a composition for treating or preventing a disease associated with growth hormone proteins, e.g. cell proliferative, inflammatory or neurological disorders or infections.

Example 2; Page 55; 84pp; English.

The present invention describes an INSP105 polypeptide comprising: (a) a 199 amino acid sequence given in SEQ ID NO:8 (ADP71313); (b) a fragment of (1) that functions as a growth hormone, or having an antigenic determinant in common with (1); or (c) a functional equivalent of (1) or the polypeptide; (2) a purified nucleic acid molecule which encodes host cell transformed with the vector; (4) a ligand which binds specifically to the growth hormone polypeptide; (5) a compound that either increases or decreases the level of expression or activity of the polypeptide; (6) a method of diagnosing a disease in a patient; (7) a pharmaceutical composition comprising the polypeptide, nucleic acid molecule, vector, host cell, ligand or compound; (8) a vaccine composition comprising the polypeptide or nucleic acid molecule; (9) a method of treating a disease in a patient; (10) a method of monitoring the therapeutic treatment of disease in a patient; (11) a method for identifying a compound for treating or diagnosing a disease; (12) a kit useful for diagnosing disease; (13) a transgenic or knockout non-human animal that has been transformed to express higher, lower or absent levels of the polypeptide; and (14) a method for screening for a compound for treating a disease. INSP105 has antiinflammatory, cytostatic, neuroprotective, virucide, osteopathic, antibacterial, fungicide, anorectic, nephrotropic and cardiant activities. The INSP105 polypeptide is useful as a growth hormone or as a modulator of growth hormone activity. The polypeptide, nucleic acid molecule, vector, host cell, ligand or compound can be used in preparing a composition for treating or preventing a disease associated with growth hormone proteins, e.g., reproductive disorders; pregnancy disorder such as gestational trophoblastic disease; developmental disorders such as Silver-Russell syndrome; growth disorders; growth hormone deficiency; Cushing's disease; endocrine disorders; cell proliferative disorders, including neoplasm, carcinoma, pituitary tumour, ovary tumour, melanoma, lung, colorectal, breast, pancreas, head and neck, placental site trophoblastic tumour; adenocarcinoma, choriocarcinoma, osteosarcoma and other solid tumours; angiogenesis; myeloproliferative disorders; autoimmune/inflammatory disorders; cardiovascular disorders; neurological disorders; pain; metabolic disorders including diabetes mellitus; osteoporosis; obesity; cachexia; AIDS; renal disease; lung injury; ageing; or infections

CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphisms data, particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolising enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy

XX Sequence 42 BP; 13 A; 16 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.7e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCTGCTCTGGAG 20

Db 19 ACCCTGCTCTGGAG 32

RESULT 31

ACH66436/c
 ID ACH66436 standard; DNA; 20 BP.

XX ACH66436;

DT 16-OCT-2003 (first entry)

DE Sense PCR primer used to amplify AOC3.

XX Promoter; ss; genomic DNA; gDNA; untranslated region; UTR;
 KW DNA high-density microarray; biosite; large scale production; gDNA probe;
 KW microarray; type I primer; PCR; primer.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /label= OTHER

FT /note= "OTHER= linked to the bacteriophage T7 promoter

FT (ACH66426)"

XX US2003073085-A1.

XX 17-APR-2003.

XX 05-OCT-2001; 2001US-00972469.

XX 05-OCT-2001; 2001US-00972469.

XX (LAIF/) LAI F.

PA (ZHOU/) ZHOU D.

XX Lai F, Zhou D;

XX WPI; 2003-555942/52.

DR Amplifying expressed genetic sequences from genomic DNA of mammalian or
 XX higher order plant species for printing on DNA microarrays, involves
 PT using the 3' untranslated region of the gene sequence.

PS Disclosure; Page 6; 15pp; English.

XX The invention discloses a method for amplifying expressed genetic
 CC sequences from genomic DNA (gDNA) from mammalian or higher order plant
 CC species. The method involves identifying a 3' untranslated region (UTR)
 CC of a gDNA sequence, designing probe, performing PCR, separating the
 CC product by size differentiation and performing a second PCR to amplify
 CC the predetermined sequence. Also claimed is a biological analysis device,
 CC comprising a substrate and an array of a set of expressed genetic
 CC sequences, located on the substrate, which are generated by the method
 CC above and a DNA high-density microarray comprising a substrate upon which
 CC are deposited an array of biosites of genomic DNA fragments having the
 CC sequence of at least one exon, and absent polyadenine and vector
 CC sequences, where the genomic DNA fragments have a sequence length of from
 CC about 75-2000 nucleotides. The method is efficient for amplifying gene
 CC sequences, enables large-scale production of gDNA sequences, generates
 CC large quantities of gDNA probes, which enables greater efficiency for
 CC printing in microarray formats, fabricates high-density DNA arrays of
 CC enhanced, widely varying genetic content and abstains from using RNA-
 CC derived sequences by simple PCR amplifications without cloning. The
 CC method produces amplified sequences that have greater specificity and
 CC size consistency than that observed with cDNA fragments, and allows for
 CC greater signal sensitivity than oligonucleotides. The sequence presented
 CC is a Type I gene specific primer which is linked at its 5' termini to the
 CC bacteriophage T7 promoter

XX Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 9; Length 20;

Best Local Similarity 88.2%; Pred. No. 2e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCCAACCCCTGCTCTGG 18

Db 17 TGCCAACCCCTACTCTGG 1

RESULT 32

ABZ84928

ID ABZ84928 standard; DNA; 20 BP.

XX ABZ84928;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 DR WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX Claim 15; SEQ ID NO 170; 872pp; English.
 XX
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: the sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 20 BP; 1 A; 10 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 57.5%; Score 13.8; DB 10; Length 20;
 Best Local Similarity 88.2%; Pred. No. 2e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGCCACCCCTGCTCTGG 18
 DB 3 TGCCACCCCTGCTCTGG 19
 RESULT 33
 ABD21158
 ID ABD21158 standard; DNA; 20 BP.
 XX
 AC ABD21158;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human transglutaminase-derived oligo SEQ ID 170.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200285309-A2.
 FN
 XX
 XX 31-OCT-2002.
 PD
 XX
 XX 23-APR-2002; 2002WO-US013143.
 PF
 XX
 XX 24-APR-2001; 2001US-0286036P.
 PR
 XX

PA (EPIC-) EPIGENESIS PHARM INC.
 XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 XX WPI; 2003-093058/08.
 DR
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 XX Claim 15; SEQ ID NO 170; 763pp; English.
 PS
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 XX Sequence 20 BP; 1 A; 10 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 57.5%; Score 13.8; DB 11; Length 20;
 Best Local Similarity 88.2%; Pred. No. 2e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGCCACCCCTGCTCTGG 18
 DB 3 TGCCACCCCTGCTCTGG 19
 RESULT 34
 ABD31281
 ID ABD31281 standard; DNA; 20 BP.
 XX
 AC ABD31281;
 XX
 XX 12-AUG-2004 (first entry)
 DT
 XX
 XX Human XT-II gene fragment for glucosaminoglycan reduction in glial scars.
 DE
 XX ss; vulnery; cell therapy; glial scar; primary proteoglycan;
 KW chain initiation enzyme; elongation enzyme; neuronal regeneration;
 KW glucosaminoglycan.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2004041197-A2.
 FN

```

XX PD 21-MAY-2004.
XX PF 31-OCT-2003; 2003WO-US034806.
XX PR 01-NOV-2002; 2002US-0423082P.
XX PR 16-MAY-2003; 2003US-0471447P.
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX PA Grimpe B, Silver J;
XX PI WPI; 2004-400518/37.
XX DR
XX PT Reducing GAG content in a glial scar comprises inhibiting the expression
XX PT of primary proteoglycans or the expression and/or activity of a chain
XX PT initiation or elongation enzyme.
XX PS Example 12; SEQ ID NO 103; 265pp; English.
XX CC The invention relates to a method of reducing glucosaminoglycan (GAG)
XX CC content in a glial scar by inhibiting the expression of primary
XX CC proteoglycans or the expression and/or activity of a chain initiation or
XX CC elongation enzyme. The method is useful in reducing GAG content in a
XX CC glial scar and promoting neuronal regeneration. This sequence corresponds
XX CC to a fragment of the human XT-II gene used to identify sequences to which
XX CC antisense oligos, ribozymes, RNAi constructs can designed.
XX SQ Sequence 20 BP; 2 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 12; Length 20;
Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CCCTGCTCTGGAGGCCT 24
Db 4 CCCTGGCTCGAGGCCT 20

RESULT 35
AAx05223/c
ID AAx05223 standard; DNA; 25 BP.
XX AC AAx05223;
XX DT 22-APR-1999 (first entry)
XX DE Murine ICE mutagenic PCR primer m8p/s.
XX KW ICE; ALS; SOD gene; interleukin-1 converting enzyme; mutant; cell death;
XX KW amyotrophic lateral sclerosis; transgenic; ICE-like caspase; apoptosis;
XX KW traumatic brain injury; TBI; neurological; neurodegenerative; kidney;
XX KW heart disease; immune system; intestinal; aging; viral infection; AIDS;
XX KW acquired immune deficiency syndrome; gene therapy; PCR primer; ss.
XX OS Synthetic.
XX OS Mus sp.
XX PN WO9857664-A1.
XX PD 23-DEC-1998.
XX PF 18-JUN-1998; 98WO-US012716.
XX PR 19-JUN-1997; 97US-0050242P.
XX PA (YUAN/) YUAN J.
XX PA (FRIE/) FRIEDLANDER R M.
XX PT Yuan J, Friedlander RM;
XX DR WPI; 1999-095294/08.
XX

Treating amyotrophic lateral sclerosis (ALS) or ALS-like symptoms -
comprises inhibiting interleukin-1 converting enzyme (ICE) by gene
therapy, useful for treating central nervous system damage.

Example 1; Page 29; 96pp; English.

The invention relates to methods of treating amyotrophic lateral
sclerosis (ALS) or ALS-like symptoms that comprises inhibiting
interleukin-1 converting enzyme (ICE) by gene therapy. A mutant ICE gene
product can also be used for modulating programmed cell death
accompanying ALS. Transgenic non-human animal (including progeny)
containing a mutant ICE and SOD (ALS phenotype) gene are used to screen
compounds for treating ALS. Inhibitors of an ICE-like caspase are used to
attenuate or prevent apoptosis resulting from traumatic brain injury
(TBI), and to reduce the formation of reactive oxygen species following
TBI. Diseases caused by acute and chronic dysregulation of cell death,
which are treated by the ICE gene product, include malignant and pre-
malignant conditions, neurological, neurodegenerative disorders, heart
disease, immune system disorders, intestinal disorders, kidney disease,
aging, viral infections and acquired immune deficiency syndrome (AIDS).
The methods, mutant genes and inhibitors of ICE enable a better
understanding of the role of cell death and what triggers cell death in
ALS, which allow treatment of the disease. They also enable understanding
of the pathways mediating post traumatic apoptosis, which lead to novel
pharmacotherapy of TBI. Sequences AAx05223-27 represent PCR mutagenic
primers of mouse ICE cDNA used for constructing vectors containing mutant
ICE sequences

Sequence 25 BP; 9 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 2; Length 25;
Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CCCTGCTCTGGAGGCCT 24
Db 21 CTCTCCTCTGGAGGCCT 5

RESULT 36
ABS55668
ID ABS55668 standard; DNA; 33 BP.
XX AC ABS55668;
XX DT 27-DEC-2002 (first entry)
XX DE CAMP dependent kinase regulation subunit 8.8 PCR primer #2.
XX KW Human; CAMP dependent kinase regulation subunit 8.8; cyclic AMP;
XX KW malignant tumour; inflammation; antagonist; reverse transcriptase PCR;
XX KW RT-PCR; primer; ss.
XX OS Homo sapiens.
XX PN CNI352179-A.
XX PD 05-JUN-2002.
XX PF 10-NOV-2000; 2000CN-00127387.
XX PR 10-NOV-2000; 2000CN-00127387.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-733428/80.
XX New human CAMP dependent protein kinase regulation subunit 8.8
XX polypeptide for treating diseases, such as, malignant tumors and
XX inflammations.

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```
XX DE Human silent SNP containing nucleic acid SEQ:612.
XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX KW protein therapy; vaccine; probe; diagnostic assay; detection;
XX KW quantitation; restorative therapy; polymorphic; ds.
XX OS Homo sapiens.
XX XX WO200140521-A2.
XX PN 07-JUN-2001.
XX PD 30-NOV-2000; 2000WO-US032758.
XX PF 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX XX (CURA-) CURAGEN CORP.
XX PA Shimkets RA, Leach M;
XX PI WPI; 2001-356160/37.
XX DR Polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy.
XX PT Claim 1; Page 241; 2653pp; English.
XX PS
XX PS AA173060 to AA179867 represent isolated human polymorphic polynucleotide
XX CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX CC AA153114 to AA153329 represent peptides related to human polymorphic
XX CC polynucleotide sequences. The sequences can be used in gene and protein
XX CC therapy, and in vaccine production. (I) and the polypeptides encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate expression of polymorphic polypeptides. For
XX CC example, (I) may be used to treat disorders by rectifying mutations or
XX CC deletions in a patient's genome that affect the activity of polypeptides
XX CC by expressing inactive proteins or to supplement the patients own
XX CC production of polypeptide. Additionally, (I) and its complementary
XX CC sequences may also be used as DNA probes in diagnostic assays to detect
XX CC and quantitate the presence of similar nucleic acids in samples, and
XX CC therefore which patients may be in need of restorative therapy. The
XX CC polypeptides encoded by (I) may be used as antigens in the production of
XX CC antibodies specific for polymorphic polypeptides. The antibodies may also
XX CC be used to down regulate expression and activity. The antibodies may also
XX CC be used as diagnostic agents for detecting the presence of polymorphic
XX CC polypeptides in samples
XX CC
XX CC Sequence 50 BP; 8 A; 16 C; 17 G; 9 T; 0 U; 0 Other;
XX SQ
XX Query Match 57.5%; Score 13.8; DB 4; Length 50;
XX Best Local Similarity 88.2%; Pred. No. 2.1e+04;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 8 CCCTGCTCTGGAGCCT 24
XX DB 33 CCATGCTCTGGAGCCT 49
XX
XX RESULT 40
XX ADP22838/c
XX ID ADP22838 standard; DNA; 20 BP.
XX XX
XX AC ADP22838;
XX XX
XX DT 26-AUG-2004 (first entry)
XX DE Human BUB1-beta target sequence ISIS 196160.
XX KW ss; BUB1-beta; hyperproliferative disorder; cancer; human.
XX XX
XX OS Homo sapiens.
XX
XX US2004110149-A1.
XX PN 10-JUN-2004.
XX PD 10-DEC-2002; 2002US-00316459.
XX PF 10-DEC-2002; 2002US-00316459.
XX PR 10-DEC-2002; 2002US-00316459.
XX XX (ISIS-) ISIS PHARM INC.
XX PA Bennett CF, Jain R;
XX PI WPI; 2004-440338/41.
XX DR New oligonucleotide compound that inhibits expression of BUB1-beta,
XX PT useful for preparing a composition for treating hyperproliferative
XX PT disorder, e.g. cancer.
XX PT Example 15; SEQ ID NO 104; 92pp; English.
XX PS The invention relates to a new compound, having a sequence targeted to a
XX CC nucleic acid encoding BUB1-beta, which specifically hybridises with the
XX CC nucleic acid encoding BUB1-beta and inhibits expression of BUB1-beta. The
XX CC oligonucleotide compound is useful for preparing a composition for
XX CC treating a hyperproliferative disorder, e.g. cancer. The present sequence
XX CC represents a human BUB1-beta target sequence.
XX CC
XX CC Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
XX SQ
XX Query Match 56.7%; Score 13.6; DB 12; Length 20;
XX Best Local Similarity 80.0%; Pred. No. 2.5e+04;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 5 CAACCCCTGCTCTGGAGCCT 24
XX DB 20 CCACTGCTCTAGAGCCT 1
XX
XX Search completed: November 18, 2005, 11:52:22
XX Job time : 167.262 secs
```

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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1147.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-3

Perfect score: 24

Sequence: 1 ATGCCAACCTGCTCTGGAGCCT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.6	60.8	35	7	T73795 yc54a06.s1
C 2	14.4	60.0	31	1	AI323319 mh78a09.x
C 3	14.4	60.0	50	1	AU102721
C 4	14	58.3	45	7	T71655 yc62e05.s1
C 5	14	58.3	48	8	BH865457 SALK 0985
C 6	13.6	56.7	31	8	AZ809714 2M0073P16
C 7	13.6	56.7	33	7	T73421 yc35a08.s1
C 8	13.6	56.7	45	8	AZ768397 1M0568D23
C 9	13.4	55.8	37	4	B034402 BJ034402
C 10	13.4	55.8	41	9	BX209782 Danio rer
C 11	13.4	55.8	45	7	T69149 yc32e08.s1
C 12	13.4	55.8	49	1	AA917511 OL52C07.8
C 13	13.2	55.0	40	4	BJ039939 BJ039939
C 14	13.2	55.0	50	1	AU103163
C 15	13.2	55.0	50	1	AU103164
C 16	13.2	55.0	50	1	AU103168
C 17	13.2	55.0	50	1	AU103176
C 18	13	54.2	38	8	AZ961550 2M0230H05
C 19	13	54.2	42	9	CG720584 1119062H0
C 20	13	54.2	43	8	AZ785692 2M0029P14
C 21	13	54.2	43	9	CG869098 AC0059 Sa
C 22	13	54.2	46	7	C0784990 BL282B A0
C 23	13	54.2	49	8	BH796330 1008093E1
C 24	12.8	53.3	35	9	DR8L23T

25	12.8	53.3	49	9	AG191198	Pan trogl
26	12.8	53.3	50	1	AU102722	AU102722
27	12.8	53.3	50	1	AU102724	AU102724
28	12.6	52.5	40	1	AI021601	ub09f01.f
29	12.6	52.5	43	8	AZ474035	1M0290F18
30	12.6	52.5	48	8	AZ475962	1M0294I21
C 31	12.6	52.5	50	1	AU103032	AU103032
C 32	12.4	51.7	25	1	AI397039	fb25e02.y
33	12.4	51.7	34	1	AU255522	AU255522
34	12.4	51.7	37	6	CA796933	Cac_BL_39
35	12.4	51.7	40	8	AZ775757	2M0008B24
36	12.4	51.7	46	7	N83841	KK3617F Hum
37	12.4	51.7	50	8	AZ766605	1M0564L13
38	12.4	51.7	50	9	CG724386	111908IA0
C 39	12.4	51.7	50	9	CL528330	ASV5B01.f
C 40	12.2	50.8	31	4	BI522142	603081524
C 41	12.2	50.8	43	1	AA482116	zva3c12.s
C 42	12.2	50.8	46	7	R48775	y769c01.s1
C 43	12.2	50.8	47	8	AZ621187	1M0454F18
C 44	12	50.0	32	8	AZ827691	2M0104H13
C 45	12	50.0	32	8	AZ830592	2M0109K23

ALIGNMENTS

RESULT 1
T73795/c

LOCUS
T73795

DEFINITION
yc54a06.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:84466 3' similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR (HUMAN); mRNA sequence.

ACCESSION
T73795

VERSION
T73795.1 GI:690470

KEYWORDS
EST.

SOURCE
Homo sapiens

ORGANISM
Homo sapiens (human)

REFERENCE
1 (bases 1 to 35)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Marais, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

AUTHORS
Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 965
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNL this clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Possible reversed clone: polyT not found
Insert Length: 965 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 1.
Location/Qualifiers
1. .35
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:501523"
/db_xref="taxon:9606"
/clone="IMAGE:84466"

```

/dev_scages="49 years old"
/lab_host="SOUR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/notes="Organ: liver; Vector: pBluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Hepatotomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

```

ORIGIN

```

Query Match      60.8%; Score 14.6; DB 7; Length 35;
Best Local Similarity 73.9%; Pred. No. 8.7e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 ATGCCAACCTGCTCTCGAGGCC 23
Db 25 ANGCCNAGCCCGCTCGAGGNC 3

```

RESULT 2

```

AI323319/c
LOCUS
DEFINITION
mh78a09.xi Soares mouse placenta 4NDMP13.5 14.5 Mus musculus CDNA
clone IMAGE:457048 3' similar to TR:Q64366 Q64366 SYNAPTOTAGMIN
VIII ;, mRNA sequence.

```

```

ACCESSION
AI323319
VERSION
AI323319.1 GI:4057748
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

```

REFERENCE

```

1 (bases 1 to 31)
Marrá M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marrá M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:273936

```

TITLE

```

JOURNAL
COMMENT
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequenced stop: 1.
Location/Qualifiers
1. .31
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:457048"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares mouse placenta 4NDMP13.5 14.5"
/notes="Organ: placenta; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5,

```

FEATURES

source

```

1. .31
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:457048"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares mouse placenta 4NDMP13.5 14.5"
/notes="Organ: placenta; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5,

```

```

TGTTACCAATCTCAAGTCGGAGCGCGCGGAATTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

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ORIGIN

```

Query Match      60.0%; Score 14.4; DB 1; Length 31;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 6 AACCTGCTCTCGAGG 21
Db 27 AAACCTGCTCTGGAGG 12

```

RESULT 3

```

AI102721
LOCUS
DEFINITION
AI102721 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS01205, mRNA sequence.
ACCESSION
AI102721
VERSION
AI102721.1 GI:13552242
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

```

REFERENCE

```

1 (bases 1 to 50)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp

```

JOURNAL

```

MEDLINE
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01205"
/clone_lib="Sugano Homo sapiens cDNA library"

```

FEATURES

source

```

1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01205"
/clone_lib="Sugano Homo sapiens cDNA library"

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ORIGIN

```

Query Match      60.0%; Score 14.4; DB 1; Length 50;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy 1 ATGCCAACCTGCTCTCGAGGCC 24
Db 23 ATGCCGCCCATCTCTCGAGAACT 46

```

RESULT 4

```

T71655/c
LOCUS
DEFINITION
T71655 yc62605.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:85280 3' similar to gb:X02162 APOLIPROTEIN A-I PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
T71655
VERSION
T71655.1 GI:686176

```



```

KEYWORDS
SOURCE      EST.
ORGANISM    Homo sapiens (human)

REFERENCE
AUTHORS     Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
            Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
            Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
            Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
            Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
            Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
            and Marra, M.

TITLE       Generation and analysis of 280,000 human expressed sequence tags
JOURNAL     Genome Res. 6 (9), 807-828 (1996)
MEDLINE     97044478
PUBMED      8889549
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 33
            High quality sequence starts: 1 High quality sequence stops: 1
            Source: IMAGE Consortium, LNL This clone is available royalty-free
            through LNL; contact the IMAGE Consortium (info@image.lnl.gov)
            for further information. Trace considered overall poor quality
            Possible reversed clone: polyt not found
            Seq primer: -21ml3
            -High quality sequence stop: 1.
            Location/Qualifiers
            1. 45
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="GDB:502337"
            /db_xref="taxon:9606"
            /clone="IMAGE:85280"
            /sex="male"
            /dev_stage="49 years old"
            /lab_host="SOUR cells (kanamycin resistant)"
            /clone_lib="Stratagene liver (H937224)"
            /note="Organ: liver; Vector: pBluescript SK; Site 1:
            EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
            Oligo dT. Hepatocytomy from normal male caucasian. Average
            insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor
            sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5'
            CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match      58.3%; Score 14; DB 7; Length 45;
Best Local Similarity 73.9%; Pred. No. 1.6e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAGGCC 23
    ||||| ||||| ||||| ||||| |||||
Db 35 ANGCCAGCCCGCGCTCGAGGAC 13

RESULT 5
BH865457
LOCUS      BH865457
DEFINITION SALK_098558 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_098558, genomic survey sequence.
ACCESSION  BH865457
VERSION     BH865457.1
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 48)

REFERENCE
1 (bases 1 to 48)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J., and Ecker, J.R.:
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. 48
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_098558"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      58.3%; Score 14; DB 8; Length 48;
Best Local Similarity 77.3%; Pred. No. 1.6e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GCCAACCTGCTCTGGAGGCC 24
    ||||| ||||| ||||| ||||| |||||
Db 6 GCCAACCGAGCTCTGGAATCT 27

RESULT 6
AZ809714
LOCUS      AZ809714
DEFINITION 2M0073P16R Mouse 10kb plasmid UUC1M library Mus musculus genomic
            clone UUC2M0073P16 R, genomic survey sequence.
ACCESSION  AZ809714
VERSION     AZ809714.1
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 31)
            1 (bases 1 to 31)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: dunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0073 row: P column: 16
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends

```

High quality sequence stop: 31.
Location/Qualifiers
1. .31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0073P16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 56.7%; Score 13.6; DB 8; Length 31;
Best Local Similarity 80.0%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| |||||
12 ATGCCAACCCCTGGCTGGTG 31

RESULT 7
T73421/c
LOCUS
DEFINITION
YC35a08.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82646 3', similar to gb:X02162 APOLIPROTEIN A-I PRECURSOR (HUMAN);, mRNA sequence.
T73421
T73421.1 GI:690096
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 33)
Hillier L., Lennon G., Becker M., Bonaldo M.F., Chiapelli B., Chisoe S., Dietrich N., Dubuque T., Favello A., Gish W., Hawkins M., Hultman M., Kucaba T., Lacy M., Le M., Le N., Mardis E., Moore B., Morris M., Parsons J., Prange C., Rifkin D., Rohlfing T., Schellenberg K., Soares M.B., Tan F., Thierry-Mieg J., Trevaskis E., Underwood K., Wohldmann P., Waterston R., Wilson R. and Marra M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 993

High quality sequence stop: 18 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found
Insert Length: 993 Std Error: 0.00
Seq primer: -21ml3
High quality sequence stop: 18.
Location/Qualifiers
1. .33
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:499703"
/db_xref="taxon:9606"
/clone="IMAGE:82646"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site 1: EORI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

Query Match 56.7%; Score 13.6; DB 7; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0

Qy 1 ATGCCAACCCCTGCTCTGGAG 21
||||| ||||| ||||| |||||
22 ANGCCAAAGCCGCGCTCGAG 2

RESULT 8
AZ768397
LOCUS
DEFINITION
1M0568D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0568D23 F, genomic survey sequence.
AZ768397
AZ768397.1 GI:12987461
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamil C., Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T., Reilly M., Rose M., Rose R., Stokes R., Tingey A., von Niederhausern A. and Wright D., Weiss R.
Plasmid inserts
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0568 row: D column: 23
Seq primer: CGTTGTAAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
1. .45
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0568D23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pW42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 [gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 56.7%; Score 13.6; DB 8; Length 45;
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGCCAACCTGCTCTGGAGG 21
 |||||
 Db 22 TGCCAACCTGGACTGATGG 41

RESULT 9

BJ034402/c
 LOCUS BJ034402 37 bp mRNA linear EST 26-SEP-2003
 DEFINITION laevis cDNA clone XL028h05 5', mRNA sequence.
 ACCESSION BJ034402
 VERSION BJ034402.1 GI:17391943
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.

Expressed genes in X. laevis embryo

Unpublished (2001)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp

The information of this clone is available through the following URL.

http://xenopus.nibb.ac.jp.

Location/Qualifiers

1..37

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="XL028h05"

/tissue_type="whole embryo"

/dev_stages="stage 15"

/clone_lib="NIBB Mochii normalized Xenopus neurula library"

FEATURES

source

ORIGIN

Query Match 55.8%; Score 13.4; DB 4; Length 37;
 Best Local Similarity 93.3%; Pred. No. 3e+05;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 TGCCAACCTGCTCT 16
 |||||
 Db 15 TGCCAACCTGTCTCT 1

RESULT 10

BX209782
 LOCUS BX209782 41 bp DNA linear GSS 29-JAN-2003
 DEFINITION Danio rerio genomic clone DKEY-250L15, genomic survey sequence.
 ACCESSION BX209782
 VERSION BX209782.1 GI:28041668
 KEYWORDS GSS.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE

1 (bases 1 to 41)
 HUMPHRAY,S.J., HUCKLE,E. and DURHAM,J.L.

AUTHORS

TITLE

JOURNAL

COMMENT

This sequence was generated from the T7 end of BAC 250L15. 250L15 is part of the Daniokey BAC library created by R. Plasterk and N.V. Keygene. Further details:
 http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

Location/Qualifiers
 1..41

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="DKEY-250L15"

/tissue_type="Testis"

/note="vector pIndigoBAC-536"

ORIGIN

Query Match 55.8%; Score 13.4; DB 9; Length 41;
 Best Local Similarity 73.9%; Pred. No. 3e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 2 TGCCAACCTGCTCTGGAGGCT 24
 |||||
 Db 19 TCCAAACTCTGCTCTGGAGGCT 41

RESULT 11

T69149/c

LOCUS T69149 45 bp mRNA linear EST 23-FEB-1995

DEFINITION yc32e08.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82406 3' similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR (HUMAN); mRNA sequence.

ACCESSION T69149

VERSION T69149.1 GI:680297

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 45)

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Kulkarni,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (3), 807-828 (1996)
97044478
8889549

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 21

High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Possible reversed clone: polyt not found
Seq primer: -21ml3
High quality sequence stop: 1.

FEATURES
source
1..45
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:499463"
/db_xref="taxon:9606"
/clone="IMAGE:82406"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Hepatotomy from normal male caucasian. Average
insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGACGAG 3' ~3' adaptor sequence: 5'
CTCAGTGTGTTTTTTTTTTTTTT 3' "

ORIGIN

Query Match 55.8%; Score 13.4; DB 7; Length 45;
Best Local Similarity 73.9%; Pred. No. 3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAGGCC 23
|||||
Db 25 AGGCACAGCCGCGCTCGAGGAC 3
|||||

RESULT 12
AA917511/c
LOCUS
DEFINITION
IMAGE:1527084 3' similar to SW:HFCL_HUMAN P51610 HOST CELL FACTOR
C1 ;, mRNA sequence.

ACCESSION
AA917511
VERSION
AA917511.1 GI:3057401
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ccgaps-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1437 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
Location/Qualifiers

source
1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1527084"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 55.8%; Score 13.4; DB 1; Length 49;
Best Local Similarity 73.9%; Pred. No. 3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGCACACCCCTGCTCTGGAGGCCCT 24
|||||
Db 26 TGCCAACCCCTGAGAGAGGCCCT 4
|||||

RESULT 13
BJ039939
LOCUS
DEFINITION
BJ039939 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL038p16 5', mRNA sequence.

ACCESSION
BJ039939.1 GI:17375714
VERSION
EST.
KEYWORDS
Xenopus laevis (African clawed frog)

SOURCE
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE
1 (bases 1 to 40)
AUTHORS
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
Kohara,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
URL.
http://xenopus.nibb.ac.jp.
Location/Qualifiers

FEATURES
source
1..40
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL038p16"
/tissue type="whole embryo"
/dev stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"

ORIGIN

Query Match 55.0%; Score 13.2; DB 4; Length 40;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      3  GCCACCTGCTCTGGAGG 21
Db      21  GNGACCTGCTCTAGAGG 39

RESULT 14
AUI03163/c
LOCUS   AUI03163 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
AUI03163 50 bp mRNA linear EST 28-JAN-2004
COLF1812, mRNA sequence.
ACCESSION AUI03163
VERSION   AUI03163.1 GI:13552684
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.,
TITLE    Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE  21270072
PUBMED   11375929
COMMENT  Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
    Location/Qualifiers
        1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="COLF5980"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7  ACCCTGCTCTGGAGGCTT 24
Db      22  ACCCAGCTCTGGCGTCTT 5

RESULT 16
AUI03168/c
LOCUS   AUI03168 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
AUI03168 50 bp mRNA linear EST 28-JAN-2004
HRC02059, mRNA sequence.
ACCESSION AUI03168
VERSION   AUI03168.1 GI:13552689
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.,
TITLE    Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE  21270072
PUBMED   11375929
COMMENT  Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
    Location/Qualifiers
        1..50
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        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="COLF1812"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. NO. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7  ACCCTGCTCTGGAGGCTT 24
Db      22  ACCCAGCTCTGGCGTCTT 5

RESULT 15
AUI03164/c
LOCUS   AUI03164 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
AUI03164 50 bp mRNA linear EST 28-JAN-2004
COLF5980, mRNA sequence.
ACCESSION AUI03164
VERSION   AUI03164.1 GI:13552685
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.,
TITLE    Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE  21270072
PUBMED   11375929
COMMENT  Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
    Location/Qualifiers
        1..50
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        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="HRC02059"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7  ACCCTGCTCTGGAGGCTT 24
Db      22  ACCCAGCTCTGGCGTCTT 5

RESULT 15
AUI03164/c
LOCUS   AUI03164 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
AUI03164 50 bp mRNA linear EST 28-JAN-2004
COLF5980, mRNA sequence.
ACCESSION AUI03164
VERSION   AUI03164.1 GI:13552685
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.,
TITLE    Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE  21270072
PUBMED   11375929
COMMENT  Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
    Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="HRC02059"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7  ACCCTGCTCTGGAGGCTT 24
Db      22  ACCCAGCTCTGGCGTCTT 5

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Db      28  ACCGAGCTCTGGCGTCCT 11
      ||||| ||||| ||||| |||||
RESULT 17
AUI031176/c
LOCUS   AUI031176 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
HMA00666, mRNA sequence.
ACCESSION AUI031176
VERSION   AUI031176.1 GI:13552697
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 50)
          Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
          Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
          Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
          Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
          ENBO Rep. 2 (5), 388-393 (2001)
          21270072
          11375929
          Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yzuku@ims.u-tokyo.ac.jp
          Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
          Sugano, S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HBMA0066"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7  ACCCTGCTCTGGAGGCCT 24
      ||||| ||||| ||||| |||||
Db      48  ACCGAGCTCTGGCGTCCT 31

RESULT 18
AUI0311550
LOCUS   AUI0311550 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
Clone UUGC2M0230H05 F, genomic survey sequence.
ACCESSION AUI0311550
VERSION   AUI0311550.1 GI:13832777
KEYWORDS GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 38)
          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
          Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
          Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
          Niederhausern, A. and Wright, D., Weiss, R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss

RESULT 19
CG720584
LOCUS   CG720584 42 bp DNA linear GSS 20-OCT-2003
DEFINITION
1119062H06.2EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION CG720584
VERSION   CG720584.1 GI:37753618
KEYWORDS GSS.
SOURCE    Zea mays
ORGANISM  Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
          1 (bases 1 to 42)
          Walbot, V.
          Maize genomic sequences found using engineered RescueMu transposon
          Unpublished (2001)
          Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA

```

```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0230 row: H column: 05
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 38.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
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                     /clone="UUGC2M0230H05"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /notes="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptor DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptor mouse DNA was annealed to
                     adaptor vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN
Query Match      54.2%; Score 13; DB 8; Length 38;
Best Local Similarity 76.2; Pred. No. 4.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1  ATGCCAACCTGCTCTGGAGG 21
      ||||| ||||| ||||| |||||
Db      14  ATGCATAAACGTGCTTTGGATG 34

RESULT 19
CG720584
LOCUS   CG720584 42 bp DNA linear GSS 20-OCT-2003
DEFINITION
1119062H06.2EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION CG720584
VERSION   CG720584.1 GI:37753618
KEYWORDS GSS.
SOURCE    Zea mays
ORGANISM  Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
          1 (bases 1 to 42)
          Walbot, V.
          Maize genomic sequences found using engineered RescueMu transposon
          Unpublished (2001)
          Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA

```



```

humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 8L23. 8L23 is
part of the Daniokey BAC Library created by R. Plastek and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1..35
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKXY-8L23"
/cisue_type="Testis"
/note="Vector pIndigoBAC-536"

ORIGIN
Query Match      53.3%; Score 12.8; DB 9; Length 35;
Best Local Similarity 70.8%; Pred. No. 5.6e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTCTGGAGGCT 24
    ||||| ||||| ||||| |||||
Db 2 ATGCAAGCTCGTCTCTGGAGGCT 25
    ||||| ||||| ||||| |||||

RESULT 25
AG191198
LOCUS      49 bp DNA linear GSS 06-MAR-2004
DEFINITION Pan troglodytes DNA, clone: RP43-067A16.T7, genomic survey
sequence.
ACCESSION  AG191198
VERSION     AG191198.1 GI:45223374
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE  1
AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43
TITLE     BAC end sequences of Library RP-43
JOURNAL   Unpublished
AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.krribb.re.kr, URL:http://phs.grc.krribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector      : pBACe3.6
R.Site 1    : EcoRI
R.Site 2    : EcoRI
Location/Qualifiers
1..49
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-067A16.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
Query Match      53.3%; Score 12.8; DB 9; Length 49;
Best Local Similarity 87.5%; Pred. NO. 5.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 7 ACCCTGCTCTGGAGGC 22
    ||||| ||||| |||||
Db 6 ACCCTGCTCTACAGGC 21
    ||||| ||||| |||||

RESULT 26
AUI02722
LOCUS      50 bp mRNA linear EST 28-JAN-2004
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS02544, mRNA sequence.
ACCESSION  AUI02722
VERSION     AUI02722
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE    21370072
PUBMED     11375929
COMMENT    Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS02544"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      53.3%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 5.6e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGCT 24
    ||||| ||||| ||||| |||||
Db 23 ATGCAGCCATCTCTCTGGAGAACT 46
    ||||| ||||| ||||| |||||

RESULT 27
AUI02724
LOCUS      50 bp mRNA linear EST 28-JAN-2004
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNG11421, mRNA sequence.
ACCESSION  AUI02724
VERSION     AUI02724
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)

```


0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.5%; Score 12.6; DB 8; Length 43;
Best Local Similarity 78.9%; Pred. No. 6.8e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CAACCCCTGCTCTGGAGCC 22
Db 12 CAACCCCTGCTCTGATGCC 30

RESULT 30

LOCUS AZ475962 48 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0294121F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0294121 F, genomic survey sequence.

ACCESSION AZ475962

VERSION AZ475962.1 GI:10634087

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 48)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ismail, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0294 row: 1 column: 21

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 48.

FEATURES

source

1..48
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0294121"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.5%; Score 12.6; DB 8; Length 48;
Best Local Similarity 78.9%; Pred. No. 6.8e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CAACCCCTGCTCTGGAGCC 23
Db 2 CAACCCCTATCTGCTGCC 20

RESULT 31

LOCUS AU103032/c 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU103032 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS05571, mRNA sequence.

ACCESSION AU103032

VERSION AU103032.1 GI:13552553

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)

REFERENCE

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

PUBMED 11375929

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997)

FEATURES

source

1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS05571"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 52.5%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.9e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CAACCCCTGCTCTGGAGCC 23
Db 40 CAACCCCTGCTCGTCAGCC 22

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RESULT 32
AI397039/c      25 bp      mRNA      linear      EST 07-JUN-2001
LOCUS          fb2se02.y1 Zebrafish WashU MPMG EST Danio rerio cDNA clone
DEFINITION     IMAGE:3712922 5' similar to SW:IQGA.HUMAN P46940 RAS
                GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 ;, mRNA sequence.
ACCESSION      AI397039
VERSION        AI397039.1 GI:42266932
KEYWORDS       EST.
SOURCE         Danio rerio (zebrafish)
ORGANISM       Danio rerio
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                Cypriniformes; Cyprinidae; Danio.
REFERENCE
AUTHORS        Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
                Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
                Underwood,K., Streptoe,M., Theising,B., Allen,M., Bowers,Y.,
                Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
                Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
                Waterston,R. and Wilson,R.
                WashU Zebrafish EST Project 1998
                Unpublished (1998)
TITLE          Contact: Stephen L. Johnson
JOURNAL        Washington University School of Medicine
COMMENT        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: zbrafish@watson.wustl.edu
                cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
                Matthew Clark. DNA Sequencing by: Washington University Genome
                Sequencing Center Clone distribution: Genome Systems, St. Louis,
                Missouri (web address: www.genomesystems.com) (email contact:
                info@genomesystems.com) and Research Genetics, Huntsville, Alabama
                (web address: www.resgen.com) (email contact: info@resgen.com) and
                RessourcenzentrumPrimarDatenbank, Berlin, Germany (web address:
                www.rzpd.de)
                Trace considered overall poor quality
                Possible reversed clone: similarity on wrong strand
                Seq primer: T3 Et from Amersham
                High quality sequence stop: 1
                POLYA=No.

FEATURES
source         Location/Qualifiers
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                /organism="Danio rerio"
                /mol_type="mRNA"
                /db_xref="taxon:7955"
                /clones="IMAGE:3712922"
                /sex="mixed"
                /tissue_type="26 somite embryos, adult livers, shield
                stage embryos"
                /lab_host="XLI-blue MRF"
                /clone_lib="Zebrafish WashU MPMG EST"
                /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st
                strand cDNA was primed with a Not I - oligo(dT)15 primer
                [5'pGACTAGTCTTAGATCGGAGCGCGCCCTTTTCTTTT3'];
                double-stranded cDNA was ligated to Sal I adaptors (BRL),
                digested with Not I and cloned into the Not I and Sal I
                sites of the pSPORT1 vector (BRL). Library was constructed
                by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
                Institut fuer Molekulare Genetik Berlin). cDNAs for EST
                analysis were selected following oligonucleotide
                hybridization fingerprinting of arrayed clones from
                zebrafish late somitogenesis (26 ss), adult liver or
                embryonic shield stage (5.6 h) libraries. Fingerprint
                data were used to computationally cluster cDNAs, and a
                single cDNA from each cluster was chosen for sequencing.
                In some cases multiple members of the same cluster were
                sequenced to assess clustering parameters or single clones
                were sequenced additional times to assess quality
                control."

ORIGIN
Query Match    51.7%; Score 12.4; DB 1; Length 34;
Best Local Similarity 72.7%; Pred. No. 8.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy             1 ATGCCAACCCCTGCTCTGGAGGC 22
               ||| ||| ||| ||| ||| |||
Db             8 ATGMAAACTTGCACCTGAAGGC 29

RESULT 34
CA796933
LOCUS          Cac_BL_3999 Cac.BL (Bean and Leaf from Amelomardo type Cacao)
DEFINITION     Theobroma cacao cDNA clone Cac_BL_3999 5', mRNA sequence.
ACCESSION      CA796933
VERSION        CA796933.1 GI:26054019
KEYWORDS       EST.
SOURCE         Theobroma cacao (cacao)
ORGANISM       Theobroma cacao
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
                Theobroma.
                1 (bases 1 to 37)
                Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
                Retzel,E.R. and Jones,C.A.
                Gene discovery and microarray analysis of cacao (Theobroma cacao
                L.) varieties
                Planta 216 (2), 255-264 (2002)
                22337596

ORIGIN
Query Match    51.7%; Score 12.4; DB 1; Length 34;
Best Local Similarity 72.7%; Pred. No. 8.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy             1 ATGCCAACCCCTGCTCTGGAGGC 22
               ||| ||| ||| ||| ||| |||
Db             8 ATGMAAACTTGCACCTGAAGGC 29

RESULT 33
AU255522
LOCUS          AU255522 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION     BED0005649 3', mRNA sequence.
ACCESSION      AU255522
VERSION        AU255522.1 GI:20318340
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                Kato,K. and Matoba,R.
                Generation of expressed sequence tags from mouse brain
                Unpublished (2002)
                Contact: Kikuya Kato
                Graduate School of Biological Sciences
                Nara Institute of Science and Technology
                8916-5 Takayama, Ikoma, Nara 630-0101, Japan
                Tel: 81-743-72-5581
                Fax: 81-743-72-5589
                Email: kkatob@bs.aist-nara.ac.jp,
                URL:http://love2.aist-nara.ac.jp/BED/index.html.
                Location/Qualifiers
                1..34
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /clone="BED0005649"
                /tissue_type="brain"
                /clone_lib="3'-directed mouse cDNA library"

ORIGIN
Query Match    51.7%; Score 12.4; DB 1; Length 34;
Best Local Similarity 72.7%; Pred. No. 8.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy             1 ATGCCAACCCCTGCTCTGGAGGC 22
               ||| ||| ||| ||| ||| |||
Db             8 ATGMAAACTTGCACCTGAAGGC 29

RESULT 34
CA796933
LOCUS          Cac_BL_3999 Cac.BL (Bean and Leaf from Amelomardo type Cacao)
DEFINITION     Theobroma cacao cDNA clone Cac_BL_3999 5', mRNA sequence.
ACCESSION      CA796933
VERSION        CA796933.1 GI:26054019
KEYWORDS       EST.
SOURCE         Theobroma cacao (cacao)
ORGANISM       Theobroma cacao
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
                Theobroma.
                1 (bases 1 to 37)
                Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
                Retzel,E.R. and Jones,C.A.
                Gene discovery and microarray analysis of cacao (Theobroma cacao
                L.) varieties
                Planta 216 (2), 255-264 (2002)
                22337596

ORIGIN

```

```

PUBMED
COMMENT
12447539
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.
FEATURES
    Location/Qualifiers
        1..37
            /organism="Theobroma cacao"
            /mol_type="mRNA"
            /strain="Amelonado type"
            /db_xref="taxon:3641"
            /clone="Cac BL 3999"
            /tissue_type="Mature leaf and mature bean"
            /cell_type="Whole organ"
            /dev_stage="maturity"
            /lab_host="XL-1 Blue MRF"
            /clone_lib="Cac_BL (Bean and Leaf from Amelonado type Cacao)"
            /note="Vector: pBK-CMV; Bean and leaf tissue from an Amelonado type Cacao tree."
ORIGIN
Query Match      51.7%; Score 12.4; DB 6; Length 37;
Best Local Similarity 69.6%; Pred. No. 8.3e+05;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  2  TGCCAACTGCTCTGGAGGCT 24
    |||||
Db   9  TGCCAACTGCTCTGGAGGCT 31

RESULT 35
AZ775757
LOCUS      40 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION 2M0008B24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0008B24 R, genomic survey sequence.
ACCESSION  AZ775757
VERSION     AZ775757.1  GI:12902623
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: B column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.
FEATURES
    Location/Qualifiers
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            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0008B24"
ORIGIN

```

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN
Query Match      51.7%; Score 12.4; DB 8; Length 40;
Best Local Similarity 72.7%; Pred. No. 8.3e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY  3  GCCAACCTGCTCTGGAGGCT 24
    |||||
Db   9  GTCTACCTGCTGCAGATGCT 30

RESULT 36
N83841
LOCUS      46 bp      mRNA      linear      EST 01-APR-1996
DEFINITION KK3617F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK3617 5' similar to STAT4, mRNA sequence.
ACCESSION  N83841
VERSION    N83841.1  GI:1259466
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
Liew,C.C.
cDNAs from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cliu@rics.bwh.harvard.edu
Seq primer: GAAATTAACCTCCTAAGGG.
FEATURES
    Location/Qualifiers
        1..46
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="KK3617"
            /lab_host="E. coli XL1-Blue"
            /clone_lib="Human fetal heart, Lambda ZAP Express"
            /note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."
ORIGIN

```

Query Match 51.7%; Score 12.4; DB 7; Length 46;
 Best Local Similarity 72.7%; Pred. No. 8.4e+05;
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGCCAACTCTGCTGTGGAGGCC 23
 |||||
 Db 16 TGCCAACTCTGCTGTGGAGGCC 37

RESULT 37
 AZ766605
 LOCUS
 DEFINITION 1M0564L13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0564L13 F, genomic survey sequence.

ACCESSION AZ766605
 VERSION AZ766605.1 GI:12883846
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 50)

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0564 row: L column: 13

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 50.

FEATURES
 Location/Qualifiers

1..50
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGC1M0564L13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.7%; Score 12.4; DB 8; Length 50;
 Best Local Similarity 92.9%; Pred. No. 8.4e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCCTGCTCTGTGGAGG 21
 |||||
 Db 26 CCCTGCTCTGTGGG 39

RESULT 38
 CG724386
 LOCUS
 DEFINITION 1119081A01.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.

ACCESSION CG724386
 VERSION CG724386
 KEYWORDS GSS.
 SOURCE Zea mays

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 50)

REFERENCE
 AUTHORS
 Walbot, V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL
 COMMENT
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1119081 row: A column: 01

Class: transposon-tagged.

FEATURES
 Location/Qualifiers

1..50
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1119 - RescueMu Grid AA"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 50;
 Best Local Similarity 72.7%; Pred. No. 8.4e+05;
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGTGGAGC 22
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 Db 26 ATGCCAACCTCTCTCTCTGCGC 47

RESULT 39
 CL528330
 LOCUS
 DEFINITION ASV5B01.fwd ASLV-vector integration sites in human 293T-TVA cells
 50 bp DNA linear GSS 17-MAY-2004
 Homo sapiens genomic clone ASV5B01.fwd, genomic survey sequence.

ACCESSION: CL528330
VERSION: CL528330.1 GI:47421526
KEYWORDS: GSS.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE: 1 (bases 1 to 50)
AUTHORS: Mitchell, R.S., Beitzel, B.F., Schroder, A.R.W., Shinn, P., Chen, H.,
Berry, C.C., Ecker, J.R. and Bushman, F.
TITLE: Retroviral DNA Integration: ASLV, HIV and MLV Show Distinct Target
Site Preferences
JOURNAL: Unpublished (2004)
COMMENT: Contact: Frederic Bushman
Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1630
Fax: 858 554 0341
Email: bushman@salk.edu
Class: PCR with specific primers.

FEATURES
source

1..50
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="ASV5B01.fwd"
/clone.lib="ASLV-vector integration sites in human
293T-TVA cells"

/note="Human 293T cells expressing the subgroup A avian
retrovirus receptor (293T-TVA) were infected with an
ASLV-based vector. DNA was isolated and cleaved with
restriction enzymes; linkers were ligated onto the cleaved
DNA and DNAs were amplified using one primer that bound to
the linker DNA and one that bound to the ASLV cDNA.
Junctions between integrated ASLV proviruses and cellular
DNA were cloned and sequenced."

ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 50;
Best Local Similarity 92.9%; Pred. No. 8.4e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 ACCCTGCTCTGGAG 20
|||||
Db 19 ACCCGGCTCTGGAG 6

RESULT 40
BI522142
LOCUS: BI522142 31 bp mRNA linear EST 29-AUG-2001
DEFINITION: 60308152471 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5221084 3',
mRNA sequence.
ACCESSION: BI522142
VERSION: BI522142.1 GI:15346934
KEYWORDS: EST.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE: 1 (bases 1 to 31)
AUTHORS: NIH-MGC <http://mgi.nci.nih.gov/>
TITLE: National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL: Unpublished (1999)
COMMENT: Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1AM1555 row: 0 column: 05
High quality sequence start: 7
High quality sequence stop: 31.

FEATURES

source

Location/Qualifiers
1..31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5221084"
/lab_host="DH10B"
/clone.lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 50.8%; Score 12.2; DB 4; Length 31;
Best Local Similarity 82.4%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCCAACCTGCTCTGGA 19
|||||
Db 14 GCTGACTCTGCTCTGGA 30

Search completed: November 18, 2005, 21:12:40
Job time : 1150.98 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 46.6312 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-3

Perfect score: 24

Sequence: 1 ATGCCAACCTGCTCTGGAGCCT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	1	US-07-989-160-3
2	16.6	69.2	25	4	US-09-396-196G-54586
3	15.8	65.8	25	4	US-09-396-196G-54585
4	15	62.5	25	4	US-09-396-196G-63266
5	15	62.5	25	4	US-09-396-196G-127234
6	14.8	61.7	25	4	US-09-396-196G-58956
7	14.8	61.7	25	4	US-09-671-317-812
8	14.6	60.8	25	4	US-09-396-196G-2325
9	14.6	60.8	25	4	US-09-396-196G-8574
10	14.6	60.8	25	4	US-09-396-196G-124901
11	14.6	60.8	25	4	US-09-422-978-2994
12	14.2	59.2	25	4	US-09-396-196G-57276
13	14.2	59.2	25	4	US-09-396-196G-70618
14	14.2	59.2	25	4	US-09-396-196G-76806
15	14	58.3	24	3	US-09-402-631A-24
16	14	58.3	35	1	US-08-375-235-6
17	13.8	57.5	25	4	US-09-396-196G-58955
18	13.6	56.7	22	3	US-08-987-326-13
19	13.6	56.7	24	3	US-08-991-862-15
20	13.6	56.7	24	4	US-09-813-156-15
21	13.6	56.7	24	4	US-09-456-886-15
22	13.6	56.7	24	4	US-09-824-647-15
23	13.6	56.7	25	4	US-09-396-196G-71340
24	13.6	56.7	25	4	US-09-396-196G-71493
25	13.6	56.7	25	4	US-09-396-196G-124900
26	13.6	56.7	50	4	US-09-907-794A-16
27	13.6	56.7	50	4	US-09-905-125A-16

c 28	13.6	56.7	50	4	US-09-902-775A-16	Sequence 16, Appl
c 29	13.6	56.7	50	4	US-09-906-700-16	Sequence 16, Appl
c 30	13.6	56.7	50	4	US-09-903-603A-16	Sequence 16, Appl
c 31	13.6	56.7	50	4	US-09-904-920A-16	Sequence 16, Appl
c 32	13.6	56.7	50	4	US-09-909-084-16	Sequence 16, Appl
c 33	13.6	56.7	50	4	US-09-905-381A-16	Sequence 16, Appl
c 34	13.6	56.7	50	4	US-09-906-618-16	Sequence 16, Appl
c 35	13.4	55.8	18	1	US-08-222-619-24	Sequence 24, Appl
c 36	13.4	55.8	18	5	PCT-US95-04075-24	Sequence 24, Appl
c 37	13.4	55.8	21	4	US-09-657-472-2169	Sequence 2169, Ap
c 38	13.4	55.8	25	4	US-09-396-196G-3026	Sequence 3026, Ap
c 39	13.4	55.8	25	4	US-09-396-196G-3027	Sequence 3027, Ap
c 40	13.4	55.8	25	4	US-09-396-196G-15020	Sequence 15020, A
c 41	13.4	55.8	25	4	US-09-396-196G-72981	Sequence 72981, A
c 42	13.4	55.8	39	4	US-09-554-572-10	Sequence 10, Appl
c 43	13.4	55.8	47	4	US-09-422-978-3461	Sequence 3461, Ap
c 44	13.2	55.0	20	3	US-09-357-072-72	Sequence 72, Appl
c 45	13.2	55.0	25	4	US-09-396-196G-4320	Sequence 4320, Ap

ALIGNMENTS

RESULT 1
US-07-989-160-3
; Sequence 3, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-07-989-160-3

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCCAACCTGCTCTGGAGCCT 24
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; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58956
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-58956

Query Match 61.7%; Score 14.8; DB 4; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAACCTGCTCTGGAGG 21
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Db 3 CCAAGCTGCTCTGAAG 20

RESULT 7

US-09-671-317-812
; Sequence 812, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 812
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 12-138-141 : polymorphic base G or A
US-09-671-317-812

Query Match 61.7%; Score 14.8; DB 4; Length 47;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAG 20
||||| ||||| ||||| |||||
Db 8 ATGCCAAGCTGATCTRGAG 27

RESULT 8

US-09-396-196G-2325
; Sequence 2325, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2325
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-2325

Query Match 60.8%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCTGCTCTGGAGGCT 24
||||| ||||| ||||| |||||
Db 1 CCAACCTGCTCAGGGCTCT 21

RESULT 9

US-09-396-196G-8574
; Sequence 8574, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8574
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-8574

Query Match 60.8%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCTGCTCTGGAGGCT 24
||||| ||||| ||||| |||||
Db 2 CCAACCTGCTAATGAGGCT 22

RESULT 10

US-09-396-196G-124901/c
; Sequence 124901, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124901


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SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Toxoplasma gondii
INDIVIDUAL ISOLATE: P30 antigen gene
IMMEDIATE SOURCE:
CLONE: Primer #5
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..18
FEATURE:
NAME/KEY: CDS
LOCATION: 19..35
US-08-375-235-6

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Query Match 58.3%; Score 14; DB 1; Length 35;
Best Local Similarity 77.3%; Pred. NO. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OV 1 ATGCCAACCTGCTCTGGAGGC 22

Qy 1 ATGCCAACCTGCTCTGGAGGC 22
|||
Db 25 ATGCCATCCCGGCTTAGAGTC 4

RESULT 17
US-09-396-196G-58955
; Sequence 58955, Application US/09396196G
: Patent No. 6821724

```

; APPLICANT: Michael Wittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58955
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-58955

Query Match          57.5%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CCAACCCCTGCTCTGGAG 20
        ||||| ||||| ||||| ||
Db      9  CCAAGCCTGCTCTGAAG 25

RESULT 18
US-08-987-326-13
; Sequence 13, Application US/08987326
; Patent No. 6057105
; GENERAL INFORMATION:
; APPLICANT: NGI/Cancer Tech Company, LLC
; TITLE OF INVENTION: Detection of Melanoma or Breast Metastasis with a
; TITLE OF INVENTION: Multiple Marker Assay
; FILE REFERENCE: NGI 20923-701 CIP
; CURRENT APPLICATION NUMBER: US/08/987,326
; CURRENT FILING DATE: 1997-12-09

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; EARLIER APPLICATION NUMBER: 08/406,307
; EARLIER FILING DATE: 1995-03-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: sequence
US-08-987-326-13

Query Match          56.7%; Score 13.6; DB 3; Length 22;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
    ||||| ||| ||| |||||
Db 1 ATGCCAACCCCTGCTCTGGAG 20

RESULT 19
US-09-991-862-15
; Sequence 15, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/963,862
; EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: primer
; LOCATION: (1)..(24)
; OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-08-991-862-15

Query Match          56.7%; Score 13.6; DB 3; Length 24;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAGGCC 23
    ||| ||||| ||| |||||
Db 5 CCAGCCCTGCTGTTAAGGCC 24

RESULT 20
US-09-813-156-15
; Sequence 15, Application US/09813156
; Patent No. 6670183
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/813,156
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: primer
; LOCATION: (1)..(24)
; OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-08-991-862-15

Query Match          56.7%; Score 13.6; DB 3; Length 24;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAGGCC 23
    ||| ||||| ||| |||||
Db 5 CCAGCCCTGCTGTTAAGGCC 24

RESULT 21
US-09-456-886-15
; Sequence 15, Application US/09456886
; Patent No. 6720159
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/456,886
; CURRENT FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US/08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: primer
; LOCATION: (1)..(24)
; OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-09-456-886-15

Query Match          56.7%; Score 13.6; DB 4; Length 24;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAGGCC 23
    ||| ||||| ||| |||||
Db 5 CCAGCCCTGCTGTTAAGGCC 24

RESULT 22
US-09-824-647-15
; Sequence 15, Application US/09824647
; Patent No. 6824775
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,647
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
```

; NAME/KEY: primer
; LOCATION: (1)..(24)
; OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-09-824-647-15

Query Match 56.7%; Score 13.6; DB 4; Length 24;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CCAACCCCTGCTCTGGAGGCC 23
||| ||||| ||||| |||||
DB 5 CCAGCCTCTGCTTGAAGGCC 24

RESULT 23
US-09-396-196G-71340
; Sequence 71340, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71340
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71340

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTGCTCTGGAG 20
||| ||||| ||||| |||||
DB 3 ATCCAGCACTGCTCTGCAG 22

RESULT 24
US-09-396-196G-74893
; Sequence 74893, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74893
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-74893

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CCAACCCCTGCTCTGGAGGCC 23
||| ||||| ||||| |||||
DB 5 CCAGTCTCTGCTGCGATGCC 24

RESULT 25
US-09-396-196G-124900/c
; Sequence 124900, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124900
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124900

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCAACCCCTGCTCTGGAGGCC 22
||| ||||| ||||| |||||
DB 25 GCCCACACAGATCTGGAGGCC 6

RESULT 26
US-09-907-794A-16/c
; Sequence 16, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-907-794A-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 27
US-09-905-125A-16/c
; Sequence 16, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-905-125A-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 28
US-09-902-775A-16/c
; Sequence 16, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 16
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
US-09-902-775A-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTCTGCTCTGGAG 20
||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 29

US-09-906-700-16/c
Sequence 16, Application US/09906700
Patent No. 6723535
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-906-700-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 30

US-09-903-603A-16/c
; Sequence 16, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903.603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-903-603A-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 31

US-09-904-920A-16/c
; Sequence 16, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904.920A

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-18
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 09/909,064
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 16
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-904-920A-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTCTCTGGAG 20
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Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 32
US-09-064-16/c
Sequence 16, Application US/09909064
Patent No. 6818449
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-18
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 16
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-909-064-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTCTCTGGAG 20
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Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 33
US-09-905-381A-16/c
Sequence 16, Application US/09905381A
Patent No. 6818746

; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe

US-09-905-381A-16
Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5,7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGCCAACCTGCTCTGGAG 20
| | | | | | | | | | | | | |
Db 22 ATGCCACAGCTGCTGGAG 3
RESULT 34
US-09-906-618-16/c
; Sequence 16, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-906-618-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCGCTCTGGAG 20
|||||
Db 22 ATGCCACAGCTGCTGGAG 3

RESULT 35

US-08-222-619-24
; Sequence 24, Application US/08222619
; Patent No. 5652352

; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-222-619-24

Query Match 55.8%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAACCCCTGCTCTGGA 19
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Db 1 CAACCCCTGCTCTGGA 15

RESULT 36

PCT-US95-04075-24
; Sequence 24, Application PC/TUS9504075
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
PCT-US95-04075-24

Query Match 55.8%; Score 13.4; DB 5; Length 18;
Best Local Similarity 93.3%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAACCCCTGCTCTGGA 19
|||||
Db 1 CAACCCCTGCTGGA 15

RESULT 37

US-09-657-472-2169/c
; Sequence 2169, Application US/09657472
; Patent No. 6727063

; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2169
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-2169

Query Match 55.8%; Score 13.4; DB 4; Length 21;
Best Local Similarity 93.3%; Pred. No. 6.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 9 CCTGCTCTGGAGGCC 23
Db 18 CCTGCTCRGGAGGCC 4

RESULT 38
US-09-396-196G-3026
; Sequence 3026, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3026
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-3026

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAGGCC 23
Db 2 ATCCAGACATGCTCTGTAGGGC 24

RESULT 39
US-09-396-196G-3027
; Sequence 3027, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3027
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-3027

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAGGCC 23
Db 1 ATCCAGACATGCTCTGTAGGGC 23

RESULT 40
US-09-396-196G-15020
; Sequence 15020, Application US/09396196G
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15020
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-15020

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAACCCCTGCTCTGGA 19
Db 9 CAAGCCTGCTCTGGA 23

Search completed: November 18, 2005, 11:21:58
Job time : 47.6312 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 322.586 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-3

Perfect score: 24

Sequence: 1 ATGCCAACCTGCTCTGGAGGCT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	8	US-08-469-172-3
2	24	100.0	24	20	US-10-788-779-3
3	19.2	80.0	25	26	US-11-036-317-8035
4	17.8	74.2	25	26	US-11-036-317-18356
5	17.8	74.2	25	26	US-11-036-317-584705

6	16.6	69.2	25	22	US-10-719-900-833111	Sequence 833111,
7	16.6	69.2	25	22 <td>US-10-719-900-924760</td> <td>Sequence 924760, A</td>	US-10-719-900-924760	Sequence 924760, A
8	16.6	69.2	25	22 <td>US-10-809-189-54586</td> <td>Sequence 54586, A</td>	US-10-809-189-54586	Sequence 54586, A
9	16.6	69.2	25	24 <td>US-10-719-956-188380</td> <td>Sequence 188380,</td>	US-10-719-956-188380	Sequence 188380,
10	16.2	67.5	25	22 <td>US-10-719-900-174561</td> <td>Sequence 174561,</td>	US-10-719-900-174561	Sequence 174561,
11	16.2	67.5	25	26 <td>US-11-036-317-584704</td> <td>Sequence 584704,</td>	US-11-036-317-584704	Sequence 584704,
12	16.2	67.5	25	26 <td>US-11-060-756-77825</td> <td>Sequence 77825, A</td>	US-11-060-756-77825	Sequence 77825, A
13	15.8	65.8	25	22 <td>US-10-719-900-53167</td> <td>Sequence 53167, A</td>	US-10-719-900-53167	Sequence 53167, A
14	15.8	65.8	25	22 <td>US-10-809-189-54585</td> <td>Sequence 54585, A</td>	US-10-809-189-54585	Sequence 54585, A
15	15.8	65.8	41	19 <td>US-10-035-833A-1677</td> <td>Sequence 1677, Ap</td>	US-10-035-833A-1677	Sequence 1677, Ap
16	15.8	65.8	41	19 <td>US-10-035-833A-7225</td> <td>Sequence 7225, Ap</td>	US-10-035-833A-7225	Sequence 7225, Ap
17	15.6	65.0	45	22 <td>US-10-887-230-21</td> <td>Sequence 21, Appl</td>	US-10-887-230-21	Sequence 21, Appl
18	15.4	64.2	25	26 <td>US-11-036-317-327390</td> <td>Sequence 327390,</td>	US-11-036-317-327390	Sequence 327390,
19	15.2	63.3	25	22 <td>US-10-719-900-170847</td> <td>Sequence 170847,</td>	US-10-719-900-170847	Sequence 170847,
20	15.2	63.3	25	22 <td>US-10-719-900-170848</td> <td>Sequence 170848,</td>	US-10-719-900-170848	Sequence 170848,
21	15.2	63.3	25	22 <td>US-10-719-900-352179</td> <td>Sequence 352179,</td>	US-10-719-900-352179	Sequence 352179,
22	15.2	63.3	25	22 <td>US-10-719-900-513335</td> <td>Sequence 513335,</td>	US-10-719-900-513335	Sequence 513335,
23	15.2	63.3	25	22 <td>US-10-719-900-796279</td> <td>Sequence 796279,</td>	US-10-719-900-796279	Sequence 796279,
24	15.2	63.3	25	22 <td>US-10-956-157-196604</td> <td>Sequence 196604,</td>	US-10-956-157-196604	Sequence 196604,
25	15.2	63.3	25	24 <td>US-10-719-956-26759</td> <td>Sequence 26759, A</td>	US-10-719-956-26759	Sequence 26759, A
26	15.2	63.3	25	24 <td>US-10-719-956-95487</td> <td>Sequence 95487, A</td>	US-10-719-956-95487	Sequence 95487, A
27	15.2	63.3	25	24 <td>US-10-719-956-671714</td> <td>Sequence 671714,</td>	US-10-719-956-671714	Sequence 671714,
28	15.2	63.3	25	26 <td>US-11-036-317-52603</td> <td>Sequence 52603, A</td>	US-11-036-317-52603	Sequence 52603, A
29	15.2	63.3	25	26 <td>US-11-036-317-194782</td> <td>Sequence 194782,</td>	US-11-036-317-194782	Sequence 194782,
30	15.2	63.3	25	26 <td>US-11-036-317-257640</td> <td>Sequence 257640,</td>	US-11-036-317-257640	Sequence 257640,
31	15.2	63.3	25	26 <td>US-11-036-317-294807</td> <td>Sequence 294807,</td>	US-11-036-317-294807	Sequence 294807,
32	15.2	63.3	25	26 <td>US-11-036-317-305597</td> <td>Sequence 305597,</td>	US-11-036-317-305597	Sequence 305597,
33	15.2	63.3	25	26 <td>US-11-036-317-311815</td> <td>Sequence 311815,</td>	US-11-036-317-311815	Sequence 311815,
34	15.2	63.3	25	26 <td>US-11-036-317-322925</td> <td>Sequence 322925,</td>	US-11-036-317-322925	Sequence 322925,
35	15.2	63.3	25	26 <td>US-11-036-317-443709</td> <td>Sequence 443709,</td>	US-11-036-317-443709	Sequence 443709,
36	15.2	63.3	25	26 <td>US-11-060-756-256216</td> <td>Sequence 256216,</td>	US-11-060-756-256216	Sequence 256216,
37	15.2	63.3	29	24 <td>US-10-885-190B-2</td> <td>Sequence 2</td>	US-10-885-190B-2	Sequence 2
38	15	62.5	25	20 <td>US-10-775-169-2685</td> <td>Sequence 2685, Ap</td>	US-10-775-169-2685	Sequence 2685, Ap
39	15	62.5	25	22 <td>US-10-719-900-13488</td> <td>Sequence 13488, A</td>	US-10-719-900-13488	Sequence 13488, A
40	15	62.5	25	22 <td>US-10-719-900-408446</td> <td>Sequence 408446,</td>	US-10-719-900-408446	Sequence 408446,
41	15	62.5	25	22 <td>US-10-719-900-833110</td> <td>Sequence 833110,</td>	US-10-719-900-833110	Sequence 833110,
42	15	62.5	25	22 <td>US-10-719-900-924759</td> <td>Sequence 924759,</td>	US-10-719-900-924759	Sequence 924759,
43	15	62.5	25	22 <td>US-10-809-189-63266</td> <td>Sequence 63266, A</td>	US-10-809-189-63266	Sequence 63266, A
44	15	62.5	25	22 <td>US-10-809-189-127234</td> <td>Sequence 127234,</td>	US-10-809-189-127234	Sequence 127234,
45	15	62.5	25	24 <td>US-10-719-956-188382</td> <td>Sequence 188382,</td>	US-10-719-956-188382	Sequence 188382,

ALIGNMENTS

RESULT 1
US-08-469-172-3
; Sequence 3, Application US/08469172
; Publication No. US200300543A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

RESULT 5
US-11-036-317-584705
; Sequence 584705, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 584705
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-584705

Query Match 74.2%; Score 17.8; DB 26; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAACCTGCTCTGGAGGCT 24
||||| ||||| ||||| |||||
Db 1 CCAACCTACTCTGATGCT 21

RESULT 6
US-10-719-900-833111
; Sequence 833111, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 833111
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-833111

Query Match 69.2%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGCCAACCTGCTCTGGAGGCT 24
||||| ||||| ||||| |||||
Db 3 TGCCAACCTTGCTCTAGAGTCT 25

RESULT 7
US-10-719-900-924760
; Sequence 924760, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 924760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-924760

Query Match 69.2%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAGGCT 23
||||| ||||| ||||| |||||
Db 3 ATGCCAACCTGCTCTGGAGGCT 25

RESULT 8
US-10-809-189-54586
; Sequence 54586, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54586
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-54586

Query Match 69.2%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGCCAACCTGCTCTGGAGGCT 24
||||| ||||| ||||| |||||
Db 1 TGCCAACCTTGCTCTAGAGTCT 23

RESULT 9
US-10-719-956-188380
; Sequence 188380, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188380
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-188380

Query Match 69.2%; Score 16.6; DB 24; Length 25;
Best Local Similarity 82.6%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77825
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-77825

Query Match      67.5%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 CCAACCCCTGCTCTGGAGGCC 24
      ||||| ||||| ||||| |||||
Db      23 CCATCCCTTCTCTGGAGTCCT 3

RESULT 10
US-10-719-900-174561/c
; Sequence 174561, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 174561
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-174561

Query Match      67.5%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TGCCACCCCTGCTCTGGAGGC 22
      ||||| ||||| ||||| |||||
Db      22 TGCCACACTGATCTGGAGGC 2

RESULT 11
US-10-036-317-584704
; Sequence 584704, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 584704
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-584704

Query Match      67.5%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 CCAACCCCTGCTCTGGAGGCC 24
      ||||| ||||| ||||| |||||
Db      1 CCAACCCCTACTCAGGATGCCT 21

RESULT 12
US-11-060-756-77825/c
; Sequence 77825, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
```

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; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77825
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-77825

Query Match      67.5%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 CCAACCCCTGCTCTGGAGGCC 24
      ||||| ||||| ||||| |||||
Db      23 CCATCCCTTCTCTGGAGTCCT 3

RESULT 13
US-10-719-900-53167
; Sequence 53167, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 53167
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-53167

Query Match      65.8%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGCCAACCCCTGCTCTGGA 19
      ||||| ||||| ||||| |||||
Db      1 AAGCCATCCCTGCTCTGGA 19

RESULT 14
US-10-809-189-54585
; Sequence 54585, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54585
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
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US-10-809-189-54585

Query Match 65.8%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAAACCTGCTCTGGAG 20
DB 7 TGCCAAACCTGCTCTAGAG 25

RESULT 15

US-10-035-833A-1677/c
; Sequence 1677, Application US/10035833A
; Publication No. US20040072156A1

GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuhō
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1677
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-1677

Query Match 65.8%; Score 15.8; DB 19; Length 41;
Best Local Similarity 81.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCT 24
DB 25 CCAAYCCTACTCTGGGCT 5

RESULT 16

US-10-035-833A-7225/c
; Sequence 7225, Application US/10035833A
; Publication No. US20040072156A1

GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuhō
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7225
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-7225

Query Match 65.8%; Score 15.8; DB 19; Length 41;
Best Local Similarity 81.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCT 24
DB 25 CCAAYCCTACTCTGGGCT 5

RESULT 17

US-10-887-230-21/c

; Sequence 21, Application US/10887230
; Publication No. US20050042218A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: MHC Class I - Peptide-Antibody Conjugates with Modified
; FILE REFERENCE: B2-Microglobulin
; FILE REFERENCE: 1843.0160002
; CURRENT APPLICATION NUMBER: US/10/887,230
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,716
; PRIOR FILING DATE: 2003-7-10
; PRIOR APPLICATION NUMBER: US 60/513,043
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer used in Production of VH Cassette/CH1/hinge
US-10-887-230-21

Query Match 65.0%; Score 15.6; DB 22; Length 45;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGC 22
DB 40 ATGCCAACCTGCTGGAGGC 19

RESULT 18

US-11-036-317-327390/c
; Sequence 327390, Application US/11036317
; Publication No. US20050214823A1

GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 327390
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-327390

Query Match 64.2%; Score 15.4; DB 26; Length 25;
Best Local Similarity 94.1%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ACCCTGCTCTGGAGGCC 23
DB 17 ACTCTGCTCTGGAGGCC 1

RESULT 19

US-10-719-900-170847
; Sequence 170847, Application US/10719900
; Publication No. US20050026164A1

GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 170847
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-170847

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCAACCTGCTCGAGGC 22
|||||
Db 2 GCCAACCTGCTTGAGC 21

RESULT 20

US-10-719-900-170848
; Sequence 170848, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 170848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-170848

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCAACCTGCTCGAGGC 22
|||||
Db 2 GCCAACCTGCTTGAGC 21

RESULT 21

US-10-719-900-352179/c
; Sequence 352179, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 352179
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-352179

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAACCTGCTCGAGGCCT 24
|||||

Db 23 CAACCAAGCTCTGGAGCCT 4

RESULT 22

US-10-719-900-513335
; Sequence 513335, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 513335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-513335

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAG 20
|||||
Db 2 ATGCCATCTTGCTCAGGAG 21

RESULT 23

US-10-719-900-796279
; Sequence 796279, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 796279
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-796279

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAACCTGCTCTGGAGCCT 24
|||||
Db 2 CAACGCTGCTGGAGCCT 21

RESULT 24

US-10-956-157-196604/c
; Sequence 196604, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04

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; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 196604
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-956-157-196604

Query Match      63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCC 23
Db 23 CCACCCCTGCTCTGAGGCC 4

RESULT 25
US-10-719-956-26759
; Sequence 26759, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 26759
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-26759

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CAACCTGCTCTGGAGGCC 24
Db 3 CGACCTGCTCTAGATGCT 22

RESULT 26
US-10-719-956-95487/c
; Sequence 95487, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 95487
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-95487

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAG 20
Db 23 ATGCCAGCCCTGCTCCGAAG 4

RESULT 27
US-10-719-956-671714/c
; Sequence 671714, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 671714
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-671714

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAG 20
Db 22 ATGACATGCTGCTCTGGAG 3

RESULT 28
US-11-036-317-52603
; Sequence 52603, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 52603
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-52603

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAG 20
Db 6 AGGCTAACCCCGCTCTGGAG 25

RESULT 29
US-11-036-317-194782/c
; Sequence 194782, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
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; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 322925
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-322925

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```
Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 3 GCCAACCTGCTCTGGAGC 22
 ||| |||||
Db 25 GCCCACCTGCTGTGCATGC 6

RESULT 35

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US-11-036-317-443709
; Sequence 443709, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443709
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-443709

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Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 5 CAACCTGCTCTGGAGGCCT 24
|||
Db 2 CAACCTGGTCTGGTGGACT 21

RESULT 36

```

US-11-060-756-256216/c
; Sequence 256216, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 256216
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-256216

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Query Match 63.3%; Score 15.2; DB 26; Length 25;

```

Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCAACCTGCTCTGGAGGCC 23
    ||| ||| ||| ||| |||
Db 20 CCATCCCTTCTCTGGAGTCC 1

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RESULT 37

```

US/10-885-1908-2/c
; Sequence 2, Application US/10885190B
; Publication No. US20050202549A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Crystal structure of OSC
; FILE REFERENCE: Case 21797
; CURRENT APPLICATION NUMBER: US/10/885.190B
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human oxidosqualene synth
; OTHER INFORMATION: (TCTAGA).
US/10-885-1908-2

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Query Match 63.3%; Score 15.2; DB 24; Length 29;
Best Local Similarity 85.0%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCAACCCCTGCTCTGGAGGC 22
||| ||| ||| ||| ||| ||| |||
Db 20 GCCACCCCTGATCTAGAGGC 1

RESULT 38

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US-10-775-169-2685/c
; Sequence 2685, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2685
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-10-775-169-2685

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```
Query Match      62.5%; Score 15; DB 20; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 2 TGCCAACCCCTGCTCTGGAGGCCT 24
||| ||| ||| ||| ||| ||| ||| |||
Dd 25 TGTCCACCCCTGCTCTGGGTACCT 3

RESULT 39

US-10-719-900-13488
; Sequence 13488, Application US/10719900
; Publication No. US20050026164A1

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; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-13488

Query Match          62.5%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. NO. 5.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGCC 23
   ||||| ||||| ||||| |||||
Db 2 AAGCCAGACCTGCGCTGGAGGAC 24

RESULT 40
US-10-719-900-408446
; Sequence 408446, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 408446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-408446

Query Match          62.5%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. NO. 5.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGCC 23
   ||||| ||||| ||||| |||||
Db 3 AAGCCAGACCTGCGCTGGAGGAC 25

Search completed: November 18, 2005, 15:41:04
Job time : 323.586 secs
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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	24	100.0	24	6	I12897		I12897 Sequence 4
2	16.2	67.5	34	6	A52065		A52065 Sequence 21
3	16.2	67.5	34	6	AR067674		AR067674 Sequence
4	16.2	67.5	34	6	AR169819		AR169819 Sequence
5	16	66.7	35	6	E22424		E22424 Method for
6	16	66.7	35	6	E58671		E58671 Novel metal
C 7	15.2	63.3	25	6	AX8663329		AX8663329 Sequence
C 8	14.8	61.7	49	6	CQ818593		CQ818593 Sequence
C 9	14.6	60.8	27	6	BD074127		BD074127 Composite
C 10	14.4	60.0	30	6	CQ857208		CQ857208 Sequence
C 11	14.4	60.0	30	6	AX793375		AX793375 Sequence
12	14.2	59.2	28	6	CQ874317		CQ874317 Sequence
13	14	58.3	36	6	AR120382		AR120382 Sequence
14	14	58.3	36	6	BD274040		BD274040 Identific
15	14	58.3	36	6	BD274049		BD274049 Identific
16	14	58.3	36	6	BD341073		BD341073 Sequence
17	14	58.3	36	6	BD063391		BD063391 Streptoco
C 18	14	58.3	38	6	AX061955		AX061955 Sequence
C 19	14	58.3	41	6	AX514615		AX514615 Sequence


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FH Key Location/Qualifiers
FT source 1..35
FT /organism='Homo sapiens (human)'.
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            /organism='Homo sapiens'
            /mol_type='genomic DNA'
            /db_xref='taxon:9606'
ORIGIN
    Query Match 66.7%; Score 16; DB 6; Length 35;
    Best Local Similarity 79.2%; Pred. No. 8.4e+03;
    Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CTTTCATGTTCCAAAGTCATGAT 24
Db 7 CCTCATCTTCTTACGGTGCATGAT 30
RESULT 7
AX663329/c
LOCUS AX663329 25 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 36 from Patent WO20061086.
ACCESSION AX663329
VERSION AX663329.1 GI:29163676
KEYWORDS
SOURCE synthetic construct
ORGANISM
    other sequences; artificial sequences.
REFERENCE
    1 Fedér,J., Ramanathan,C. and Mintier,G.
    Human leucine-rich repeat containing protein, expressed
    predominantly in small intestine. HLRRS11
    Patent: WO 02061086-A 36 08-AUG-2002;
    Bristol-Myers Squibb Company (US)
FEATURES
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        Location/Qualifiers
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            /organism='synthetic construct'
            /mol_type='unassigned DNA'
            /db_xref='taxon:32630'
            /note='Synthesized oligonucleotide.'
ORIGIN
    Query Match 63.3%; Score 15.2; DB 6; Length 25;
    Best Local Similarity 85.0%; Pred. No. 2.2e+04;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTTTCATGTTCCAAAGTCGA 20
Db 23 CTTTCGTGGCTCCAAAGTCGA 4
RESULT 8
CQ818593/c
LOCUS CQ818593 49 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 23 from Patent WO2004039825.
ACCESSION CQ818593
VERSION CQ818593.1 GI:48427205
KEYWORDS
SOURCE synthetic construct
ORGANISM
    other sequences; artificial sequences.
REFERENCE
    1 freskg Rd,P.O., Franch,T., Gouliaev,A.H., Lundorf,M.D., Felding,J.,
    Olsen,E.K., Holtmann,A., Jakobsen,S.R., Sama,C., Glad,S.S.,
    Jensen,K.B. and Pedersen,H.
    Enzymatic encoding
    Patent: WO 2004039825-A 23 13-MAY-2004;
    Nuevolution A/S (DK)
FEATURES
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        Location/Qualifiers
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            /organism='synthetic construct'
            /mol_type='unassigned DNA'
            /db_xref='taxon:32630'
            /note='Artificially produced'
ORIGIN
    Query Match 61.7%; Score 14.8; DB 6; Length 49;
    Best Local Similarity 88.9%; Pred. No. 3.3e+04;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TTCATGTTCCAAAGTCG 19
Db 40 TTCATGTTCCAAAGTCG 23
RESULT 9
BD074127/c
LOCUS BD074127 27 bp DNA linear PAT 27-AUG-2002
DEFINITION Composition binding specifically to colorectal cancer and
utilization thereof.
ACCESSION BD074127
VERSION BD074127.1 GI:22619730
KEYWORDS JP 2001512666-A/18.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
    1 (bases 1 to 27)
    Waldman,S.A., Pearlman,J.M., Barber,M.T., Schultz,S. and
    Parkinson,S.J.
    Composition binding specifically to colorectal cancer and
    utilization thereof
    Patent: JP 2001512666-A 18 28-AUG-2001;
    THOMAS JEFFERSON UNIVERSITY
    OS Unidentified
    PN JP 2001512666-A/18
    PD 28-AUG-2001
    PR 07-AUG-1998 JP 2000506228
    PF 07-AUG-1997 US 08/908643
    PI SCOTT A WALDMAN,JOSHUA M PEARLMAN,MICHAEL T BARBER,STEPHANIE
    PI SCHULTZ
    PI SCOTT J PARKINSON
    PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68,G01N33/
    PC 574//
    PC A61K31/7088,A61K39/00,A61K39/395,A61K48/00,A61P35/
    PC 00,A61P35/04,
    PC C12N15/00,C12N5/00
    CC Strandedness: Double;
    CC Topology: linear;
    CC Composition binding specifically to colorectal cancer and CC
    thereof
    FH Key Location/Qualifiers
    FT source 1..27
    FT /organism='Unidentified'.
FEATURES
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        Location/Qualifiers
            1..27
            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'
ORIGIN
    Query Match 60.8%; Score 14.6; DB 6; Length 27;
    Best Local Similarity 81.0%; Pred. No. 4.4e+04;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CATCTTTCCAAAGTCATGAT 24
Db 26 CATATGTTCCAAAGACGAGAT 6
RESULT 10
CQ857208/c
LOCUS CQ857208 30 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 550 from Patent WO2004069997.
    source
        Location/Qualifiers
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            /organism='synthetic construct'
            /mol_type='unassigned DNA'
            /db_xref='taxon:32630'
            /note='Artificially produced'
ORIGIN
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ACCESSION	CQ857208
VERSION	CQ857208.1 GI:51851583
KEYWORDS	
SOURCE	Helicobacter pylori
ORGANISM	Helicobacter pylori
REFERENCE	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
AUTHORS	Thiberge,J.M., Labigne,A., Coppee,J.Y. and Lacroix,C.
TITLE	Method for the production of a composition of dna sequences or the expression products thereof permitting the identification of the strains of helicobacter pylori and use thereof in a prognostic or diagnostic method
JOURNAL	PATENT: WO 2004069997-A 550 19-AUG-2004;
FEATURES	INSTITUT PASTEUR (FR)
source	Location/Qualifiers
ORIGIN	1..30 /organism="Helicobacter pylori" /mol_type="unassigned DNA" /db_xref="taxon:210"
Query Match	60.0%; Score 14.4; DB 6; Length 30;
Best Local Similarity	75.0%; Pred.No.5.5e+04;
Matches	18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	1 CTTTCATTGTTCCAAAGTGCAATGAT 24
Db	28 CTTTCATTGTTCTTAGTGCATGAT 5
RESULT 11	
AX793975/c	
LOCUS	AX793975 30 bp DNA linear PAT 17-JUL-2003
DEFINITION	Sequence 6439 from Patent WO02066501.
ACCESSION	AX793975
VERSION	AX793975.1 GI:32959422
KEYWORDS	
SOURCE	Helicobacter pylori
ORGANISM	Helicobacter pylori
REFERENCE	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
AUTHORS	Legrain,P., Rain,J.C., Colland,F., de Reuse,H. and Labigne,A.
TITLE	Protein-protein interactions in Helicobacter pylori
JOURNAL	Patent: WO 02066501-A 6439 29-AUG-2002;
HYBRIDIZATION	Hybridogenics (FR); INSTITUT PASTEUR (FR)
FEATURES	Location/Qualifiers
source	1..30 /organism="Helicobacter pylori" /mol_type="unassigned DNA" /db_xref="taxon:210"
ORIGIN	
Query Match	60.0%; Score 14.4; DB 6; Length 30;
Best Local Similarity	75.0%; Pred.No.5.5e+04;
Matches	18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	1 CTTTCATTGTTCCAAAGTGCAATGAT 24
Db	28 CTTTCATTGTTCTTAGTGCATGAT 5
RESULT 12	
CQ874317	
LOCUS	CQ874317 28 bp DNA linear PAT 27-SEP-2004
DEFINITION	Sequence 13 from Patent WO2004076618.
ACCESSION	CQ874317
VERSION	CQ874317.1 GI:52747832
KEYWORDS	
ORGANISM	synthetic construct
SOURCE	synthetic construct
OTHER SEQUENCES	artificial sequences.

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

TITLE
Streptococcus pneumoniae antigens and vaccines

JOURNAL

FEATURES

source

1. .36

Location/Qualifiers

Patent: US 6573082-A 258 03-JUN-2003;

/organism="unknown"

/mol type="genomic DNA"

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/organism="unknown"
/mol_type="genomic DNA"
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Query Match	58.3%;	Score 14;	DB 6;	Length 36;
Best Local Similarity	77.3%;	Pred. NO. 8.6e+04;		
Matches 17;	Conservative	0;	Mismatches 5;	Indels 0;
Gaps	0;			
QY	3	TCATGTTTCCAAAGTCATGAT	24	
Db	3	TCAAAGCTTCCAAACTGTTTGAT	24	

RESULT	17
BD063391	
LOCUS	
DEFINITION	BD063391 36 bp DNA linear
	Streptococcus pneumoniae antigens and vaccines.
	PAT 27-AUG-2002

ACCESSION	BD063391
VERSION	BD063391.1
KEYWORDS	GI:22608994
SOURCE	JP 2001505415-A/145.
ORGANISM	unidentified
	unclassified.
REFERENCE	1 (bases 1 to 36)
AUTHORS	Kunsch,C.A., Choi,G.H., Johnson,S.L. and Hromockyj,A.
TITLE	Streptococcus pneumoniae antigens and vaccines
JOURNAL	Patent: JP 2001505415-A 145 24-APR-2001;
	HUMAN GENOME SCIENCES INC

COMMENT	PN	JP	2001505415-A/145
	PD	24-APR-2001	
	PF	30-OCT-1997	JP 1998520667
	PR	31-OCT-1996	US 60/029960
	PI	CHARLES A KUNSCH, GIL H CHOI, SYDNOR L JOHNSON, ALEX HROMOKEYJ PC C12N15/31, C12N5/18, C12N1/21, C07K14/315, C12Q1/68, A61K39/09, PC	
	G01N33/569		
	PC	G01N33/68	
	CC	Strandedness: Double;	
	CC	Topology: Linear;	
	PH	Key	Location/Qualifiers.
FEATURES			Location/Qualifiers

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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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ORIGIN

[illegible]

RESULTS						PAT 24-JAN-2001
AX061955/c						
LOCUS	AX061955	Sequence 3 from Patent WO0100837.	38 bp	DNA	linear	
DEFINITION	AX061955					
ACCESSION	AX061955.1	GI:12539939				
VERSION						
KEYWORDS	.					

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SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    other sequences; artificial sequences.
1
AUTHORS      Thonnard,J.S.
TITLE        Babilii polypeptide and polynucleotide from moraxella catharrhalis
JOURNAL      Patent: WO 0100817-A 3 04-JAN-2001;
SMITHKLINE BEECHAM BIOLOGICALS (S.A.)
FEATURES     Location/Qualifiers
source       1..38
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Primer"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 38;
Best Local Similarity 77.3%; Pred. No. 8.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 TTCATGTTTCCAAAGTGCATGA 23
Db 35 TTAATTTTACCAAAATTCATGA 14

RESULT 19
AX514615/c
LOCUS          AX514615              41 bp      DNA      linear      PAT 05-OCT-2002
DEFINITION     Sequence 813 from Patent WO02052044.
ACCESSION      AX514615
VERSION        AX514615.1 GI:23561172
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE          Detection of genetic polymorphisms
JOURNAL        Patent: WO 02052044-A 813 04-JUL-2002;
               Riken (JP)
FEATURES       Location/Qualifiers
source         1..41
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 41;
Best Local Similarity 70.8%; Pred. No. 8.5e+04;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTTCATGTTTCCAAAGTGCATGAT 24
Db 24 CATATGTTTCCAAACTGCTGAAT 1

RESULT 20
AX520557/c
LOCUS          AX520557              41 bp      DNA      linear      PAT 05-OCT-2002
DEFINITION     Sequence 6755 from Patent WO02052044.
ACCESSION      AX520557
VERSION        AX520557.1 GI:23571178
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1
AUTHORS        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE          Detection of genetic polymorphisms
JOURNAL        Patent: WO 02052044-A 6755 04-JUL-2002;
               Riken (JP)
FEATURES       Location/Qualifiers
source         1..41
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 41;
Best Local Similarity 70.8%; Pred. No. 8.5e+04;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTTCATGTTTCCAAAGTGCATGAT 24
Db 24 CATATGTTTCCAAACTGCTGAAT 1

RESULT 21
AX697195
LOCUS          AX697195              46 bp      DNA      linear      PAT 02-APR-2003
DEFINITION     Sequence 263 from Patent WO0078961.
ACCESSION      AX697195
VERSION        AX697195.1 GI:29498140
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      1
AUTHORS        Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
               Eaton,D.L., Gao,W.O., Pan,J., Botstein,D., Fong,S., Goddard,A.,
               Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
               Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
               Secreted and transmembrane polypeptides and nucleic acids encoding
               the same
JOURNAL        Patent: WO 0078961-A 263 28-DEC-2000;
               Genentech Inc. (US)
FEATURES       Location/Qualifiers
source         1..46
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 46;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CTTCATGTTTCCAAAGTGCATG 22
Db 13 CTTCATGATGCTCAAGTACATG 34

RESULT 22
AR355880
LOCUS          AR355880              50 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION     Sequence 1998 from patent US 6593114.
ACCESSION      AR355880
VERSION        AR355880.1 GI:33761964
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 50)
AUTHORS        Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and
               Rosen,C.A.
Staphylococcus aureus polynucleotides and sequences
JOURNAL        Patent: US 6593114-A 1998 15-JUL-2003;
               Location/Qualifiers
FEATURES       Location/Qualifiers
source         1..50
               /organism="unknown"
               /mol_type="genomic DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 50;
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Best Local Similarity 73.9%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTCATGAT 24
Db 7 TTGATGNTCTCAAGAACATGAT 29

RESULT 23
AR537436
LOCUS AR537436 50 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1998 from patent US 6737248.
ACCESSION AR537436
VERSION AR537436.1 GI:53928653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6737248-A 1998 18-MAY-2004;
FEATURES
source
Location/Qualifiers
1..50
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 50;
Best Local Similarity 73.9%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTCATGAT 24
Db 7 TTGATGNTCTCAAGAACATGAT 29

RESULT 24
AR533926
LOCUS AR533926 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 173 from patent US 6733965.
ACCESSION AR533926
VERSION AR533926.1 GI:53923959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Unclassified.
TITLE (bases 1 to 20)
AUTHORS Echt,C.S. and Nelson,C.D.
TITLE Microsatellite DNA markers and uses thereof
JOURNAL Patent: US 6733965-A 173 11-MAY-2004;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTG 18
Db 3 TTGATGTTTCCAAATGT 19

RESULT 25
BD002832
LOCUS BD002832 31 bp DNA linear PAT 31-JAN-2002
DEFINITION Gene composition and method.
ACCESSION BD002832
VERSION BD002832.1 GI:18630793

Best Local Similarity 73.9%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

KEYWORDS JP 2000245487-A/498.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Sha,N., Walinton,J. and Patel,N.
TITLE Gene composition and method
JOURNAL Patent: JP 2000245487-A 498 12-SEP-2000;
COMMENT AFIMETRICS INC
OS Unknown
PN JP 2000245487-A/498
PD 12-SEP-2000
PF 27-JAN-2000 JP 200019392
PI 27-JAN-1999 US 09/238.402
PI NIRA SHA,JANET WALINTON,NIRA PATEL
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..31
FT /organism="Unknown".
FEATURES
source
Location/Qualifiers
1..31
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 31;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TGTTCCAAAGTCATGAT 24
Db 1 TGTTCCAAAGTTGAYGAT 19

RESULT 26
AX931884/c
LOCUS AX931884 35 bp DNA linear PAT 22-DEC-2003
DEFINITION Sequence 41 from Patent WO03087829.
ACCESSION AX931884
VERSION AX931884.1 GI:40312497
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Thunnissen,F.B., Klaassen,C.H. and Prinsen,C.F.
TITLE Human papilloma virus detection with dna microarray
JOURNAL Patent: WO 03087829-A 41 23-OCT-2003;
JOURNAL Dot Diagnostics B.V. (NL)
FEATURES
source
Location/Qualifiers
1..35
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: based on
genomic DNA sequence from Human Papilloma Virus"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 35;
Best Local Similarity 88.2%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGT 17
Db 33 CTACATGTTTCCAAATGT 17

RESULT 27
AR284732
LOCUS AR284732 47 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 784 from patent US 6528260.
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ACCESSION AR284732
VERSION AR284732.1 GI:29721636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Blumenfeld, M., Chumakov, I., Bougueleret, L. and Cohen, A.
TITLE Biallelic markers related to genes involved in drug metabolism
JOURNAL Patent: US 6528260-A 784 04-MAR-2003;
FEATURES Location/Qualifiers
 source 1..47
 /organism="unknown"
 /mol_type="genomic DNA"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 47;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 6 TGTTCCTCAAAAGTGCATGAT 24
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Db 9 TGTCTCAAAAGTTGAYGAT 27
RESULT 28
AR565646
LOCUS AR565646 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 10 from patent US 6767738.
ACCESSION AR565646
VERSION AR565646.1 GI:53981680
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gage, F.H., Palmer, T., Safar, P.G., Takahashi, J. and Takahashi, M.
TITLE Method of isolating adult mammalian CNS-derived progenitor stem cells using density gradient centrifugation
JOURNAL Patent: US 6767738-A 10 27-JUL-2004;
FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="genomic DNA"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CATGTTTCCAAAGTGCATGA 23
 ||||| ||||| |||||
Db 1 CATGTAATTCAAAGACCATGA 20
RESULT 29
CQ880137
LOCUS CQ880137 26 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 1 from Patent EP1464710.
ACCESSION CQ880137
VERSION CQ880137.1 GI:54033904
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Yamamoto, N., Ogura, M., Kawaguchi, M., Tsukada, M., Yoshii, H., Suzuki, T., Ishii, M. and Fukui, T.
TITLE Infectious etiologic agent detection probe and probe set, carrier, and genetic screening method
JOURNAL Patent: EP 1464710-A 1 06-OCT-2004;
FEATURES Location/Qualifiers
 source 1..26
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /notes="Complementary DNA Sequence of Synthesized DNA probe PA-1"

source 1..26
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /notes="Synthesized DNA probe named PA-1"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CATGTTTCCAAAGTGCATGA 23
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Db 7 CATGGTTCAAAAGTGAAGA 26
RESULT 30
CQ880249/c
LOCUS CQ880249 26 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 113 from Patent EP1464710.
ACCESSION CQ880249
VERSION CQ880249.1 GI:54034016
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Yamamoto, N., Ogura, M., Kawaguchi, M., Tsukada, M., Yoshii, H., Suzuki, T., Ishii, M. and Fukui, T.
TITLE Infectious etiologic agent detection probe and probe set, carrier, and genetic screening method
JOURNAL Patent: EP 1464710-A 113 06-OCT-2004;
FEATURES Location/Qualifiers
 source 1..26
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /notes="Complementary DNA Sequence of Synthesized DNA probe PA-1"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CATGTTTCCAAAGTGCATGA 23
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Db 20 CATGGTTTCAAAAGTGAAGA 1
RESULT 31
BD170377/c
LOCUS BD170377 27 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel formate dehydrogenase and process for producing the same.
ACCESSION BD170377
VERSION BD170377.1 GI:27876189
KEYWORDS WO 0246427-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Takaoka, Y. and Namba, H.
TITLE Novel formate dehydrogenase and process for producing the same
JOURNAL Patent: WO 0246427-A 7 13-JUN-2002;
COMMENT KANEKA CORP., YASUKO TAKAOKA, HIROKAZU NAMBA
 OS Artificial Sequence
 PN WO 0246427-A/7
 PD 13-JUN-2002
 PF 04-DEC-2001 WO 2001JP010569
 PR 04-DEC-2000 JP 00P 368838
 PI YASUKO TAKAOKA, HIROKAZU NAMBA
 PC C12N15/53, C12N9/04, C12N1/21


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CC . Description of Artificial Sequence: primer-5
FH Key      Location/Qualifiers
FT source   1..27
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FEATURES
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            /organism='synthetic construct'
            /mol_type='genomic DNA'
            /db_xref='taxon:32630'
ORIGIN
Query Match      56.7%; Score 13.6; DB 6; Length 27;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 TCATGTTTCCAAAGTGCATG 22
Db 24 TCATGTCGACGGTGCATG 5
RESULT 32
LOCUS AR290927/c 47 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2662 from patent US 6537751.
ACCESSION AR290927
VERSION AR290927.1 GI:31678211
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 2662 25-MAR-2003;
    source Location/Qualifiers
    1..47
    /organism='unknown'
    /mol_type='genomic DNA'
ORIGIN
Query Match      56.7%; Score 13.6; DB 6; Length 47;
Best Local Similarity 72.7%; Pred. No. 1.4e+05;
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 3 TCATGTTTCCAAAGTGCATG 24
Db 33 TCATGAATYAAATTCATGAT 12
RESULT 33
LOCUS AR190122/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5610 from patent US 6346398.
ACCESSION AR190122
VERSION AR190122.1 GI:20236087
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6346398-A 5610 12-FEB-2002;
    source Location/Qualifiers
    1..17
    /organism='unknown'
    /mol_type='unassigned DNA'
ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GTTTCCTCCAAAGTGCAT 21
Db 16 GTTTCCTCCAAAGAGCAT 2
RESULT 34
LOCUS AR190123/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5611 from patent US 6346398.
ACCESSION AR190123
VERSION AR190123.1 GI:20236088
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6346398-A 5611 12-FEB-2002;
    source Location/Qualifiers
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    /organism='unknown'
    /mol_type='unassigned DNA'
ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GTTTCCTCCAAAGTGCAT 21
Db 15 GTTTCCTCCAAAGAGCAT 1
RESULT 35
LOCUS AR325098/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2500 from patent US 6566127.
ACCESSION AR325098
VERSION AR325098.1 GI:33710906
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6566127-A 2500 20-MAY-2003;
    source Location/Qualifiers
    1..17
    /organism='unknown'
    /mol_type='unassigned RNA'
ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GTTTCCTCCAAAGTGCAT 21
Db 16 GTTTCCTCCAAAGAGCAT 2
RESULT 36
LOCUS AR325099/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2501 from patent US 6566127.
ACCESSION AR325099
VERSION AR325099.1 GI:33710907
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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 2501 20-MAY-2003;
FEATURES    Location/Qualifiers
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTCCAAAGTCAT 21
    |||||
Db 15 GTTCCAAAGCAT 1

RESULT 37
DOGP47701/c
LOCUS      DOGP47701      18 bp      DNA      linear      MAM 19-JAN-1996
DEFINITION Dog (Clone: CXK.477) primer for STS 477, 5' end.
ACCESSION L24354
VERSION   L24354.1 GI:404031
KEYWORDS  PCR identification; PCR primer; STS.
SEGMENT   1 of 2
ORGANISM  Canis familiaris (dog)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
TITLE      One hundred and one new simple sequence repeat-based markers for
            the canine genome
JOURNAL    Mamm. Genome 6 (3), 192-195 (1995)
MEDLINE    95268214
PUBMED     7749226
COMMENT    Original source text: Canis familiaris (library: E. Ostrander, in
            pBluescript+) adult spleen DNA.
            Submitted by:
            Fred Hutchinson Cancer Research Center
            Transplantation Biology Dept
            1124 Columbia; Mailstop M318
            Seattle, WA 98104, USA
            e-mail: EAOstrander@bl.gov
            PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
            PCR Profile: Denaturation: 94 degrees C for 1.00 minute
            Annealing: 55 or 59 degrees C for 0.45 minutes
            Polymerization: 74 degrees C for 1.00 minutes
            PCR Cycles: 33
            Final Extension: 74 degrees C for 5.00 minutes.
FEATURES    Location/Qualifiers
            1..18
            /organism="Canis familiaris"
            /mol_type="genomic DNA"
            /db_xref="taxon:9615"
            /tissue_type="spleen"
            /dev_stages="adult"
            /tissue_lib="E. Ostrander, in pBluescript+"
            primer_bind 1..18

ORIGIN
Query Match      55.8%; Score 13.4; DB 4; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TTTCCAAAGTCATG 22
    |||||
Db 15 TTTCCAAAGGCATG 1

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 2501 20-MAY-2003;
FEATURES    Location/Qualifiers
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTCCAAAGTCAT 21
    |||||
Db 15 GTTCCAAAGCAT 1

RESULT 38
AX462495
LOCUS      AX462495      20 bp      DNA      linear      PAT 15-JUL-2002
DEFINITION Sequence 239 from Patent EP1217079.
ACCESSION AX462495
VERSION   AX462495.1 GI:21885708
KEYWORDS
SOURCE     Aegilops tauschii
ORGANISM   Aegilops tauschii
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Pooideae; Triticeae; Aegilops.
REFERENCE  1
AUTHORS    Bernard,M., Sourdille,P. and Guyomarch,H.
TITLE      Microsatellite markers from Triticum tauschii
JOURNAL    Patent: EP 1217079-A 239 26-JUN-2002;
          INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES    Location/Qualifiers
            1..20
            /organism="Aegilops tauschii"
            /mol_type="unassigned DNA"
            /db_xref="taxon:37682"

ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TTCCAAAGTCATGA 23
    |||||
Db 4 TTCCAAAGTCATGA 18

RESULT 39
AB166618/c
LOCUS      AB166618      23 bp      DNA      linear      SYN 07-OCT-2004
DEFINITION Synthetic construct DNA, forward primer for microsatellite
            NRD1KM020.
ACCESSION AB166618
VERSION   AB166618.1 GI:51850034
KEYWORDS  synthetic construct
SOURCE     other sequences; artificial sequences.
ORGANISM   1
REFERENCE   1
AUTHORS     Ihara,N.; Takasuga,A., Mizoshita,K., Takeda,H., Sugimoto,M.,
            Mizoguchi,Y., Hirano,T., Itoh,T., Watanabe,T., Reed,K.M.,
            Snelling,W.M., Kappes,S.M., Beattie,C.W., Bennett,G.L. and
            Sugimoto,Y.
TITLE      A comprehensive genetic map of the cattle genome based on 3802
            microsatellites
JOURNAL    Genome Res. 14 (10), 1987-1998 (2004)
PUBMED     15466297
REFERENCE   2 (bases 1 to 23)
AUTHORS     Sugimoto,Y., Ihara,N. and Mizoshita,K.
TITLE      Direct Submission
JOURNAL    Submitted (04-MAR-2004) Yoshikazu Sugimoto, Shirakawa Institute of
            Animal Genetics; Odakura, Nishigo, Nishi-shirakawa, Fukushima
            961-8061, Japan (E-mail:kazusugi@siag.or.jp, Tel:81-248-25-5641,
            Fax:81-248-25-5725)
FEATURES    Location/Qualifiers
            1..23
            /organism="synthetic construct"
            /mol_type="other DNA"
            /db_xref="taxon:32630"
            /chromosome="20"
            misc_feature 1..23
            /note="forward primer for microsatellite NRD1KM020"

ORIGIN

```

Query Match 55.8%; Score 13.4; DB 12; Length 23;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAG 16
Db 16 TTCATGTTTACCAAG 2

RESULT 40
A94624/c A94624 29 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 7 from Patent EP0943679.
ACCESSION A94624
VERSION A94624.1 GI:6778935
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 29)
AUTHORS
TITLE Novel RNase-like protein and its use
JOURNAL Patent: EP 0943679-A 7 22-SEP-1999;
FEATURES
source
1..29
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 29;
Best Local Similarity 73.9%; Pred. No. 1.7e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATGA 23
Db 26 CTTTAGGTTTCCAGACTGCTCGA 4

Search completed: November 18, 2005, 17:42:53
Job time : 667.986 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 165.262 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-4
Perfect score: 24
Sequence: 1 CTTCAAGTTTCCAAAGTCATGAT 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	2	AAQ91124 Beta-card
2	24	100.0	24	9	ACA63114 Human bet
3	24	100.0	24	13	ADR05300 Human bet
4	16.4	68.3	41	4	AHA46257 Aldenhyde/
5	16.2	67.5	34	2	AAT34642 Primer fo
6	16	66.7	35	2	AA18400 Primer MI
7	16	66.7	35	4	AAH20236 Human ADA
8	15.2	63.3	25	6	ABS63500 HLRRS11,
9	15	62.5	38	6	ADP30162 HA-tagged
10	14.8	61.7	20	12	ADP21883 Ornithine
11	14.8	61.7	20	12	ADP21988 Ornithine
12	14.6	61.7	49	12	ADO04093 Identifie
13	14.6	60.8	27	2	AAH27821 CRCA-1 co
14	14.6	60.8	34	12	ADO41360 Oligo 3-2
15	14.6	60.8	41	10	AAH57225 Oligonuc
16	14.6	60.8	41	10	AAH57224 Oligonuc
17	14.4	60.0	30	6	ABX70212 Novel Hel
18	14.4	60.0	30	13	ADR23060 DNA/RNA p
19	14.4	60.0	33	6	AAH45772 Human aci
20	14.4	60.0	37	8	ABT42676 Human G-p

21	14.2	59.2	20	4	AAF87048 PCR prime
22	14.2	59.2	20	12	ADL59164 Human ESM
23	14.2	59.2	20	12	ADL5982 Human ESM
24	14.2	59.2	33	6	ABW74729 Human cia
25	14.2	59.2	50	6	ABZ04574 Human leu
26	14.2	59.2	50	10	ADG33666 Human DNA
27	14.2	59.2	50	12	ADP10108 50-mer ol
28	14	58.3	25	9	ACK15268 Human mic
29	14	58.3	27	10	ABX95855 PCR prime
30	14	58.3	28	12	ADH27316 Ferritin
31	14	58.3	28	12	ADH27295 Ferritin
32	14	58.3	28	12	ADH27302 Ferritin
33	14	58.3	28	12	ADH27288 Ferritin
34	14	58.3	29	12	ADH27309 Ferritin
35	14	58.3	32	13	ADR33465 Human nic
36	14	58.3	33	6	ABK11366 NADH dehy
37	14	58.3	36	2	AAV27468 Streptoco
38	14	58.3	36	3	AAA70860 Molecular
39	14	58.3	36	3	AAA70869 Molecular
40	14	58.3	36	6	ABQ84936 Streptoco
41	14	58.3	36	10	ADC45339 S. pneumo
42	14	58.3	38	4	AAF30041 Moraxella
43	14	58.3	41	6	ABS55299 Human leu
44	14	58.3	46	3	AAA37264 Human PRO
45	14	58.3	46	4	AAF54390 Primer #7

ALIGNMENTS

RESULT 1
AAQ91124
ID AAQ91124 standard; cDNA; 24 BP.
XX
AC AAQ91124;
XX
DT 19-FEB-1996 (first entry)
XX
DE Beta-cardiac myosin heavy chain PCR primer B'.
XX
KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
diagnosis; primer; mutation; detection; ss.
OS Synthetic.
XX
FN US429923-A.
XX
PD 04-JUL-1995.
XX
PF 11-DEC-1992; 92US-00989160.
XX
PR 11-DEC-1992; 92US-00989160.
XX
(HARD) HARVARD COLLEGE.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
(GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.
Seidman J, Seidman C, Watkins H, Rosenzweig A;
WPI; 1995-245715/32.
Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
useful for testing asymptomatic individual(s).
Example 1; Col 10; 22pp; English.

AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria
 CC
 SQ Sequence 24 BP; 6 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 |||||
 DB 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 |||||
 RESULT 2
 ACA63114
 ID ACA63114 standard; DNA; 24 BP.
 XX
 AC ACA63114;
 XX
 DT 28-AUG-2003 (first entry)
 XX
 DE Human beta cardiac myosin heavy chain PCR primer B'.
 XX
 KW Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
 KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
 KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
 KW phenylketonuria; cystic fibrosis.
 XX
 OS Homo sapiens.
 XX
 XX US2003054343-A1.
 XX
 XX 20-MAR-2003.
 XX
 XX 06-JUN-1995; 95US-00469172.
 XX
 XX 11-DEC-1992; 92US-00989160.
 XX
 XX (SEID/) SEIDMAN C.
 XX (SEID/) SEIDMAN J.
 XX (WATK/) WATKINS H.
 XX (ROSE/) ROSENZWEIG A.
 XX
 XX Seidman C, Seidman J, Watkins H, Rosenzweig A;
 XX WPI; 2003-512374/48.
 XX
 XX Detecting a presence or absence of a mutation associated with
 XX hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
 XX hemophilia, by detecting a mutation in an amplified product of a beta
 XX cardiac myosin heavy-chain DNA.
 XX
 XX Example 1; Page 5; 22pp; English.
 XX
 XX The invention relates to detecting the presence or absence of a mutation
 XX associated with hypertrophic cardiomyopathy (sporadic or familial SHC
 XX and FHC) comprises detecting a mutation associated with hypertrophic
 XX cardiomyopathy in an amplified product of a beta cardiac myosin heavy
 XX chain DNA. The mutations associated with SHC/FHC are detected in the
 XX myosin gene isolated from blood, by detecting mis-matched areas in RNA-
 XX DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
 XX sample). FHC associated point mutation can be classified and used to
 XX determine life expectancy in affected individuals e.g. using a Kaplan-
 XX Meier curve for the classified type of FHC causing point mutation. Also
 XX included are an RNA probe comprising ribonucleotides arranged in a
 XX sequence which is complementary to at least a portion of beta-cardiac
 XX myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
 XX amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a nested PCR primer used to amplify a region of the beta cardiac
 CC myosin heavy chain cDNA containing an FHC-associated mutation
 XX
 SQ Sequence 24 BP; 6 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 |||||
 DB 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 |||||
 RESULT 3
 ADR05300
 ID ADR05300 standard; DNA; 24 BP.
 XX
 AC ADR05300;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human beta cardiac myosin heavy chain mutation detection primer B'.
 XX
 KW Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
 KW familial hypertrophic cardiomyopathy;
 KW sporadic hypertrophic cardiomyopathy.
 XX
 OS Homo sapiens.
 XX
 XX US2004152121-A1.
 XX
 XX 05-AUG-2004.
 XX
 XX 27-FEB-2004; 2004US-00788779.
 XX
 XX 11-DEC-1992; 92US-00989160.
 XX
 XX 06-JUN-1995; 95US-00469172.
 XX
 XX (SEID/) SEIDMAN C.
 XX (SEID/) SEIDMAN J.
 XX (WATK/) WATKINS H.
 XX (ROSE/) ROSENZWEIG A.
 XX
 XX Seidman C, Seidman J, Watkins H, Rosenzweig A;
 XX WPI; 2004-592586/57.
 XX
 XX Detecting mutations associated with hypertrophic cardiomyopathy to
 XX diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
 XX myosin heavy-chain DNA and detecting the mutation in the amplified
 XX product.
 XX
 XX Claim 18; SEQ ID NO 4; 22pp; English.
 XX
 XX The invention relates to detecting the presence or absence of a mutation
 XX associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
 XX SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
 XX comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
 XX amplified product, and detecting the presence or absence of a mutation
 XX associated with hypertrophic cardiomyopathy in the amplified product,
 XX thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
 XX included are a set of DNA oligonucleotide primers for amplifying beta-
 XX cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

XX Sequence 24 BP; 6 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 24; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCATGTTTCCAAAGTGCATGAT 24
DB 1 CTTTCATGTTTCCAAAGTGCATGAT 24

RESULT 4
AAH46257/c
ID AAH46257 standard; DNA; 41 BP.
XX
AC AAH46257;
XX
DT 25-SEP-2001 (first entry)
XX
DE Aldehyde/ketone reductase 9 probe, SEQ ID NO:8.
XX
KW Aldehyde/ketone reductase 9; human; recombinant production;
KW malignant tumour; cancer; blood disease; HIV infection;
KW human immunodeficiency virus; immune disorder; inflammatory condition;
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.
XX
OS Homo sapiens.
XX
FN WO200146433-A1.
XX
PD 28-JUN-2001.
XX
PF 18-DEC-2000; 2000WO-CN000607.
XX
PR 22-DEC-1999; 99CN-00125681.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-441679/47.
XX
PT Aldehyde/ketone reductase 9 and encoded polynucleotide, applicable in
PT diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT immunological diseases and various inflammation.
XX
PS Example 7; Page 16; 39pp; Chinese.

XX The invention relates to aldehyde/ketone reductase 9 (AAH98900), nucleic
CC acids encoding it (AAH46257), and a method for the recombinant production
CC of the protein. The present invention additionally discloses an agonist
CC of aldehyde/ketone reductase 9 for therapeutic use, and an antibody which
CC specifically binds to aldehyde/ketone reductase 9. Aldehyde/ketone
CC reductase 9, and nucleotides which encode it may be used for treating a
CC variety of diseases, such as malignant tumours, blood diseases, HIV
CC (human immunodeficiency virus) infection, immune disorders and
CC inflammatory conditions. The protein may also be used to screen for
CC modulators of its activity or for peptide fingerprinting identification.
CC The polynucleotide can be used as a primer for nucleic acid amplification
CC reactions or as a probe for hybridisation reactions, or in producing gene
CC chips or microarrays. Sequences AAH46257-AAH46258 represent aldehyde/
CC ketone reductase 9 probes used in an exemplification of the invention
XX

SQ Sequence 41 BP; 10 A; 11 C; 10 G; 10 T; 0 U; 0 Other;
Query Match 68.3%; Score 16.4; DB 4; Length 41;
Best Local Similarity 94.4%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATGTTTCCAAAGTGCA 20
DB 37 TCATGTTTCCAAAGTGCA 20

RESULT 5
AAT34642
ID AAT34642 standard; DNA; 34 BP.
XX
AC AAT34642;
XX
DT 14-FEB-1997 (first entry)
XX
DE Primer for human phosphodiesterase type IV D.
XX
KW Phosphodiesterase; screening; identification; inhibitor; inhibition; PDE;
KW treatment; prophylaxis; inflammatory disease; inflamed lung; asthma.
XX
OS Synthetic.
XX
FN WO9620281-A1.
XX
PD 04-JUL-1996.
XX
PF 21-DEC-1995; 95WO-GB003006.
XX
PR 23-DEC-1994; 94GB-00026227.
PR 26-JUN-1995; 95GB-00012996.
XX
PA (CLLT) CELLTech THERAPEUTICS LTD.
XX
PI Owens RJ, Perry MJ, Lumb SM;
XX
DR WPI; 1996-321854/32.
XX
PT Human phosphodiesterase type IVC and selective inhibitors - used in the
PT treatment of inflammatory disease, esp. asthma.
XX
PS Disclosure; Page 15; 50pp; English.

XX Recombinant phosphodiesterase (PDE) type IVC may be used to screen for
CC inhibitors of PDE IVC. The inhibitors may be used in pharmaceutical for
CC the treatment and prophylaxis of inflammatory diseases, especially
CC inflamed lung associated with asthma. Multiple isoforms of PDE exist
CC opening the possibility for individual inhibitors of each isoform. The
CC distribution of PDE IV isoform mRNAs in different human tissues was
CC analysed by northern blotting. Human multiple tissue northern blots were
CC hybridised with isoform specific probes generated by PCR from the 3' non-
CC translated region of each gene. Either HL-60 genomic DNA (probes A and C)
CC or a cDNA library prepared from eosinophil enriched mRNA (probes B and D)
CC were used as templates for the PCR reaction with two primers (AAT34642,


```

PD 08-AUG-2002.
XX
XX PF 20-DEC-2001; 2001WO-US049739.
XX
XX PR 22-DEC-2000; 2000US-0257774P.
XX
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX PI Feder J, Ramanathan C, Mintier G;
XX
XX WPI; 2002-619252/66.
XX
XX PT New isolated nucleic acid molecules encoding HLRRS11 polypeptides, or
XX their fragments and homologues, useful for preventing, treating and
XX ameliorating medical conditions, e.g. proliferative, gastrointestinal, or
XX renal disorders.
XX
XX PS Example 57; Page 287; 336pp; English.
XX
XX CC The invention relates to isolated nucleic acid molecules (I) encoding
XX human leucine-rich repeat small intestine I (HLRRS11) polypeptides. The
XX nucleic acid molecules and polypeptides are useful for preventing,
XX treating and ameliorating medical conditions, such as proliferative,
XX gastrointestinal, renal, neural, or reproductive disorders; or disorders
XX related to aberrant calcium regulation or apoptosis modulation, either
XX directly or indirectly. They are also useful for treating, preventing
XX and/or diagnosing diseases, disorders and/or conditions of: immune system
XX by activating or inhibiting the proliferation, differentiation, or
XX mobilisation of immune cells; haematopoietic cells e.g. thrombocytopenia,
XX anaemia; immunologic deficiency syndromes, e.g. human immune deficiency
XX virus (HIV) infection, HTLV-BLV infection; blood coagulation disorders,
XX e.g. arterial thrombosis; autoimmune disorders, e.g. Addison's disease,
XX myasthenia gravis; asthma or allergic reactions; inflammatory conditions,
XX e.g. chronic prostatitis, sepsis; proliferative disorders, e.g. cancer;
XX cardiovascular disorders, e.g. arrhythmia, myocardial ischaemias,
XX aneurysms; neurological disorders, e.g. Alzheimer's disease, Huntington's
XX chorea; infectious diseases, e.g. measles, mumps, pneumonia, or viral,
XX bacterial, and fungal infections. The HLRRS11 polypeptides are useful for
XX modulating cytokine production, antigen presentation or other processes
XX such as boosting immune responses. ABS63485-ABS63504 represent HLRRS11
XX coding sequences and PCR primers of the invention
XX
XX SQ Sequence 25 BP; 5 A; 7 C; 7 G; 4 T; 2 U; 0 Other;
Query Match 63.3%; Score 15.2; DB 6; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCA 20
Db 23 CTTTCGTGGCTCCAAAGTGCA 4

RESULT 9
AAD30162/c
ID AAD30162 standard; DNA; 38 BP.
XX
XX AC AAD30162;
XX
XX DT 17-MAY-2002 (first entry)
XX
XX DE HA-tagged human MCIP1 splice variant 4 isolating PCR primer #1.
XX
XX KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
XX heart failure; cardiomyopathy; heart disease; human; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200204491-A2.
XX
XX PD 17-JAN-2002.
XX
XX PF 06-JUL-2001; 2001WO-US021652.
XX
XX PD 07-JUL-2000; 2000US-0216601P.
XX
XX PR 13-FEB-2001; 2001US-00782953.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PA (WILL/) WILLIAMS S R.
XX
XX PA (ROTH/) ROTHERMEL B.
XX
XX PI Williams SR, Rothermel B;
XX
XX WPI; 2002-179698/23.
XX
XX PT Screening for modulators of muscle calcineurin interacting protein (MCIP)
XX binding, expression or phosphorylation, useful for treating cardiac
XX hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a
XX test compound.
XX
XX PS Example 1; Page 78; 174pp; English.
XX
XX CC The invention relates to muscle calcineurin interacting proteins (MCIPs)
XX and nucleic acid molecules encoding such proteins. MCIPs form a physical
XX complex with the catalytic subunit of calcineurin and increased levels of
XX MCIPs correspond to a reduced ability of calcineurin to stimulate
XX transcriptions of certain target genes. The invention also relates to
XX methods for identifying modulators of MCIP binding, expression or
XX phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
XX may be used for treating cardiac hypertrophy and heart failure.
XX Antibodies to MCIP can be used in characterising the MCIP content of
XX healthy and diseased tissues and subsequently for determining the
XX presence or absence of cardiomyopathy or as predictor of heart disease.
XX The present sequence is a PCR primer used to isolate HA-tagged human
XX MCIP1 splice variant 4
XX
XX SQ Sequence 38 BP; 14 A; 6 C; 5 G; 13 T; 0 U; 0 Other;
Query Match 62.5%; Score 15; DB 6; Length 38;
Best Local Similarity 78.3%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCAATGAT 24
Db 26 TTAAGTTTCTTAAAGTGCATGGT 4

RESULT 10
ADP21883
ID ADP21883 standard; DNA; 20 BP.
XX
XX AC ADP21883;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Ornithine decarboxylase 1 antisense oligonucleotide seqid 31.
XX
XX KW cytosolic; gene therapy; ornithine decarboxylase 1;
XX ornithine decarboxylase 1 associated disorder;
XX hyperproliferative disorder; cancer; human; antisense oligonucleotide;
XX antisense technology; ss.
XX
XX OS Homo sapiens.
XX
XX PH Key Location/Qualifiers
XX
XX FT modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "OTHER= Phosphorothioate backbone. All cytidines
XX FT are 5-methylcytidines"
XX FT modified_base 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX FT modified_base 15..20
XX FT /*tag= c

```

```

FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FN US2004110148-A1.
PD 10-JUN-2004.
XX
XX 10-DEC-2002; 2002US-00316244.
XX
XX 10-DEC-2002; 2002US-00316244.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie KW;
XX WPI; 2004-440337/41.
DR
XX New oligonucleotide compound that inhibits expression of ornithine
XX decarboxylase 1, useful for preparing a composition for treating
XX hyperproliferative disorder, e.g. cancer.
XX
XX Example 15; SEQ ID NO 31; 69pp; English.
XX
XX The invention describes a new compound, having a sequence comprising 8-80
XX bp targeted to a nucleic acid encoding ornithine decarboxylase 1,
XX specifically hybridises with the nucleic acid encoding ornithine
XX decarboxylase 1 comprising 2035-bp sequence and inhibits expression of
XX ornithine decarboxylase 1 in cells or tissues; screening for a
XX modulator of ornithine decarboxylase 1; identifying a disease state; a
XX kit or assay device comprising the compound; and treating an animal
XX having a disease or condition associated with ornithine decarboxylase 1.
XX The oligonucleotide compound is useful for preparing a composition for
XX treating hyperproliferative disorder, e.g. cancer. This sequence
XX represents an ornithine decarboxylase 1 antisense oligonucleotide.
XX
XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 61.7%; Score 14.8; DB 12; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAGTGCAAT 21
Db 1 CATGTTTCCAAGAGCAT 18

RESULT 11
ADP21988/c
ID ADP21988 standard; DNA; 20 BP.
AC ADP21988;
XX
XX 26-AUG-2004 (first entry)
XX
XX Ornithine decarboxylase 1 antisense oligonucleotide seqid 136.
XX
XX cytostatic; gene therapy; ornithine decarboxylase 1;
XX ornithine decarboxylase 1 associated disorder;
XX hyperproliferative disorder; cancer; human; antisense oligonucleotide;
XX antisense technology; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone. All cytidines
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER

```

```

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX
XX US2004110148-A1.
XX
XX 10-JUN-2004.
XX
XX 10-DEC-2002; 2002US-00316244.
XX
XX 10-DEC-2002; 2002US-00316244.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie KW;
XX WPI; 2004-440337/41.
DR
XX New oligonucleotide compound that inhibits expression of ornithine
XX decarboxylase 1, useful for preparing a composition for treating
XX hyperproliferative disorder, e.g. cancer.
XX
XX Example 16; SEQ ID NO 136; 69pp; English.
XX
XX The invention describes a new compound, having a sequence comprising 8-80
XX bp targeted to a nucleic acid encoding ornithine decarboxylase 1,
XX specifically hybridises with the nucleic acid encoding ornithine
XX decarboxylase 1 comprising 2035-bp sequence and inhibits expression of
XX ornithine decarboxylase 1. Also described are: inhibiting the expression
XX of ornithine decarboxylase 1 in cells or tissues; screening for a
XX modulator of ornithine decarboxylase 1; identifying a disease state; a
XX kit or assay device comprising the compound; and treating an animal
XX having a disease or condition associated with ornithine decarboxylase 1.
XX The oligonucleotide compound is useful for preparing a composition for
XX treating hyperproliferative disorder, e.g. cancer. This sequence
XX represents an ornithine decarboxylase 1 antisense oligonucleotide.
XX
XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 61.7%; Score 14.8; DB 12; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAGTGCAAT 21
Db 20 CATGTTTCCAAGAGCAT 3

RESULT 12
AD004093/c
ID AD004093 standard; DNA; 49 BP.
XX
XX AD004093;
XX
XX 29-JUL-2004 (first entry)
XX
XX Identifier oligonucleotide.
XX
XX Bifunctional complex; ss.
XX
XX Synthetic.
XX
XX WO2004039825-A2.
XX
XX 13-MAY-2004.
XX
XX 30-OCT-2003; 2003WO-DK000739.
XX
XX 30-OCT-2002; 2002DK-00001652.
XX
XX 30-OCT-2002; 2002US-0422167P.
XX
XX 19-DEC-2002; 2002DK-00001955.

```

PR 19-DEC-2002; 2002US-0434425P.
PR 11-JUL-2003; 2003DK-00001064.
PR 11-JUL-2003; 2003US-0486199P.
XX (NUEV-) NUEVOLUTION AS.
XX
PI Freskgard P, Franch T, Gouliaev AH, Lundorf MD, Felding J;
PI Olsen EK, Holtmann A, Jakobsen SN, Sams C, Glad SS, Jensen KB;
PI Pedersen H;
XX
DR WPI; 2004-376154/35.
XX
PT Obtaining bifunctional complex with display molecule and coding part,
PT where bifunctional complex with priming site for adding tag is reacted at
PT reaction site with reactants and provided with tag identifying reactant
PT at priming site.
XX
PS Example 5; Page 125; 220pp; English.
XX
CC The present invention relates to a method (M1) for obtaining a
CC bifunctional complex. (M1) comprises a display molecule part and a coding
CC part, where a nascent bifunctional complex comprising a chemical reaction
CC site and a priming site for enzymatic addition of a tag is reacted at the
CC chemical reaction site with reactant(s), and provided with respective
CC tag(s) identifying the reactant(s) at the priming site using one or more
CC enzymes. The present sequence was used to illustrate the invention.
XX
SQ Sequence 49 BP; 16 A; 12 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 61.7%; Score 14.8; DB 12; Length 49;
Best Local Similarity 88.9%; Pred. No. 4.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTCATGTTCCAAAGTGC 19
|||||
DB 40 TTCATGTTCCAAAGTGC 23

RESULT 13
AAAX27821/c
ID AAAX27821 standard; DNA; 27 BP.
XX
AC AAAX27821;
XX
DT 02-JUN-1999 (first entry)
XX
DE CRCA-1 coding sequence fragment.
XX
KW CRCA-1; colorectal cancer associated transcript; marker; detection;
KW colorectal cancer cell; diagnosis; human; ss.
XX
OS Homo sapiens.
XX
PN WO9907726-A1.
XX
PD 18-FEB-1999.
XX
PF 07-AUG-1998; 98WO-US016440.
XX
PR 07-AUG-1997; 97US-00908643.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Waldman SA, Pearlman JM, Barber MT, Schulz S, Parkinson SJ;
XX
DR WPI; 1999-180474/15.
DR P-PSDB; AAY00966.
XX
CC CRCA-1 transcript, a specific marker for colorectal cancer cells - used
PT for in vitro diagnosis, staging and monitoring colorectal cancer and
PT assessing its metastasis.
XX
PS Disclosure; Page 115; 133pp; English.

XX This sequence is a fragment of the CRCA-1 (colorectal cancer associated)
CC transcript of the invention. The CRCA-1 transcript is a specific marker
CC for colorectal cancer cells and detecting it is used to identify/confirm
CC cells as colorectal cancer cells and to examine the extent of which they
CC have migrated, especially for diagnosis, staging and post-operative
CC monitoring, also for screening subjects at risk. The CRCA-1 DNA is used
CC to express the corresponding expression products and its fragments are
CC useful as oligonucleotide probes, primers and antisense agents
XX
SQ Sequence 27 BP; 6 A; 6 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 2; Length 27;
Best Local Similarity 81.0%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CATGTTTCCAAAGTGCATGAT 24
|||||
DB 26 CATATGTCCAAAGAGCAGGAT 6

RESULT 14
ADO41360
ID ADO41360 standard; DNA; 34 BP.
XX
AC ADO41360;
XX
DT 15-JUL-2004 (first entry)
XX
DE Oligo 3-2 used to diagnose Staphylococcus saprophyticus pathogen.
XX
KW Bacterial pathogen; diagnosis; meningitis; therapy; ss.
XX
OS Staphylococcus saprophyticus.
XX
PN US2004010129-A1.
XX
PD 15-JAN-2004.
XX
PF 28-OCT-2002; 2002US-00281845.
XX
PR 01-NOV-2001; 2001TW-00127119.
XX
PA (HSUP/) HSU P.
PA (CHIA/) CHIANG Y.
PA (HUAN/) HUANG H L.
PA (CHAO/) CHAO S Y.
XX
PI Hsu P, Chiang Y, Huang HL, Chao SY;
XX
DR WPI; 2004-224188/21.
XX
PT Nucleic acid kit for diagnosis of bacterial pathogens that cause
PT meningitis comprises nucleic acid sequences designed for 20 bacterial
PT pathogens e.g., Staphylococcus aureus, S.epidermidis, Streptococcus
PT saprophyticus, S.agalactiae.
XX
PS Claim 4; SEQ ID NO 10; 9pp; English.
XX
CC The present invention relates to a nucleic acid kit for bacterial pathogen
CC diagnosis and method for using the same which provides with a quick
CC diagnosis for 20 species of bacterial pathogens. The invention is useful
CC for diagnosis of bacterial meningitis pathogens or can be conjugated to a
CC substrate (e.g., biochips) and serve as probes. The present sequence is
CC an oligonucleotide used to diagnose Staphylococcus saprophyticus
CC pathogen. This sequence is used in the invention.
XX
SQ Sequence 34 BP; 10 A; 6 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 12; Length 34;
Best Local Similarity 81.0%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTGCATG 24
|||||
Db 13 CATGGTTCCTAAGTGAAAGAT 33

RESULT 15

AAL57225/c
ID AAL57225 standard; DNA; 41 BP.

XX AAL57225;

XX 04-DEC-2003 (first entry)

XX Oligonucleotide probe 2 related to human protein 46-53.

XX Human protein 46.53; cancer; HIV infection; probe; ss.

XX Homo sapiens.

XX CNL381487-A.

XX 27-NOV-2002.

XX 18-APR-2001; 2001CN-00112636.

XX 18-APR-2001; 2001CN-00112636.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2003-258240/26.

XX Polypeptide-human protein-46.53 containing bromo structure domain and polynucleotide for coding it.

XX Example 7; Page 23; Opp; Chinese.

XX This invention relates to the novel human protein 46.53, containing a bromo structure, and the cDNA sequence encoding it. The invention may be useful in the treatment of diseases such as cancer and HIV infection. The present sequence is that of oligonucleotide probe 2 related to the human 46.53 protein of the invention and used in example 7 of the specification

XX Sequence 41 BP; 17 A; 8 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 10; Length 41;

Best Local Similarity 81.0%; Pred. No. 5.2e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22

|||||
Db 37 TTCATGGTGCCAAATTCATG 17

RESULT 16

AAL57224/c

ID AAL57224 standard; DNA; 41 BP.

XX AAL57224;

XX 04-DEC-2003 (first entry)

XX Oligonucleotide probe 1 related to human protein 46-53.

XX Human protein 46.53; cancer; HIV infection; probe; ss.

XX Homo sapiens.

XX CNL381487-A.

XX 27-NOV-2002.

PF 18-APR-2001; 2001CN-00112636.
XX
PR 18-APR-2001; 2001CN-00112636.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;

XX WPI; 2003-258240/26.

XX Polypeptide-human protein-46.53 containing bromo structure domain and polynucleotide for coding it.

XX Example 7; Page 23; Opp; Chinese.

XX This invention relates to the novel human protein 46.53, containing a bromo structure, and the cDNA sequence encoding it. The invention may be useful in the treatment of diseases such as cancer and HIV infection. The present sequence is that of oligonucleotide probe 1 related to the human 46.53 protein of the invention and used in example 7 of the specification

XX Sequence 41 BP; 16 A; 8 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 10; Length 41;

Best Local Similarity 81.0%; Pred. No. 5.2e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22

|||||
Db 37 TTCATGGTGCCAAATTCATG 17

RESULT 17

ABX70212/c

ID ABX70212 standard; DNA; 30 BP.

XX ABX70212;

XX 07-MAY-2003 (first entry)

XX Novel Helicobacter pylori gene PCR primer #3183.

XX Protein-protein interaction; ulcer; selected interacting domain; SID; PCR; primer; ss.

XX Helicobacter pylori.

XX WO200266501-A2.

XX 29-AUG-2002.

XX 28-DEC-2001; 2001WO-EP015428.

XX 02-JAN-2001; 2001US-0259302P.

XX (HYBR-) HYBRIGENICS.

XX (INSP) INST PASTEUR.

XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;

XX WPI; 2002-674910/72.

XX New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing ulcers in mammals.

XX Example 9; Page 587; 642pp; English.

XX The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be

CC used for treating or preventing ulcers in a human or animal. This
 CC sequence represents a primer used to isolate polynucleotides encoding
 CC Helicobacter pylori proteins for studies on protein-protein interactions
 XX
 SQ Sequence 30 BP; 13 A; 6 C; 5 G; 3 T; 3 U; 0 Other;
 Query Match 60.0%; Score 14.4; DB 6; Length 30;
 Best Local Similarity 75.0%; Pred. No. 6.1e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 ||||| | | |||||
 Db 28 CTTTCATTCATTCTTAGTGCATGAT 5
 RESULT 18
 ADR23060/c
 ID ADR23060 standard; DNA; 30 BP.
 XX
 AC ADR23060;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE DNA/RNA primer 550 used to amplify H. pylori strain typing ORF DNA.
 XX
 KW strain typing; geographical origin; gastric ulcer; duodenal ulcer;
 KW inflammation; stomach cancer; gastric cancer; DNA/RNA hybrid; PCR;
 KW primer; ss.
 XX
 OS Helicobacter pylori.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 1..9
 FT /*tag= a
 FT /note= "RNA bases"
 XX
 FN FR2850667-A1.
 XX
 PD 06-AUG-2004.
 XX
 PF 30-JAN-2003; 2003FR-00001235.
 XX
 PR 30-JAN-2003; 2003FR-00001235.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Thiberge JM, Labigne A, Coppee JY, Lacroix C;
 XX
 PS WPI; 2004-563635/55.
 XX
 PS Disclosure; SEQ ID NO 550; 126pp; French.
 XX
 CC The invention relates to a novel method for preparing a set of DNA
 CC fragments or their expression products that allows typing of Helicobacter
 CC pylori strains. The method comprises preparing genomic DNA components
 CC from clinical isolates and strains of H. pylori that can be
 CC distinguished, particularly from their geographical origin or their
 CC particular associated pathology. Subsequently a set of non-ubiquitous
 CC open reading frames (ORFs) may be identified from amongst the ORFs
 CC present in the genome of a reference strain by comparison with the DNA
 CC prepared in the first stage and a composition may be prepared containing
 CC the identified ORFs, or fragments, their expression products or
 CC antibodies against these expression products. The method of the invention
 CC may be used to provide unequivocal differentiation between clinical
 CC isolates of H. pylori according to their geographical origin and
 CC particular pathologies. H. pylori infection is particularly associated
 CC with gastric and duodenal ulcers or inflammation, as well as cancer of
 CC the stomach or gastric system. The current sequence is that of a DNA/RNA
 CC hybrid PCR primer of the invention which was used to amplify H. pylori

CC ORF DNA for strain typing.
 XX
 SQ Sequence 30 BP; 13 A; 6 C; 5 G; 3 T; 3 U; 0 Other;
 Query Match 60.0%; Score 14.4; DB 13; Length 30;
 Best Local Similarity 75.0%; Pred. No. 6.1e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 ||||| | | |||||
 Db 28 CTTTCATTCATTCTTAGTGCATGAT 5
 RESULT 19
 AAL45772/c
 ID AAL45772 standard; DNA; 33 BP.
 XX
 AC AAL45772;
 XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Human acid phosphatase family protein 11 cDNA PCR primer #3.
 XX
 KW Human; acid phosphatase family protein 11; cancer; haemopathy;
 KW cytosstatic; haemostatic; virucide; immunomodulatory; antiinflammatory;
 KW immune disease; HIV infection; phlogosis; gene therapy; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200220579-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 19-JUN-2001; 2001WO-CN001011.
 XX
 PR 21-JUN-2000; 2000CN-00116667.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-329869/36.
 XX
 PT Homo acid phosphatase family protein 11 and encoding polynucleotide, used
 PT in diagnosis and treatment of malignant tumors, hemopathy, human
 PT immunodeficiency virus infection, immunological diseases and
 PT inflammation.
 XX
 PS Example 4; Page 13; 39pp; Chinese.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC acid phosphatase family protein 11. The sequences can be used in the
 CC treatment of cancer, haemopathy, HIV infection, immune diseases and
 CC phlogosis. The present sequence is a PCR primer for the coding sequence
 CC of the invention
 XX
 SQ Sequence 33 BP; 9 A; 8 C; 5 G; 11 T; 0 U; 0 Other;
 Query Match 60.0%; Score 14.4; DB 6; Length 33;
 Best Local Similarity 75.0%; Pred. No. 6.2e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 ||||| | | |||||
 Db 33 CTTAATGATGAGAAAGTGCATCAT 10
 RESULT 20
 ABT42676
 ID ABT42676 standard; DNA; 37 BP.
 XX
 AC ABT42676;
 XX

DT 17-SEP-2003 (first entry)

DE Human G-protein coupled receptor HGRBMY28 DNA SEQ ID 138.

XX Neuroprotective; antiinflammatory; immunosuppressive; cytostatic; neural;

KW nephrotropic; cardiac; human G-protein receptor; HGRBMY28; HGRBMY29;

KW HGRBMY29v1; HGRBMY29v2; HGRBMY28; HGRBMY29; immune disorder; pulmonary;

KW inflammatory; haematopoietic; gastrointestinal; small intestine; cancer;

KW proliferative; aberrant p27 regulation; FEN1; cell cycle; DNA repair;

KW apoptosis; spleen; lung; reproductive; oesophageal; metabolic;

KW endocrine; colon; cervix; lung; squamous cell; renal; cardiovascular;

KW placental; testis; heart; gene therapy; ds.

XX Homo sapiens.

OS WO200283856-A2.

FN 24-OCT-2002.

PD 11-APR-2002; 2002WO-US011525.

PF 11-APR-2001; 2001US-0283145P.

PR 11-APR-2001; 2001US-0283161P.

PR 03-MAY-2001; 2001US-0288468P.

PR 25-JUN-2001; 2001US-0300619P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

FA Bol D, Feder J, Mintier G, Ramanathan C, Hawken DR;

XX WPI; 2003-075538/07.

XX New G-protein coupled receptors, HGRBMY28 and HGRBMY29, and their

PT variants, useful for treating, preventing or ameliorating e.g.

PT hematopoietic, neural, pulmonary, gastrointestinal, inflammatory or

PT proliferative disorders.

XX Example 24; Page 386; 501pp; English.

PS This invention relates to an isolated nucleic acid molecule comprising a

CC polynucleotide encoding a human G-protein receptor, including HGRBMY28,

CC HGRBMY29, HGRBMY29v1 or HGRBMY29v2 polypeptides. The HGRBMY28 or

CC HGRBMY29 polypeptides and nucleic acids are useful for treating,

CC preventing or ameliorating a medical condition, e.g. an immune disorder,

CC an inflammatory disorder, an inflammatory disorder in which G-protein

CC coupled receptors are either directly or indirectly associated with the

CC disorder, a haematopoietic disorder, a neural disorder, a pulmonary

CC disorder, a gastrointestinal disorder, a disorder affecting the small

CC intestine, a proliferative disorder, a cancer, a disorder related to

CC aberrant p27 regulation, a disorder related to aberrant FEN1 regulation,

CC a disorder related to aberrant cell cycle regulation, a disorder related

CC to aberrant DNA repair regulation, a disorder related to aberrant

CC apoptosis regulation, a disorder of the spleen, a disorder of the lymph

CC nodes, a male or female reproductive disorder, an oesophageal disorder, a

CC metabolic disorder, an endocrine disorder, a proliferative disorder

CC afflicting the colon, cervix, lung, squamous cells or tissues, a renal

CC disorder, a cardiovascular disorder, a placental disorder, and a disorder

CC of the testes, heart or lymph nodes. The isolated polynucleotides of the

CC invention may be used to treat disorders by gene therapy. This

CC polynucleotide sequence represents the Human G-protein coupled receptor

CC HGRBMY28 DNA of the invention

XX

SQ Sequence 37 BP; 12 A; 9 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 8; Length 37;

Best Local Similarity 75.0%; Pred. No. 6.4e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTTGATGTTTCCAAAGTCATGAT 24

Db 13 CATAATGGTTCCAAACAGCAGGAT 36

RESULT 21

AAF87048

ID AAF87048 standard; DNA; 20 BP.

XX

XX AAF87048;

AC

DT 18-SEP-2001 (first entry)

XX

DE PCR primer for Mash1 gene.

XX

KW PCR primer; neuroectoderm cell; cell production; Parkinson's disease;

KW early primitive ectoderm-like cell; EPL cell; cell therapy;

KW transgenic animal; gene therapy; neuronal disease; Huntington's disease;

KW lysosomal storage disease; multiple sclerosis; memory disorder;

KW behavioural disorder; Alzheimer's disease; organ transplant;

KW spinal cord disorder; Mash1; ss.

XX

OS Unidentified.

XX WO200151611-A1.

FN 19-JUL-2001.

PD

XX 12-JAN-2001; 2001WO-AU000030.

PF

XX 14-JAN-2000; 2000AU-00005098.

PR 20-APR-2000; 2000AU-00007045.

PR 27-APR-2000; 2000AU-00007143.

XX (BRES-) BRESAGEN LTD.

PA

XX Rathjen PD, Rathjen J;

FI WPI; 2001-432908/46.

DR

XX Producing neuroectoderm cells for treatment of Parkinson's and

PT Alzheimer's and for transplantation comprises culturing early primitive

PT ectoderm-like cells in conditioned medium.

XX

PS Example 3; Page 41; 91pp; English.

XX This sequence represents a PCR primer for the Mash1 gene, used within the

CC scope of the invention. The invention relates to a method for producing

CC neuroectoderm cells (I) comprises: (a) providing a source of early

CC primitive ectoderm-like (EPL) cells and a neural-inducing conditioned

CC medium (CW) or extract of it; and (b) contacting the EPL cells with the

CC CM or extract for a time sufficient to generate controlled

CC differentiation to (I). The cells or partially differentiated progeny are

CC useful in human, or animal cell therapy, transgenic animal production,

CC human or animal gene therapy, the screening of pharmaceutical that induce

CC a biological response in neuroectoderm cells or their partially

CC differentiated progeny and evaluation of biological molecules that direct

CC differentiation of neural cells. The method is useful for producing or

CC neuroectoderm cells. It is also useful for producing differentiated or

CC partially differentiated cells from neural ectoderm cells. The method can

CC is also useful for maintaining neuroectoderm cells in vitro in

CC homogeneous cell populations. It can also be used for producing

CC genetically modified neuroectoderm cells. The cells can be used in the

CC treatment of neuronal diseases, including Parkinson's disease,

CC Huntington's disease, lysosomal storage diseases, multiple sclerosis,

CC memory and behavioural disorders, and Alzheimer's disease. The method can

CC also be used for preparation of tissue or organs for transplant. Neural

CC crest cells produced by the method are useful for the treatment of spinal

CC cord disorders and Schwann cells produced by the method are used for the

CC treatment of multiple sclerosis

XX

SQ Sequence 20 BP; 4 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 4; Length 20;

Best Local Similarity 84.2%; Pred. No. 7.2e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTCAT 21

```
Db      1  ||| ||| ||| ||| ||| ||| ||| |||
          TCCTGCTTCCAAAGTCCAT 19

RESULT 22
ADL59164
ID      ADL59164 standard; DNA; 20 BP.
XX
XX      ADL59164;
XX
XX      03-JUN-2004 (first entry)
XX
DE      Human ESM-1 antisense oligonucleotide seqid 1413.
XX
KW      cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW      gene therapy; endothelial specific molecule-1; ESM-1;
KW      ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW      angiogenic disorder; immunological disorder; cardiovascular disorder;
KW      neurological disorder; antisense technology; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..20
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "OTHER= phosphorothioate backbone. All cytidine
FT      residues are 5-methylcytidines"
FT      modified_base 1..5
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT      modified_base 16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX      WO2004021978-A2.
XX
XX      18-MAR-2004.
XX
XX      19-AUG-2003; 2003WO-US025833.
XX
XX      19-AUG-2002; 2002US-040495P.
XX
XX      (PHAA ) PHARMACIA CORP.
XX
XX      Weinstein EJ, Griggs DW;
XX
XX      WPI; 2004-248358/23.
XX
XX      New antisense compound, having a sequence targeted to a nucleic acid
XX      encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
XX      disorder.
XX
XX      Claim 3; SEQ ID NO 1413; 555pp; English.
XX
XX      The invention describes a new antisense compound, having a sequence
XX      comprising 8-30 bp targeted to a nucleic acid encoding endothelial
XX      specific molecule-1 (ESM-1), that specifically hybridises with the
XX      nucleic acid ESM-1 and inhibits its expression. Also described are: a
XX      composition; inhibiting the expression of ESM-1 in cells or tissues; and
XX      treating an animal having a disease or condition associated with ESM-1.
XX      The compound is useful for preparing a composition for treating diabetes,
XX      cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
XX      cardiovascular or neurological disorder. This sequence represents an
XX      antisense oligonucleotide that can be used to modulate expression of
XX      endothelial specific molecule-1 (ESM-1).
XX
XX      Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
XX
XX      Query Match      59.2%; Score 14.2; DB 12; Length 20;
```

```
Best Local Similarity 84.2%; Pred. NO. 7.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CTTTCATGTTTCCAAAGTGC 19
          ||| ||| ||| ||| ||| ||| ||| |||
Db      2  CTTTCATGTTTCCCAAGCTGC 20

RESULT 23
ADL58982
ID      ADL58982 standard; DNA; 20 BP.
XX
XX      ADL58982;
XX
XX      03-JUN-2004 (first entry)
XX
DE      Human ESM-1 antisense oligonucleotide seqid 1231.
XX
KW      cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
KW      gene therapy; endothelial specific molecule-1; ESM-1;
KW      ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW      angiogenic disorder; immunological disorder; cardiovascular disorder;
KW      neurological disorder; antisense technology; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..20
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "OTHER= phosphorothioate backbone. All cytidine
FT      residues are 5-methylcytidines"
FT      modified_base 1..5
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT      modified_base 16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX      WO2004021978-A2.
XX
XX      18-MAR-2004.
XX
XX      19-AUG-2003; 2003WO-US025833.
XX
XX      19-AUG-2002; 2002US-040495P.
XX
XX      (PHAA ) PHARMACIA CORP.
XX
XX      Weinstein EJ, Griggs DW;
XX
XX      WPI; 2004-248358/23.
XX
XX      New antisense compound, having a sequence targeted to a nucleic acid
XX      encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
XX      disorder.
XX
XX      Claim 3; SEQ ID NO 1231; 555pp; English.
XX
XX      The invention describes a new antisense compound, having a sequence
XX      comprising 8-30 bp targeted to a nucleic acid encoding endothelial
XX      specific molecule-1 (ESM-1), that specifically hybridises with the
XX      nucleic acid ESM-1 and inhibits its expression. Also described are: a
XX      composition; inhibiting the expression of ESM-1 in cells or tissues; and
XX      treating an animal having a disease or condition associated with ESM-1.
XX      The compound is useful for preparing a composition for treating diabetes,
XX      cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
XX      cardiovascular or neurological disorder. This sequence represents an
XX      antisense oligonucleotide that can be used to modulate expression of
XX      endothelial specific molecule-1 (ESM-1).
```

```
XX SQ Sequence 20 BP; 2 A; 8 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGC 19
|||||
Db 1 CTTTCATGTTTCCCAAGTGC 19

RESULT 24
ABV74729
ID ABV74729 standard; DNA; 33 BP.
XX AC ABV74729;
XX DT 03-FEB-2003 (first entry)
XX DE Human clathrin light chain 13.64 PCR primer #4.
XX KW Human; clathrin light chain 13.64; tumour; haemopathy; HIV infection;
XX KW immunological disease; inflammation; cytostatic; anti-HIV; PCR; primer;
XX KW ss.
XX OS Homo sapiens.
XX PN CN1352131-A.
XX PD 05-JUN-2002.
XX PF 06-NOV-2000; 2000CN-00127271.
XX PR 06-NOV-2000; 2000CN-00127271.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-644460/70.
XX DE New human clathrin light chain 13.64 polypeptide for treating malignant
XX PT tumors, hemopathy, human immunodeficiency virus infection, immunological
XX PT diseases and various inflammations.
XX PS Example 4; Page 18 (Disclosure); 34pp; Chinese.
XX CC The present invention relates to human clathrin light chain 13.64 (see
XX CC AB98794). The protein and its coding sequence can be used for treating
XX CC various diseases, such as malignant tumours, haemopathy, HIV infection,
XX CC immunological diseases and various inflammations. The present sequence is
XX CC a PCR primer, which was used in an example from the invention
XX SQ Sequence 33 BP; 6 A; 12 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 6; Length 33;
Best Local Similarity 84.2%; Pred. No. 7.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGC 19
|||||
Db 14 CCTGATGTTTCCCAATTGC 32

RESULT 25
ABZ04574
ID ABZ04574 standard; DNA; 50 BP.
XX AC ABZ04574;
XX DT 09-JAN-2003 (first entry)
XX OS Homo sapiens.
```

```
DE DE Human leukocyte gene expression profiling probe SEQ ID NO 4565.
XX KW T7; leukocyte; gene expression profiling; allograft rejection;
XX KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX KW ss.
XX OS Homo sapiens.
XX PN WO200257414-A2.
XX PD 25-JUL-2002.
XX PF 22-OCT-2001; 2001WO-US047856.
XX PR 20-OCT-2000; 2000US-0241994P.
XX PR 08-JUN-2001; 2001US-0296764P.
XX PA (BIOC-) BIOCARDIA INC.
XX PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX PI Ly N, Woodward R, Quertermous T, Johnson F;
XX WPI; 2002-636525/68.
XX DE New system for leukocyte expression profiling, diagnosing a disease, or
XX PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX PS Claim 1; Page 473; Opp; English.
XX CC The invention relates to a system for detecting gene expression, which
XX CC comprises one or two isolated DNA molecules that detect expression of a
XX CC gene, where the gene corresponds to any of 8143 oligonucleotides
XX CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX CC for leukocyte expression profiling. It is particularly useful for
XX CC diagnosing a disease, monitoring (rate of) progression of a disease,
XX CC predicting therapeutic outcome, determining prognosis for a patient,
XX CC predicting disease complications in an individual or monitoring response
XX CC to treatment in an individual. The diseases include cardiac allograft
XX CC rejection, kidney allograft rejection, liver allograft rejection,
XX CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX SQ Sequence 50 BP; 16 A; 12 C; 12 G; 10 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 6; Length 50;
Best Local Similarity 84.2%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGC 19
|||||
Db 10 CTTTCATGTTTCCCAAGTGC 28

RESULT 26
ADG33666
ID ADG33666 standard; DNA; 50 BP.
XX AC ADG33666;
XX DT 26-FEB-2004 (first entry)
XX DE Human DNA probe used to monitor expression of diagnostic genes SeqID990.
XX KW human; ss; autoimmune; chronic inflammatory disease; SLE;
XX KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
XX KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
XX KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;
XX KW diverticulitis; primary biliary sclerosis; probe.
XX OS Homo sapiens.
```



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PN WO2003090694-A2.
XX
PD 06-NOV-2003.
XX
PF 24-APR-2003; 2003WO-US013015.
XX
PR 24-APR-2002; 2002US-00131827.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgenuth J, Fry K, Woodward R, Ly N;
XX WPI; 2003-877243/81.
DR
XX
PT Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT colitis, psoriasis and asthma by detecting the expression level of one or
PT more genes.
XX
PS Claim 1; SEQ ID NO 990; 877pp; English.
XX
CC This invention relates to novel methods for diagnosing and monitoring
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC the identification of genes that have a clinical utility as diagnostic
CC tools for the management of, in particular, patients with systemic lupus
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC present invention describes a method for determining the levels of
CC multiple differentially expressed genes of a patient, in a concerted
CC manner, in order to achieve an improved diagnostic assay with sensitivity
CC and specificity for the disease in question. As such, these genes are
CC useful for the diagnosis of various other inflammatory disorders
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC This oligonucleotide is a human DNA probe used to monitor the expression
CC level of the differentially expressed diagnostic genes of the invention.
XX
SQ Sequence 50 BP; 16 A; 12 C; 12 G; 10 T; 0 U; 0 Other;

Query Match          59.2%; Score 14.2; DB 10; Length 50;
Best Local Similarity 84.2%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTTTCATGTTTCCCAAGTGC 19
    ||||| || |||||
Db 10 CTTTCATCTTCCCAAGTGC 28

RESULT 27
ADP10108
ID ADP10108 standard; DNA; 50 BP.
XX
XX ADP10108;
XX
XX 12-AUG-2004 (first entry)
XX
XX 50-mer oligonucleotide marker probe of the invention #117.
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO2004042346-A2.
XX
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
XX
XX 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

Query Match          59.2%; Score 14.2; DB 12; Length 50;
Best Local Similarity 84.2%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTTTCATGTTTCCCAAGTGC 19
    ||||| || |||||
Db 10 CTTTCATCTTCCCAAGTGC 28

RESULT 28
ACK15268
ID ACK15268 standard; DNA; 25 BP.
XX
XX ACK15268;
XX
XX 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 115249.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX OS
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (APFY-) AFFYMETRIX INC.
XX
XX Mittmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.

```

PS Claim 1; SEQ ID NO 115249; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 5 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAA 14
| | | | | | | | | |
Db 1 CTTTCATGTTTCCAA 14

RESULT 29

ID ABX95855/c
AC ABX95855 standard; DNA; 27 BP.

AC ABX95855;

DT 01-AUG-2003 (first entry)

XX PCR primer J for detecting DNA derived from cotton event 757.

XX Lepidoptera resistant cotton; transgenic plant; cotton; PV-GHBRK04;
KW cotton event 757 recombinant; progeny; transgene; transgenic; PCR;
KW primer; ss.

XX Gossypium hirsutum.
OS Synthetic.

OS US2003024005-A1.

PN 30-JAN-2003.

FD 16-NOV-2001; 2001US-00990659.

PF 17-NOV-2000; 2000US-0249757P.

XX (HILL/) HILLYARD J R.
FA (ROBE/) ROBERTS J K.
PA (YEMM/) YE M.

XX Hillyard JR, Roberts JK, Ye M;
PI WPI; 2003-456316/43.

DR New cotton plant event PV-GHBRK04 (757) nucleic acid sequences, useful for
XX detecting DNA from the cotton plant event 757 in a sample for determining
PT whether the progeny of a sexual cross contain a transgene of interest.

XX Claim 3; Page 16; 32pp; English.

XX The present invention relates to a Lepidoptera resistant transgenic cotton (Gossypium hirsutum) plant referred to as PV-GHBRK04 or cotton event 757. The invention provides polynucleotide sequences contained within cotton event 757 and methods for detecting DNA from the cotton plant event 757 in a sample. The methods are useful for determining whether the progeny of a sexual cross contain a transgene of interest. The present sequence represents a PCR primer that may be used to detect DNA derived from the cotton event 757 in a sample

XX Sequence 27 BP; 11 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 10; Length 27;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
| | | | | | | | | | | | | | | |
Db 23 TTCTTCTTTCGTAAGTGCATCA 2

RESULT 30

ID ADH27316
AC ADH27316 standard; DNA; 28 BP.

AC ADH27316;

DT 11-MAR-2004 (first entry)

XX Ferritin related oligonucleotide Bin#5 structure 3.

DE detection; conserved structure; RNA structural element; fitness; ss.
XX Synthetic.

XX WO2003104478-A2.

PN 18-DEC-2003.

PD 10-JUN-2003; 2003WO-US018573.

PF 10-JUN-2002; 2002US-0387342P.

XX (ISIS-) ISIS PHARM INC.

XX Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VW;
PI WPI; 2004-062371/06.

DR Detecting a conserved structures in an RNA sequence by generating an
XX offspring group from the parent group and selecting at least one group
PT from the parent and offspring groups with the highest fitness.

XX Example 1; Fig 13; 52pp; English.

XX The present invention describes a method for detecting a conserved structure in an RNA sequence. The method comprises: (a) placing 2 structures from structures generated for 2 RNA sequences from 2 organisms into a parent group; (b) generating an offspring group from the parent group; (c) determining fitness of the parent and offspring groups; (d) comparing the fitness of the parent and offspring groups; and (e) selecting at least one group from the parent and offspring groups with the highest fitness, where the conserved structure in the RNA is present within the at least one group. The method is useful for detecting a conserved structure in an RNA sequence. The present sequence is used in the exemplification of the present invention.

XX Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 12; Length 28;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;

```
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 TTCATGTTTCCAAAGTGCATGA 23
Db 1 TTCTGCTTCAACAGTGTCTGA 22

RESULT 31
ADH27295
ID ADH27295 standard; DNA; 28 BP.
XX
AC ADH27295;
XX
DT 11-MAR-2004 (first entry)
XX
DE Ferritin related oligonucleotide Bin#2 structure 3.
XX
KW detection; conserved structure; RNA structural element; fitness; ss.
XX
OS Synthetic.
XX
PN WO2003104478-A2.
XX
PD 18-DEC-2003.
XX
PF 10-JUN-2003; 2003WO-US018573.
XX
PR 10-JUN-2002; 2002US-0387342P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VW;
DR WPI; 2004-062371/06.
XX
PT Detecting a conserved structures in an RNA sequence by generating an
offspring group from the parent group and selecting at least one group
from the parent and offspring groups with the highest fitness.
XX
PS Example 1; Fig 13; 52pp; English.
XX
CC The present invention describes a method for detecting a conserved
structure in an RNA sequence. The method comprises: (a) placing 2
structures from structures generated for 2 RNA sequences from 2 organisms
into a parent group; (b) generating an offspring group from the parent
group; (c) determining fitness of the parent and offspring groups; (d)
comparing the fitness of the parent and offspring groups; and (e)
selecting at least one group from the parent and offspring groups with
the highest fitness, where the conserved structure in the RNA is present
within the at least one group. The method is useful for detecting a
conserved structure in an RNA sequence. The present sequence is used in
the exemplification of the present invention.
XX
SQ Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 12; Length 28;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
Db 1 TTCTGCTTCAACAGTGTCTGA 22

RESULT 32
ADH27302
ID ADH27302 standard; DNA; 28 BP.
XX
AC ADH27302;
XX
DT 11-MAR-2004 (first entry)
XX
DE Ferritin related oligonucleotide Bin#3 structure 3.
XX
KW detection; conserved structure; RNA structural element; fitness; ss.
XX
OS Synthetic.
XX
PN WO2003104478-A2.
XX
PD 18-DEC-2003.
XX
PF 10-JUN-2003; 2003WO-US018573.
XX
PR 10-JUN-2002; 2002US-0387342P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VW;
```

```
XX
KW detection; conserved structure; RNA structural element; fitness; ss.
XX
OS Synthetic.
XX
PN WO2003104478-A2.
XX
PD 18-DEC-2003.
XX
PF 10-JUN-2003; 2003WO-US018573.
XX
PR 10-JUN-2002; 2002US-0387342P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VW;
DR WPI; 2004-062371/06.
XX
PT Detecting a conserved structures in an RNA sequence by generating an
offspring group from the parent group and selecting at least one group
from the parent and offspring groups with the highest fitness.
XX
PS Example 1; Fig 13; 52pp; English.
XX
CC The present invention describes a method for detecting a conserved
structure in an RNA sequence. The method comprises: (a) placing 2
structures from structures generated for 2 RNA sequences from 2 organisms
into a parent group; (b) generating an offspring group from the parent
group; (c) determining fitness of the parent and offspring groups; (d)
comparing the fitness of the parent and offspring groups; and (e)
selecting at least one group from the parent and offspring groups with
the highest fitness, where the conserved structure in the RNA is present
within the at least one group. The method is useful for detecting a
conserved structure in an RNA sequence. The present sequence is used in
the exemplification of the present invention.
XX
SQ Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 12; Length 28;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
Db 1 TTCTGCTTCAACAGTGTCTGA 22

RESULT 33
ADH27288
ID ADH27288 standard; DNA; 28 BP.
XX
AC ADH27288;
XX
DT 11-MAR-2004 (first entry)
XX
DE Ferritin related oligonucleotide Bin#1 structure 3.
XX
KW detection; conserved structure; RNA structural element; fitness; ss.
XX
OS Synthetic.
XX
PN WO2003104478-A2.
XX
PD 18-DEC-2003.
XX
PF 10-JUN-2003; 2003WO-US018573.
XX
PR 10-JUN-2002; 2002US-0387342P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VW;
```

XX WPI; 2004-062371/06.
DR
XX Detecting a conserved structures in an RNA sequence by generating an
PT offspring group from the parent group and selecting at least one group
PT from the parent and offspring groups with the highest fitness.
XX
XX Example 1; Fig 13; 52pp; English.
XX
XX The present invention describes a method for detecting a conserved
CC structure in an RNA sequence. The method comprises: (a) placing 2
CC structures from structures generated for 2 RNA sequences from 2 organisms
CC into a parent group; (b) generating an offspring group from the parent
CC group; (c) determining fitness of the parent and offspring groups; (d)
CC comparing the fitness of the parent and offspring groups; and (e)
CC selecting at least one group from the parent and offspring groups with
CC the highest fitness, where the conserved structure in the RNA is present
CC within the at least one group. The method is useful for detecting a
CC conserved structure in an RNA sequence. The present sequence is used in
CC the exemplification of the present invention.
XX
XX Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
SQ

Query Match 58.3%; Score 14; DB 12; Length 28;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
||| ||| ||| ||| ||| |||
Db 1 TTCCTGCTTCAACAGTGTCTGA 22

RESULT 34
ADH27309
ID ADH27309 standard; DNA; 29 BP.
XX
AC ADH27309;
XX
DT 11-MAR-2004 (first entry)
XX
DE Ferritin related oligonucleotide Bin#4 structure 3.
XX
KW detection; conserved structure; RNA structural element; fitness; ss.
XX
OS Synthetic.
XX
FN WO2003104478-A2.
XX
PD 18-DEC-2003.
XX
PF 10-JUN-2003; 2003WO-US018573.
XX
PR 10-JUN-2002; 2002US-0387342P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Sampath R, Becker DJ, Griffey RH, Fogel GB, Porto VW;
XX
DR WPI; 2004-062371/06.
XX
PT Detecting a conserved structures in an RNA sequence by generating an
PT offspring group from the parent group and selecting at least one group
PT from the parent and offspring groups with the highest fitness.
XX
XX Example 1; Fig 13; 52pp; English.
XX
XX The present invention describes a method for detecting a conserved
CC structure in an RNA sequence. The method comprises: (a) placing 2
CC structures from structures generated for 2 RNA sequences from 2 organisms
CC into a parent group; (b) generating an offspring group from the parent
CC group; (c) determining fitness of the parent and offspring groups; (d)
CC comparing the fitness of the parent and offspring groups; and (e)
CC selecting at least one group from the parent and offspring groups with

CC the highest fitness, where the conserved structure in the RNA is present
CC within the at least one group. The method is useful for detecting a
CC conserved structure in an RNA sequence. The present sequence is used in
CC the exemplification of the present invention.
XX
XX Sequence 29 BP; 7 A; 7 C; 6 G; 9 T; 0 U; 0 Other;
SQ

Query Match 58.3%; Score 14; DB 12; Length 29;
Best Local Similarity 77.3%; Pred. No. 9.5e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
||| ||| ||| ||| ||| |||
Db 2 TTCCTGCTTCAACAGTGTCTGA 23

RESULT 35
ADR33465/c
ID ADR33465 standard; DNA; 32 BP.
XX
AC ADR33465;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent target DNA #1006.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
FN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX
DR WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 1; Page 87; 238pp; English.
XX
XX The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species.
CC subpecies, and especially strains or individuals of the subpecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for

CC bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.

XX
 SQ Sequence 32 BP; 10 A; 8 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 58.3%; Score 14; DB 13; Length 32;
 Best Local Similarity 77.3%; Pred. No. 9.6e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATGAT 24

Db 29 TCATTTTCCATAGACATGGT 8

RESULT 36

ABK11366

ID ABK11366 standard; DNA; 33 BP.

AC ABK11366;

DT 05-JUN-2002 (first entry)

DE NADH dehydrogenase 51Kd subunit 10 PCR primer #1.

XX ss; PCR; NADH dehydrogenase 51Kd subunit 10; malignant tumour;
 KW haemopathy; human immunodeficiency virus infection; HIV; primer;
 KW immunological disease; inflammation; cytostatic; haemostatic; virucide;
 KW immunomodulatory; anti-inflammatory; metabolic disturbance.

XX Unidentified.

XX WO200202618-A1.

XX 10-JAN-2002.

XX 18-JUN-2001; 2001WO-CN000991.

XX 19-JUN-2000; 2000CN-00116593.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-090538/12.

XX NADH-dehydrogenase 51 and encoded polynucleotide, used in diagnosis and
 PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
 PT infection, immunological diseases and inflammation.

PS Example 5; Page 13; 35pp; Chinese.

XX The invention relates to an isolated polypeptide of NADH-dehydrogenase 51
 CC Kd subunit 10, the cDNA encoding it, and its fragment, analogue or
 CC derivative. Also included are vectors expressing the protein, a host cell
 CC comprising the vector, the isolation of modulators of the protein and an
 CC anti-NADH-dehydrogenase 51 antibody. The protein and nucleic acid are
 CC used in diagnosis and treatment of a malignant tumour, haemopathy, human
 CC immunodeficiency virus (HIV) infection, immunological diseases, various
 CC inflammations, metabolic disturbance of carbohydrate, lipid and protein.
 CC The present sequence is a PCR primer used to clone the cDNA encoding the
 CC NADH- dehydrogenase 51Kd subunit 10

XX Sequence 33 BP; 8 A; 8 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 33;

Best Local Similarity 77.3%; Pred. No. 9.7e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATGAT 24

Db 8 TGATGTTTCCCATATACATGAT 29

RESULT 37

AAV27468

ID AAV27468 standard; DNA; 36 BP.

AC AAV27468;

DT 02-OCT-1998 (first entry)

DE Streptococcus pneumoniae ORF cloning primer SEQ ID NO:258.

XX Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
 KW detection; pneumonia; otitis media; meningitis; cloning primer; ss.

XX Synthetic.

OS Streptococcus pneumoniae.

XX WO9818930-A2.

XX 07-MAY-1998.

XX 30-OCT-1997; 97WO-US019422.

XX 31-OCT-1996; 96US-0029960P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kunsch CA, Choi GH, Johnson LS, Hromockyj A;

XX WPI; 1998-272224/24.

XX Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae
 PT - or their epitope-containing fragments, useful in protective or
 PT therapeutic vaccines, and for diagnosis.

XX Example 1; Page 106; 118pp; English.

XX The present sequence represents a cloning primer used in an example from
 CC the present invention which describes proteins from Streptococcus
 CC pneumoniae. Nucleic acid sequence encoding Streptococcus pneumoniae
 CC proteins can be useful in vaccines for inducing protective antibodies
 CC against Streptococcus pneumoniae, for treatment or prevention of
 CC infection e.g. pneumonia, otitis media or meningitis. Probes based on the
 CC nucleic acids are used to detect Streptococcus infection (by usual
 CC hybridisation or amplification methods), also for isolating Streptococcus
 CC genes or their allelic variants. The proteins can be used similarly to
 CC detect specific antibodies in standard immunoassays, especially for
 CC diagnosing or monitoring infections. Antibodies which bind the proteins
 CC are used to detect corresponding antigens, to purify the proteins and for
 CC passive immunisation (optionally coupled to a toxin). Vaccines are
 CC administered, e.g. by injection, orally or through the skin, typically at
 CC 0.01-1000 (especially 10-300) mu g/ml per dose. The cloning primers used
 CC in the present invention are given in AAV27437 to AAV27562 and AAV39870
 CC to AAV39869

XX SQ Sequence 36 BP; 11 A; 10 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 2; Length 36;

Best Local Similarity 77.3%; Pred. No. 9.8e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATGAT 24

Db 3 TCAGCTTCCAAACTGGTGTAT 24

RESULT 38

AAA70860

ID AAA70860 standard; DNA; 36 BP.

XX

```

AC AAA70860;
XX
XX 27-APR-2001 (first entry)
XX
XX Molecular interaction site DNA #13.
XX
XX Modulator; identification; molecular interaction; virtual library; ss.
XX
XX Xenopus sp.
XX
XX WO9958947-A2.
XX
XX 18-NOV-1999.
XX
XX 12-MAY-1999; 99WO-US010361.
XX
XX 12-MAY-1998; 98US-00076404.
XX
XX 12-MAY-1998; 98US-0085092P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX
XX Example 2; Fig 63; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX with members of the virtual library of compounds to generate a hierarchy
XX of the compounds ranked in accordance with their respective ability to
XX form physical interactions with the molecular interaction site. The
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX nucleotides but not more than 70 nucleotides and having secondary
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX internal loop region; (c) 4 nucleotides forming a first side of a second
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; (f) 4
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAAUACUUGUACAGAAAAUC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX or industrial compounds
XX
XX Sequence 36 BP; 7 A; 11 C; 9 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 58.3%; Score 14; DB 3; Length 36;
XX Best Local Similarity 77.3%; Pred. No. 9.8e+03;
XX Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX Qy 2 TTCATGTTTCCAAAGTGCATGA 23
XX ||| ||| ||| ||| ||| |||
XX Db 3 TTCCTGCTTCAACAGTGTCTGA 24
XX
XX RESULT 39
XX AAA70869
XX ID AAA70869 standard; RNA; 36 BP.
XX
XX AC AAA70869;

```

```

XX
XX 27-APR-2001 (first entry)
XX
XX Molecular interaction site RNA #55.
XX
XX Modulator; identification; molecular interaction; virtual library; ss.
XX
XX Xenopus sp.
XX
XX WO9958947-A2.
XX
XX 18-NOV-1999.
XX
XX 12-MAY-1999; 99WO-US010361.
XX
XX 12-MAY-1998; 98US-00076404.
XX
XX 12-MAY-1998; 98US-0085092P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX
XX Example 2; Fig 66; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX with members of the virtual library of compounds to generate a hierarchy
XX of the compounds ranked in accordance with their respective ability to
XX form physical interactions with the molecular interaction site. The
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX nucleotides but not more than 70 nucleotides and having secondary
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX internal loop region; (c) 4 nucleotides forming a first side of a second
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; (f) 4
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAAUACUUGUACAGAAAAUC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX or industrial compounds
XX
XX Sequence 36 BP; 7 A; 11 C; 9 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 58.3%; Score 14; DB 3; Length 36;
XX Best Local Similarity 45.5%; Pred. No. 9.8e+03;
XX Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
XX
XX Qy 2 TTCATGTTTCCAAAGTGCATGA 23
XX ::| ::| ::| ::| ::| ::|
XX Db 3 UUCUCGCUCAACACAGUCUUGA 24
XX
XX RESULT 40
XX ABQ84936
XX ID ABQ84936 standard; DNA; 36 BP.
XX
XX AC ABQ84936;
XX

```

DT 04-SEP-2002 (first entry)
 XX Streptococcus pneumoniae ORF cloning primer SEQ ID NO:258.
 DE
 XX
 KW Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
 KW antibacterial; Streptococcal infection; detection; primer; ss.
 XX
 OS Streptococcus pneumoniae.
 OS Synthetic.
 XX
 XX US2002061545-A1.
 FN
 XX 23-MAY-2002.
 PD
 XX
 XX 22-JAN-2001; 2001US-00765272.
 PF
 XX
 XX 30-OCT-1997; 97US-00961083.
 PR
 XX (CHOI/) CHOI G H.
 PA (KUNS/) KUNSCH C A.
 PA (BARA/) BARASH S C.
 PA (DILL/) DILLON P J.
 PA (DOUG/) DOUGHERTY B.
 PA (FANN/) FANNON M R.
 PA (ROSE/) ROSEN C A.
 XX
 PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR,
 PI Rosen CA;
 XX
 XX WPI; 2002-479261/51.
 DR
 XX
 XX New Streptococcus pneumoniae antigens, useful for detecting Streptococcus
 PT and for preventing or attenuating disease caused by Streptococcus
 PT infection.
 XX
 XX Example 1; Page 62; 70pp; English.
 PS
 XX ABO84792 to ABO84904 represents nucleic acids which encode the
 CC Streptococcus pneumoniae antigens given in ABO84557 to ABO84669. The S.
 CC pneumoniae antigens have antibacterial activity and can be used in
 CC vaccines. The S. pneumoniae antigens can also be used to prevent or
 CC attenuate a Streptococcal infection in an animal. The polynucleotides
 CC encoding the S. pneumoniae antigens can be used to detect Streptococcus
 CC nucleic acids. ABO84905 to ABO85130 represent primers used in the cloning
 CC of S. pneumoniae ORFs (open reading frames) which are used in an example
 CC from the present invention
 XX
 SQ Sequence 36 BP; 11 A; 10 C; 6 G; 9 T; 0 U; 0 Other;
 Query Match 58.3%; Score 14; DB 6; Length 36;
 Best Local Similarity 77.3%; Pred. No. 9.8e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 TCATGTTTCCAAAGTCATGAT 24
 ||| ||||| |||||
 Db 3 TCAAGCTTCCAACTGTTGAT 24
 ||| ||||| |||||

Search completed: November 18, 2005, 11:52:25
 Job time : 168.262 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1147.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-4

Perfect score: 24

Sequence: 1 CTTTCATGTTTCCAAAGTCATGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.6	65.0	44	8	BH810239
2	14.2	59.2	42	1	AV845171
3	14.2	59.2	47	9	AL974349
4	14	58.3	43	1	AA423162
5	14	58.3	48	1	AA930873
6	14	58.3	48	1	AI172854
7	14	58.3	48	1	AA386692
8	13.6	56.7	40	8	AZ651473
9	13.4	55.8	26	8	AZ637079
10	13.4	55.8	27	9	TA46H06P
11	13.4	55.8	42	7	T73611
12	13.2	55.0	31	8	AZ307496
13	13.2	55.0	33	1	AU014420
14	13.2	55.0	35	9	CU213211
15	13.2	55.0	41	9	AL753405
16	13.2	55.0	41	9	BX891114
17	13.2	55.0	45	9	CC888123
18	13	54.2	29	8	BZ762504
19	13	54.2	37	2	BE548888
20	13	54.2	40	9	BX572262
21	13	54.2	43	2	BE788148
22	13	54.2	43	8	BH790838
23	13	54.2	44	4	BJ076538
24	12.8	53.3	28	7	W11835

25	12.8	53.3	36	8	AZ794096
26	12.8	53.3	36	9	CC796901
27	12.8	53.3	43	1	AA955598
28	12.8	53.3	46	8	CC049873
29	12.6	52.5	26	8	BZ290816
30	12.6	52.5	31	8	BZ661378
31	12.6	52.5	32	9	CG712334
32	12.6	52.5	37	8	BH850177
33	12.6	52.5	38	5	BW593923
34	12.6	52.5	40	7	H95706
35	12.6	52.5	41	9	TA202B01Q
36	12.6	52.5	43	1	AI280742
37	12.6	52.5	43	8	BZ766776
38	12.4	51.7	37	8	AZ388487
39	12.4	51.7	41	8	BH866468
40	12.4	51.7	42	9	TA232A04Q
41	12.4	51.7	47	8	AZ830439
42	12.4	51.7	47	8	BZ584043
43	12.2	50.8	25	8	AZ826147
44	12.2	50.8	33	8	AZ762777
45	12.2	50.8	33	8	BH911010

ALIGNMENTS

RESULT 1
BH810239
LOCUS
DEFINITION
SALK_048259 Arabidopsis thaliana DNA linear GSS 02-MAY-2002
thaliana genomic clone SALK_048259, genomic survey sequence.

ACCESSION
BH810239

VERSION
BH810239.1 GI:20388057

KEYWORDS
GSS.

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana

REFERENCE
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmermann,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

TITLE
Arabidopsis thaliana (thale cress)

JOURNAL
COMMENT

FEATURES
source
Class: TDNA tagged.
Location/Qualifiers
1..44
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_048259"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 65.0%; Score 15.6; DB 8; Length 44;

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 58.3%; Score 14; DB 1; Length 43;
Best Local Similarity 77.3%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTTTCATGTTTCCAAAGTGCGATG 22
||||| ||||| ||||| |||||
Db 37 CTTCCATGTCCTCCATGTCGATG 16

RESULT 5
AA930873/c

LOCUS AA930873 48 bp mRNA linear EST 23-APR-1998
DEFINITION v271e07.s1 Soares mammary gland NbMMG Mus musculus cDNA clone
IMAGE:1331940 3' similar to gb:M90696 CATHEPSIN S PRECURSOR
(HUMAN); mRNA sequence.

ACCESSION AA930873
VERSION AA930873.1 GI:3080261
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 48)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:691484

Trace considered overall poor quality

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1..48
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1331940"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NbMMG"

/note="Organ: mammary gland; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

ORIGIN

Query Match 58.3%; Score 14; DB 1; Length 48;
Best Local Similarity 77.3%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TCATGTTTCCAAAGTGCGATGAT 24
||||| ||||| ||||| |||||
Db 34 TCATGTCCTCCCAAGTGGTTTCAT 13

RESULT 6
AII172854/c

LOCUS AII172854 48 bp mRNA linear EST 07-OCT-1998
DEFINITION uc10c07.r1 Soares mammary gland NbMMG Mus musculus cDNA clone
IMAGE:1397580 5' similar to gb:M90696 CATHEPSIN S PRECURSOR
(HUMAN); mRNA sequence.

ACCESSION AII172854

VERSION AII172854.1 GI:3720434

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 48)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:909296

Trace considered overall poor quality

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1..48
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1397580"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NbMMG"
/note="Organ: mammary gland; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

ORIGIN

Query Match 58.3%; Score 14; DB 1; Length 48;
Best Local Similarity 77.3%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY      3 TCATGTTTCCAAAGTCATGAT 24
      ||||| ||| ||||| |||
DB      34 TCATGTCCTCCCAAGTGGTTCAT 13

RESULT 7
AA386692/c      48 bp      mRNA      linear      EST 23-APR-1997
LOCUS      V55C05.r1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone
DEFINITION      IMAGE:760904 5' similar to gb:M90696 CATHEPSIN S PRECURSOR
                (HUMAN); mRNA sequence.
ACCESSION      AA386692
VERSION        AA386692.1 GI:2039656
KEYWORDS       Mus musculus (house mouse)
SOURCE         EST.
ORGANISM       Mus musculus
REFERENCE      1 (bases 1 to 48)
AUTHORS        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
                Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
                Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                Waterston,R.
TITLE          The WashU-HHMI Mouse EST Project
JOURNAL        Unpublished (1996)
COMMENT        Contact: Marra M/Mouse EST Project
                WashU-HHMI Mouse EST Project
                Washington University School of MedicineP
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: mouseest@watson.wustl.edu
                This clone is available royalty-free through LNL ; contact the
                IMAGE Consortium (info@image.llnl.gov) for further information.
                MGI:461824
Trace considered overall poor quality
High quality sequence stop: 1.
FEATURES       source
               Location/Qualifiers
                1..48
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:760904"
                /sex="pooled"
                /tissue_type="embryo"
                /dev_stage="11.5dpc"
                /lab_host="DH10B"
                /clone_lib="Ko mouse embryo 11 5dpc"
                /note="Organ: embryo; Vector: pSPORT1; Site 1: SalI;
                Site 2: NotI; Total RNAs were extracted from 11.5 dpc
                embryos (excluding placenta and yolk sac). The
                double-stranded cDNA was synthesized with an oligo (drr)-1
                primer GAGAGAGCTAGTCTAGATCGAGCGCGCTTTTTCATTTTTCATTTT
                3'. The cDNAs were ligated to LL-Sal3A: 5'
                GGTATTGACGTCGACTATCC 3' and LL-Sal3B: 5'
                GGATAGTCGACGTCATCAAT 3'. The cDNAs were size-selected and
                amplified by long-range PCR using Ex Taq polymerase for 18
                cycles. The PCR-amplifiable cDNA mixture went through
                one round of equalization and was digested with SalI/NotI
                and cloned into the SalI/NotI sites of the pSPORT1
                plasmid vector (Life Technologies). The library was
                constructed by Dr. Minoru S. H. Ko and Dr. Xiachong
                Wang."
ORIGIN

Query Match      58.3%; Score 14; DB 1; Length 48;
Best Local Similarity 77.3%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 TCATGTTTCCAAAGTCATGAT 24

```

```

DB      34 TCATGTCCTCCCAAGTGGTTCAT 13
      ||||| ||| ||||| |||
RESULT 8
AZ651473/c      40 bp      DNA      linear      GSS 14-DEC-2000
LOCUS      1M0522N07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      Clone UUGC1M0522N07 F, genomic survey sequence.
ACCESSION      AZ651473
VERSION        AZ651473.1 GI:11787002
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      1 (bases 1 to 40)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Kelly,M., Rose,M., Rose,R., Stokes,R., Fingey,A., von
                Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0522 row: N column: 07
                Seq primer: CGTTGTAACAGCAGCGCCAGT
                Class: plasmid ends
                High quality sequence stop: 40.
FEATURES       source
               Location/Qualifiers
                1..40
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0522N07"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN

Query Match      56.7%; Score 13.6; DB 8; Length 40;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 ATGTTTCCAAAGTCATGAT 24

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Db      23  ATGTTTCCCAAGTCATGA 4
|||||
RESULT 9
AZ637079/c
LOCUS   1M0496F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION
clone UUGC1M0496F09 F, genomic survey sequence.
ACCESSION
AZ637079
VERSION 1
KEYWORDS
GSS.
SOURCE  AZ637079.1 GI:11759185
        Mus musculus (house mouse)
ORGANISM
        Mus musculus
REFERENCE
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS  1 (bases 1 to 26)
        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
        Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
        Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
        Niederhausern, A. and Wright, D. Weiss, R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
        University of Utah Genome Center
        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
        84112, USA
        Tel: 801 585 5606
        Fax: 801 585 7177
        Email: ddunn@genetics.utah.edu
        Insert Length: 10000 Std Error: 0.00
        Plate: 0496 row: F column: 09
        Seq primer: CCGTGAACACGACGCCAGT
        Class: plasmid ends
        High quality sequence stop: 26.
FEATURES
        Location/Qualifiers
            1..26
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0496F09"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWB42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match      55.8%; Score 13.4; DB 8; Length 26;
Best Local Similarity 93.3%; Pred. No. 2.2e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9  TTCCAAAGTCATGA 23
|||||
RESULT 9
AZ637079/c
LOCUS   1M0496F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION
clone UUGC1M0496F09 F, genomic survey sequence.
ACCESSION
AZ637079
VERSION 1
KEYWORDS
GSS.
SOURCE  AZ637079.1 GI:11759185
        Mus musculus (house mouse)
ORGANISM
        Mus musculus
REFERENCE
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS  1 (bases 1 to 26)
        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
        Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
        Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
        Niederhausern, A. and Wright, D. Weiss, R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
        University of Utah Genome Center
        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
        84112, USA
        Tel: 801 585 5606
        Fax: 801 585 7177
        Email: ddunn@genetics.utah.edu
        Insert Length: 10000 Std Error: 0.00
        Plate: 0496 row: F column: 09
        Seq primer: CCGTGAACACGACGCCAGT
        Class: plasmid ends
        High quality sequence stop: 26.
FEATURES
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            1..26
                /organism="Mus musculus"
                /mol_type="genomic DNA"
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                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWB42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match      55.8%; Score 13.4; DB 8; Length 26;
Best Local Similarity 93.3%; Pred. No. 2.2e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9  TTCCAAAGTCATGA 23
|||||
Db      23  ATGTTTCCCAAGTCATGA 4
|||||
RESULT 9
AZ637079/c
LOCUS   1M0496F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION
clone UUGC1M0496F09 F, genomic survey sequence.
ACCESSION
AZ637079
VERSION 1
KEYWORDS
GSS.
SOURCE  AZ637079.1 GI:11759185
        Mus musculus (house mouse)
ORGANISM
        Mus musculus
REFERENCE
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS  1 (bases 1 to 26)
        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
        Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
        Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
        Niederhausern, A. and Wright, D. Weiss, R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
        University of Utah Genome Center
        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
        84112, USA
        Tel: 801 585 5606
        Fax: 801 585 7177
        Email: ddunn@genetics.utah.edu
        Insert Length: 10000 Std Error: 0.00
        Plate: 0496 row: F column: 09
        Seq primer: CCGTGAACACGACGCCAGT
        Class: plasmid ends
        High quality sequence stop: 26.
FEATURES
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                /organism="Mus musculus"
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                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWB42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match      55.8%; Score 13.4; DB 8; Length 26;
Best Local Similarity 93.3%; Pred. No. 2.2e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9  TTCCAAAGTCATGA 23
|||||
Db      15  TTCCAGAGTCATGA 1
|||||
RESULT 10
TA46H06P/c
LOCUS   T. brucei sheared genomic DNA clone 46h06, forward sequence,
DEFINITION
genomic survey sequence.
ACCESSION
AL454437
VERSION 1
KEYWORDS
GSS.
SOURCE  AL454437.1 GI:11856289
        Trypanosoma brucei
        Trypanosoma
        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
        Trypanosoma.
REFERENCE
        1 (bases 1 to 27)
        Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
        Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
        Melville, S.E., Rajandream, M.A. and Barrell, B.G.
        Direct Submission
        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
        project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
        Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
        nh@sanger.ac.uk
        Constructed at the Institute for Genomic Research (TIGR),
        Rockville, MD. Genomic DNA isolated from a cloned population of
        Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
        to give a tight size distribution (
        4 kb). The v + i method used for the library construction is
        described in detail in Smith, H. and Venter, J.C. (Making small
        insert libraries for whole genome shotgun sequencing projects. In
        Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
        Barrell, Oxford University Press, 1999).
        Email: nelsayed@tigr.org
        Details of T. brucei sequencing at the Sanger Centre are available
        at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
        Location/Qualifiers
            1..27
                /organism="Trypanosoma brucei"
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                /clone="46h06"
ORIGIN
Query Match      55.8%; Score 13.4; DB 9; Length 27;
Best Local Similarity 93.3%; Pred. No. 2.2e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8  TTTCAGAGTCATG 22
|||||
Db      27  TTTCACAGTCATG 13
|||||
RESULT 11
T73611/c
LOCUS   YC36h11.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
DEFINITION
IMAGE:82821 3', similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION
T73611
VERSION 1
KEYWORDS
EST.
SOURCE  T73611.1 GI:690286
        Homo sapiens (human)
        Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
        1 (bases 1 to 42)
        Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
        Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
        Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
        Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

```

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohldmann, P., Waterston, K., Wilson, R. and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

PUBMED 889549

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1676

High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Insert Length: 1676 Std Error: 0.00
Seq primer: -21ml3

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

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1. .42
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:499878"
/cb_xref="taxon:9606"
/clone="IMAGE:82821"
/sex="male"
/dev stages="49 years old"
/lab_host="SOUR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Hepatotomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATCGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"
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ORIGIN

Query Match 55.8%; Score 13.4; DB 7; Length 42;
Best Local Similarity 82.4%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTG 18

| | | | | | | | | | | | | | | | | | | | | |

Db 23 TANANGTTTCCAAAGTG 7

RESULT 12

AZ307496/c

LOCUS

DEFINITION AZ307496 31 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0009F14 F, genomic survey sequence.

ACCESSION AZ307496

VERSION AZ307496.1 GI:10346554

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 31)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0009 row: F column: 14

Seq primer: CGTGTAAACGAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 31.

Location/Qualifiers

FEATURES

source

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1. .31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0009F14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

ORIGIN

Query Match 55.0%; Score 13.2; DB 8; Length 31;
Best Local Similarity 83.3%; Pred. No. 2.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TGTTCCAAAGTGCATGA 23

| | | | | | | | | | | | | | | | | | | | | |

Db 30 TGTTTCCTAAATGTATGA 13

RESULT 13

AU014420

LOCUS

DEFINITION AU014420 33 bp mRNA linear EST 03-AUG-1998
Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc09814, mRNA sequence.

ACCESSION AU014420

VERSION AU014420.1 GI:3369211

KEYWORDS EST.

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM Schizosaccharomyces pombe

Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomycetes.

1 (bases 1 to 33)

Moriyomo, M. and Mita, K.

Identification of expressed sequence tags of Schizosaccharomycetes

pombe

Unpublished (1998)

Contact: Mitsuaki Moriyomo

Genome Research Group

National Institute of Radiological Sciences

9-1, Anagawa-4-chome, Inage-ku, Chiba 263-8555, Japan

Email: moriyomo@nirs.go.jp

Location/Qualifiers

FEATURES

```

source
1. .33
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc09814"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M3mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M3mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN
Query Match 55.0%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. NO. 2.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TGTTCCTCAAGTCATGA 23
Db 9 TGTTCCTATGATGA 26

RESULT 14
LOCUS CL213211 35 bp mRNA linear GSS 30-JUN-2004
DEFINITION A045A04 GATC Gene Trap Library GV03C04 Mus musculus cDNA clone
VERSION CL213211
GSS. CL213211.2 GI:49489584
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schmutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P. A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
JOURNAL 22810117
MEDLINE 12904583
PUBMED 12904583
COMMENT On Jun 30, 2004 this sequence version replaced gi:40730112.
Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
p1ribetageo gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=A045A04' ES cell line harboring insertion mutation of target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 08991
Class: Gene Trap.
Location/Qualifiers
FEATURES
source
1. .35
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="A045A04"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells 129S2 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV03C04"
/note="Vector: p1ribetageo"

ORIGIN
Query Match 55.0%; Score 13.2; DB 9; Length 35;
Best Local Similarity 83.3%; Pred. NO. 2.8e+05;

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 TCATGTTTCCAAAGTCGA 20
Db 1 TCATGTTTGCACAGTCCA 18

RESULT 15
LOCUS AL753405/c 41 bp DNA linear GSS 31-MAR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-049G05-013871, genomic survey sequence.
ACCESSION AL753405
VERSION AL753405.1 GI:21485903
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weissshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL 22755829
MEDLINE 12874060
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weissshaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4
AUTHORS Li, Y., Strizhov, N., Rosso, M.G. and Weissshaar, B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1-3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/
Location/Qualifiers
FEATURES
source
1. .41
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-049G05-013871"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion.

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T-DNA derived sequences were removed."

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ORIGIN
Query Match          55.0%; Score 13.2; DB 9; Length 41;
Best Local Similarity 83.3%; Pred. No. 2.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  5 ATGTTTCCAAAGTCATG 22
    ||||| ||||| |||||
Db   21 ATGTTTCTAAAGTTCAAG 4

RESULT 16
BX891114          41 bp      DNA      linear      GSS 05-APR-2004
LOCUS             Arabidopsis thaliana T-DNA flanking sequence GK-446C12-023804,
DEFINITION        genomic survey sequence.
ACCESSION         BX891114
VERSION           BX891114.1 GI:39923609
KEYWORDS          GSS.
SOURCE            Arabidopsis thaliana (thale cress)
ORGANISM          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS           Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weishaar,B.
TITLE             GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
                  the identification of T-DNA insertion mutants in Arabidopsis
                  thaliana
JOURNAL            Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE            22755829
PubMed            12874060
REFERENCE
AUTHORS           Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
                  Weishaar,B.
TITLE             An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
                  flanking sequence tag-based reverse genetics
JOURNAL            Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE            23117147
PubMed            14756321
REFERENCE
AUTHORS           Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
                  Weishaar,B.
TITLE             High-throughput generation of sequence indexes from T-DNA
                  mutagenized Arabidopsis thaliana lines
JOURNAL            Biotechniques 35 (6), 1164-1168 (2003)
MEDLINE            14682050
PubMed
REFERENCE
AUTHORS           Li,Y., Strizhov,N., Rosso,M.G. and Weishaar,B.
TITLE             Direct Submission
JOURNAL            Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
                  Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
                  This sequence has been recovered from the left border of the T-DNA.
                  It indicates an insertion within the locus defined by BAC clone
                  K21P3. Details on the protocols used for generation of the sequence
                  are described in References 1-3. The sequences are generated at the
                  MPI for Plant Breeding Research in the context of the GABI-Kat
                  project. GABI-Kat is part of the German Plant Genomics program
                  designated 'GABI'. Information on line availability can be found
                  at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES             location/Qualifiers
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                        /organism="Arabidopsis thaliana"
                        /mol_type="genomic DNA"
                        /strain="Columbia 0"
                        /db_xref="taxon:3702"
                        /clone="GK-446C12-023804"
                        /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                        /note="PCR was performed on DNA from Arabidopsis thaliana
                        plants (Ti) which were transformed with the T-DNA from
                        vector pAC161 (GenBank accession number: AJ537514). The

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lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

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ORIGIN
Query Match          55.0%; Score 13.2; DB 9; Length 41;
Best Local Similarity 83.3%; Pred. No. 2.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  6 TGTTCACAAAGTCATGA 23
    ||||| ||||| |||||
Db   4 TTTTCCAAATTCNAGA 21

RESULT 17
CC888123          45 bp      DNA      linear      GSS 31-JUL-2003
LOCUS             SALK_151365.21.90.x Arabidopsis thaliana TDNA insertion lines
DEFINITION        Arabidopsis thaliana genomic clone SALK_151365.21.90.x, genomic
                  survey sequence.
ACCESSION         CC888123
VERSION           CC888123.1 GI:33364479
KEYWORDS          GSS.
SOURCE            Arabidopsis thaliana (thale cress)
ORGANISM          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
                  Shinn,P., Zimmermann,J. and Ecker,J.R.
                  A Sequence-Indexed Library of Insertion Mutations in the
                  Arabidopsis Genome
JOURNAL            Unpublished (2001)
COMMENT           Contact: Joseph R. Ecker
                  Salk Institute Genomic Analysis Laboratory (SIGnAL)
                  The Salk Institute for Biological Studies
                  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                  Tel: 858 453 4100 x1752
                  Fax: 858 558 6379
                  Email: ecker@salk.edu
                  This is single pass sequence recovered from the left border of
                  TDNA.
                  Class: TDNA tagged.

FEATURES             location/Qualifiers
                     1..45
                        /organism="Arabidopsis thaliana"
                        /mol_type="genomic DNA"
                        /ecotype="Col-0"
                        /db_xref="taxon:3702"
                        /clone="SALK_151365.21.90.x"
                        /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                        /note="PCR was performed on Arabidopsis thaliana lines
                        each of which contains one or more TDNA insertion
                        elements. The resultant fragment for each line was
                        directly sequenced to determine the genomic sequence at
                        the site of insertion. Details of the protocols used can
                        be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          55.0%; Score 13.2; DB 9; Length 45;
Best Local Similarity 83.3%; Pred. No. 2.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  6 TGTTCACAAAGTCATGA 23
    ||||| ||||| |||||
Db   24 TGTTCACCAATGTCATGA 7

RESULT 18
BZ762504/c

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LOCUS BZ762504 29 bp DNA linear GSS 13-MAR-2003
 DEFINITION SALK_105087.19.80.n Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_105087.19.80.n, genomic
 survey sequence.

ACCESSION BZ762504
 VERSION BZ762504.1 GI:28933057
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 29)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 The Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel.: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.

Class: TDNA tagged.
 Location/Qualifiers
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 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_105087.19.80.n"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 54.2%; Score 13; DB 8; Length 29;
 Best Local Similarity 76.2%; Pred. No. 3.3e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCAT 21
 Db 27 CATGGTGATCCAAAGTCCAT 7

RESULT 19
 BE548888
 LOCUS BE548888 37 bp mRNA linear EST 09-AUG-2000
 DEFINITION G01073346F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3459586 5',
 mRNA sequence.

ACCESSION BE548888
 VERSION BE548888.1 GI:9777533
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 37)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

ORIGIN

Query Match 54.2%; Score 13; DB 8; Length 29;
 Best Local Similarity 76.2%; Pred. No. 3.3e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCAT 21
 Db 27 CATGGTGATCCAAAGTCCAT 7

RESULT 19
 BE548888
 LOCUS BE548888 37 bp mRNA linear EST 09-AUG-2000
 DEFINITION G01073346F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3459586 5',
 mRNA sequence.

ACCESSION BE548888
 VERSION BE548888.1 GI:9777533
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 37)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

ORIGIN

Query Match 54.2%; Score 13; DB 8; Length 29;
 Best Local Similarity 76.2%; Pred. No. 3.3e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCAT 21
 Db 27 CATGGTGATCCAAAGTCCAT 7

RESULT 19
 BE548888
 LOCUS BE548888 37 bp mRNA linear EST 09-AUG-2000
 DEFINITION G01073346F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3459586 5',
 mRNA sequence.

ACCESSION BE548888
 VERSION BE548888.1 GI:9777533
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 37)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

ORIGIN

Query Match 54.2%; Score 13; DB 8; Length 29;
 Best Local Similarity 76.2%; Pred. No. 3.3e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCAT 21
 Db 27 CATGGTGATCCAAAGTCCAT 7

RESULT 19
 BE548888
 LOCUS BE548888 37 bp mRNA linear EST 09-AUG-2000
 DEFINITION G01073346F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3459586 5',
 mRNA sequence.

cdNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM8452 row: k column: 11
 High quality sequence stop: 37.

FEATURES
 source
 1..37
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3459586"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 37;
 Best Local Similarity 76.2%; Pred. No. 3.5e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22
 Db 8 TTCCTGCTTCAACAGTCTTG 28

RESULT 20
 BX572262
 LOCUS BX572262 40 bp DNA linear GSS 04-APR-2004
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-544G08-020964,
 genomic survey sequence.

ACCESSION BX572262
 VERSION BX572262.1 GI:33412435
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1
 Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL MEDLINE 22755829
 PUBMED 12874060
 REFERENCE 2

AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
 Weissshaar,B.
 TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL MEDLINE 23117147
 PUBMED 14756321
 REFERENCE 3

AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
 Weissshaar,B.
 TITLE High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 BioTechniques 35 (6), 1164-1168 (2003)

JOURNAL MEDLINE 14682050
 PUBMED 14682050
 REFERENCE 4 (bases 1 to 40)

AUTHORS Rosso,M.G., Li,Y., Strizhov,N. and Weissshaar,B.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50629, Germany

ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 37;
 Best Local Similarity 76.2%; Pred. No. 3.5e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22
 Db 8 TTCCTGCTTCAACAGTCTTG 28

RESULT 20
 BX572262
 LOCUS BX572262 40 bp DNA linear GSS 04-APR-2004
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-544G08-020964,
 genomic survey sequence.

ACCESSION BX572262
 VERSION BX572262.1 GI:33412435
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1
 Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL MEDLINE 22755829
 PUBMED 12874060
 REFERENCE 2

AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
 Weissshaar,B.
 TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL MEDLINE 23117147
 PUBMED 14756321
 REFERENCE 3

AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
 Weissshaar,B.
 TITLE High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 BioTechniques 35 (6), 1164-1168 (2003)

JOURNAL MEDLINE 14682050
 PUBMED 14682050
 REFERENCE 4 (bases 1 to 40)

AUTHORS Rosso,M.G., Li,Y., Strizhov,N. and Weissshaar,B.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50629, Germany

ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 37;
 Best Local Similarity 76.2%; Pred. No. 3.5e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22
 Db 8 TTCCTGCTTCAACAGTCTTG 28

RESULT 20
 BX572262
 LOCUS BX572262 40 bp DNA linear GSS 04-APR-2004
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-544G08-020964,
 genomic survey sequence.

ACCESSION BX572262
 VERSION BX572262.1 GI:33412435
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1
 Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Atlg32090. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source
1. .40
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-54G08-020964"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 54.2%; Score 13; DB 9; Length 40;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTCATGA 23
||||| ||||| ||||| |||||

Db 14 TCATCTTACAAAGGATGA 34
||||| ||||| ||||| |||||

RESULT 21
BE788148
LOCUS 601480079F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882835 5',
DEFINITION mRNA sequence.
VERSION BE788148.1 GI:10209346
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/BTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LIA9653 row: n column: 20
High quality sequence stop: 43.
Location/Qualifiers
1. .43

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3882835"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

FEATURES

source
1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3882835"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 43;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCAATGTTTCCAAAGTCATG 22
||||| ||||| ||||| |||||

Db 14 TTCTGCTTCAACAGTCTTG 34
||||| ||||| ||||| |||||

RESULT 22
BH790838/c

LOCUS SALK_058022.27.05.x Arabidopsis thaliana T-DNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_058022.27.05.x, genomic survey sequence.
ACCESSION BH790838
VERSION BH790838.1 GI:19893973
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 43)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of T-DNA. This sequence lies within an annotated exon of At3g41627.
Class: T-DNA tagged.
Location/Qualifiers
1. .43
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_058022.27.05.x"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

Query Match 54.2%; Score 13; DB 8; Length 43;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCAATGTTTCCAAAGTCATG 22
||||| ||||| ||||| |||||

Db 37 TTCATCTTACACACTGCATG 17
||||| ||||| ||||| |||||

RESULT 23

BJ076538

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

LOCUS

DEFINITION

BJ076538 NIBB Mochii normalized Xenopus tailbud library

laevis cDNA clone XL051f21 3', mRNA sequence.
ACCESSION BJ076538
VERSION BJ076538.1 GI:17521454
KEYWORDS EST
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 44)
AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.

TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
http://xenopus.nibb.ac.jp.

FEATURES
source Location/Qualifiers
1..44
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL051f21"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud library"

ORIGIN

Query Match 54.2%; Score 13; DB 4; Length 44;
Best Local Similarity 81.2%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGT 17
Db 11 TTNANGTTTCCAAANT 26

RESULT 24

W11835/c
LOCUS W11835 28 bp mRNA linear EST 02-OCT-1997
DEFINITION mb20h01.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:330001 5', similar to SW:CATK_RABIT P43236 CATHEPSIN K PRECURSOR ;, mRNA sequence.

ACCESSION W11835
VERSION W11835.1 GI:1286140
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 28)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HWMI Mouse EST Project
JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
WashU-HWMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through INL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI: 211401

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: mob.REGA+ET

High quality sequence stop: 1.

FEATURES
source Location/Qualifiers

1..28
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:330001"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares mouse p3NMF19.5"
/note="Vector: pRT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

ORIGIN

Query Match 53.3%; Score 12.8; DB 7; Length 28;
Best Local Similarity 87.5%; Pred. No. 4.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTG 18
Db 20 TCATGTTCTCCCAAGT 5

RESULT 25

AZ794096

LOCUS

DEFINITION 2M0047P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0047P10 R, genomic survey sequence.

ACCESSION AZ794096

VERSION AZ794096.1 GI:12939715

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 36)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0047 row: P column: 10

Seq primer: CACACAGGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 36.

FEATURES

source Location/Qualifiers

1..36

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC2M0047P10"
/sex="Male"
/lab_hosts="E. Coli strain Xl10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli Xl10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

```
Query Match      53.3%; Score 12.8; DB 8; Length 36;
Best Local Similarity 70.8%; Pred. No. 4.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

Qy	1	CTTCATGTTTCCAAAGTCATGAT	24
Db	2	CTGTATACATCCAAATTTCATGAT	25

RESULT	26
CC796901/c	
LOCUS	
CC796901	36 bp DNA linear GSS 01-JUL-2003
DEFINITION	SALK_144210.22.90.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_144210.22.90.x, genomic survey sequence.

FEATURES
source

```
1: 20
/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
```

ORIGIN

```
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_144210.22.90.x"
/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tDNA\_protocols.html"
```

ORIGIN

Query Match	53.3%	Score 12.8;	DB 9;	Length 36;
Best Local Similarity	70.8%	Pred. No. 4.2e+05;		
Matches 17; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATGAT 24
Db 30 CATGGTGTAGCCAAAGTCCGTGAT 7

RESULT 27	AA995598	AA995598	43 bp	mrna	linear	EST 27-AUG-1998
LOCUS	OS22H03.s1	NCI_CGAP_Kid5 Homo sapiens	cdna	clone IMAGE:1606133	3'	
DEFINITION	similar to TR:O14949 O14949 LOW MOLECULAR MASS UBIQUINONE-BINDING PROTEIN. ;, mRNA sequence.					

Trace considered overall poor quality
Insert Length: 475 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES	SOURCE

```

Query Match      53.3%; Score 12.8; DB 1; Length 43;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2  TTCATGTTTCCAAAGT 17
    ||||| ||||| |||||
DB   24  TTCATATTTCCTCAACT 39

RESULT 28
CC049873/c
LOCUS      CC049873
DEFINITION 01S0518-03B1-B06 UniformMu MutTAIL Library Zea mays genomic clone
            01S-518-3-7tol2-B06, genomic survey sequence.
ACCESSION  CC049873
VERSION     CC049873.1 GI:29464764
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 46)
AUTHORS   Latschaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE     Sequence tagged transposon insertions from the UniformMu maize
            population
JOURNAL   Unpublished (2003)
COMMENT   Contact: Donald R. McCarty
            Plant Molecular and Cellular Biology Program
            University of Florida
            PO 110690 Gainesville, FL 32611-0690, USA
            Tel: 352-392-1928 x322
            Email: drmc@ufl.edu
            Sequence flanking probable Mu insertion site in UniformMu line:
            01S-518-3
            Class: transposon insertion site.
            Location/Qualifiers
                source          1..46
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="W22 (ACR, bz1-m9)"
                /cultivar="UniformMu"
                /db_xref="taxon:4577"
                /clone="01S-518-3-7tol2-B06"
                /clone_lib="UniformMu MutTAIL Library"
                /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
            insertions in Mu inactive lines were extracted from the
            UniformMu maize population by the thermo asymmetric
            interlaced PCR (TAIL) protocol using primers specific for
            the Mu terminal inverted repeat and a set of 16 arbitrary
            primers. Amplicons were size enriched using Sepharose 400
            spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match      53.3%; Score 12.8; DB 8; Length 46;
Best Local Similarity 70.8%; Pred. No. 4.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  1  CTTCATGTTTCCAAAGTGCATGAT 24
    ||||| ||||| |||||
DB   36  CCTCATGTTTGATACAGGGCATGTT 13

RESULT 29
BZ290816/c
LOCUS      BZ290816
DEFINITION SALK_091529.28.85.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_091529.28.85.x, genomic
            survey sequence.
ACCESSION  BZ290816
VERSION     BZ290816.1 GI:24334846
KEYWORDS   GSS.

Query Match      53.3%; Score 12.8; DB 8; Length 46;
Best Local Similarity 70.8%; Pred. No. 4.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  1  CTTCATGTTTCCAAAGTGCATGAT 24
    ||||| ||||| |||||
DB   36  CCTCATGTTTGATACAGGGCATGTT 13

RESULT 28
CC049873/c
LOCUS      CC049873
DEFINITION 01S0518-03B1-B06 UniformMu MutTAIL Library Zea mays genomic clone
            01S-518-3-7tol2-B06, genomic survey sequence.
ACCESSION  CC049873
VERSION     CC049873.1 GI:29464764
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 46)
AUTHORS   Latschaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE     Sequence tagged transposon insertions from the UniformMu maize
            population
JOURNAL   Unpublished (2003)
COMMENT   Contact: Donald R. McCarty
            Plant Molecular and Cellular Biology Program
            University of Florida
            PO 110690 Gainesville, FL 32611-0690, USA
            Tel: 352-392-1928 x322
            Email: drmc@ufl.edu
            Sequence flanking probable Mu insertion site in UniformMu line:
            01S-518-3
            Class: transposon insertion site.
            Location/Qualifiers
                source          1..46
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="W22 (ACR, bz1-m9)"
                /cultivar="UniformMu"
                /db_xref="taxon:4577"
                /clone="01S-518-3-7tol2-B06"
                /clone_lib="UniformMu MutTAIL Library"
                /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
            insertions in Mu inactive lines were extracted from the
            UniformMu maize population by the thermo asymmetric
            interlaced PCR (TAIL) protocol using primers specific for
            the Mu terminal inverted repeat and a set of 16 arbitrary
            primers. Amplicons were size enriched using Sepharose 400
            spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match      53.3%; Score 12.8; DB 8; Length 46;
Best Local Similarity 70.8%; Pred. No. 4.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  1  CTTCATGTTTCCAAAGTGCATGAT 24
    ||||| ||||| |||||
DB   36  CCTCATGTTTGATACAGGGCATGTT 13

RESULT 29
BZ290816/c
LOCUS      BZ290816
DEFINITION SALK_091529.28.85.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_091529.28.85.x, genomic
            survey sequence.
ACCESSION  BZ290816
VERSION     BZ290816.1 GI:24334846
KEYWORDS   GSS.

Query Match      52.5%; Score 12.6; DB 8; Length 26;
Best Local Similarity 78.9%; Pred. No. 5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  3  TCATGTTTCCAAAGTGCAT 21
    ||||| ||||| |||||
DB   26  TAAAGTTTAAAGTGCT 8

RESULT 30
BZ661378/c
LOCUS      BZ661378
DEFINITION SALK_024848.36.30.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_024848.36.30.x, genomic
            survey sequence.
ACCESSION  BZ661378
VERSION     BZ661378.1 GI:28174525
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 31)
            Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Query Match      52.5%; Score 12.6; DB 8; Length 26;
Best Local Similarity 78.9%; Pred. No. 5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  3  TCATGTTTCCAAAGTGCAT 21
    ||||| ||||| |||||
DB   26  TAAAGTTTAAAGTGCT 8

RESULT 30
BZ661378/c
LOCUS      BZ661378
DEFINITION SALK_024848.36.30.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_024848.36.30.x, genomic
            survey sequence.
ACCESSION  BZ661378
VERSION     BZ661378.1 GI:28174525
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 31)
            Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Source
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 26)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
Atlg29620 and 300 bases of the 5' end of Atlg29630.
Class: TDNA tagged.
Location/Qualifiers
    source          1..26
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /ecotype="Col-0"
    /db_xref="taxon:3702"
    /clone="SALK_091529.28.85.x"
    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
    /note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

```

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..31 /organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_024848.36.30.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES
source

ORIGIN

Query Match 52.5%; Score 12.6; DB 8; Length 31;
Best Local Similarity 78.9%; Pred. No. 5.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCAT 21

||||| ||||| ||||| ||||| |||||

Db 25 TCATGTTTCCAAATTTCAT 7

RESULT 31

CG712334/c

LOCUS

DEFINITION 1119026A11.2EL.x1 1119 - RescueMu Grid AA Zea mays genomic, GSS 20-OCT-2003

survey sequence.

ACCESSION CG712334

VERSION CG712334.1

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 32)

Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

TITLE

JOURNAL

COMMENT

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119026 row: A column: 11

Class: transposon-tagged.

Location/Qualifiers

1..32 /organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue type="leaf"

/dev stage="adult"

/lab_host="DH10B"

/clone_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI, Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.fastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 52.5%; Score 12.6; DB 9; Length 32;

Best Local Similarity 78.9%; Pred. No. 5.1e+05;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTTCAATGTTTCCAAAGTGC 19

||||| ||||| ||||| ||||| |||||

Db 23 CTTCTGCTTCCAGATTC 5

RESULT 32

BH850177/c

LOCUS

DEFINITION SALK_070912.49.55.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_070912.49.55.x, genomic

survey sequence.

ACCESSION BH850177

VERSION BH850177.1

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 37)

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..37

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_070912.49.55.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 52.5%; Score 12.6; DB 8; Length 37;

Best Local Similarity 78.9%; Pred. No. 5.2e+05;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TTCAATGTTTCCAAAGTGC 20

||||| ||||| ||||| ||||| |||||

Db 35 TTCAATGTTTCCAAAGTGC 17

Source: IMAGE Consortium, LNLN
This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: polyT not found
Insert Length: 597 Std Error: 0.00
Seq primer: Promega -21ml3.

FEATURES
source
1. 40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3862089"
/db_xref="taxon:9606"
/clone="IMAGE:232098"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_pineal_gland_N3HPG"
/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Patima Bonaldo."

ORIGIN
Query Match 52.5%; Score 12.6; DB 5; Length 38;
Best Local Similarity 75.0%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3' TCATGTTTCCAAAGTGCATG 22
|||||
Db 16 TCTTGATGCGAGTGCATG 35

RESULT 34
H95706/c
LOCUS
DEFINITION
IMAGE:232098 3', similar to gb|M73048|HUMU3AAAA Human U3 small nuclear RNA (rRNA);, mRNA sequence.

ACCESSION
H95706
VERSION
H95706.1 GI:1108848
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 40)

REFERENCE
AUTHORS
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1

FEATURES
source
1. 38
/organism="Ciona savignyi"
/mol_type="mRNA"
/db_xref="taxon:51511"
/clone="csef028024"
/dev_stage="egg"
/clone_lib="Yutaka Satou unpublished cDNA library (csef2)"

ORIGIN
Query Match 52.5%; Score 12.6; DB 5; Length 38;
Best Local Similarity 75.0%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3' TCATGTTTCCAAAGTGCATG 22
|||||
Db 16 TCTTGATGCGAGTGCATG 35

RESULT 33
BW593923
LOCUS
DEFINITION
BW593923 Yutaka Satou unpublished cDNA library (csef2) Ciona savignyi cDNA clone csef028024 3', mRNA sequence.

ACCESSION
BW593923
VERSION
BW593923.1 GI:51844723
KEYWORDS
EST.
SOURCE
Ciona savignyi
ORGANISM
Ciona savignyi
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 38)
AUTHORS
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
TITLE
Expressed genes in Ciona savignyi (Satou, Shin-i, Kohara, Satoh)
JOURNAL
Unpublished (2004)
COMMENT
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1. 38
/organism="Ciona savignyi"
/mol_type="mRNA"
/db_xref="taxon:51511"
/clone="csef028024"
/dev_stage="egg"
/clone_lib="Yutaka Satou unpublished cDNA library (csef2)"

ORIGIN
Query Match 52.5%; Score 12.6; DB 5; Length 38;
Best Local Similarity 75.0%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3' TCATGTTTCCAAAGTGCATG 22
|||||
Db 16 TCTTGATGCGAGTGCATG 35

RESULT 35
TA202B01Q/c
LOCUS
DEFINITION
TA202B01Q 41 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 202b01, reverse sequence, genomic survey sequence.

ACCESSION
AL477015
VERSION
AL477015.1 GI:11843470
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
1 (bases 1 to 41)

REFERENCE
AUTHORS
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

TITLE
JOURNAL
COMMENT
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1. 41
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"


```

/strain="TREU927"
/db_xref="taxon:5691"
/clone="202b01"

ORIGIN
Query Match      52.5%; Score 12.6; DB 9; Length 41;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTGCATG 22
    ||||| ||||| |||||
Db 21 CACGCTTCAGAGTGCATG 3

RESULT 36
AI280742
LOCUS      43 bp mRNA linear EST 23-NOV-1998
DEFINITION Qw07c06.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:1990378 3'
            similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN. ; mRNA
            sequence.
ACCESSION  AI280742
VERSION     AI280742.1 GI:3918975
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 43)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            Cloning Distribution by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..43
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1990378"
                     /tissue_type="poorly-differentiated endometrial
                     adenocarcinoma, 2 pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI-CGAP_Ut3"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
                     Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.45 kb. Life Technologies catalog #:
                     11541-018"

ORIGIN
Query Match      52.5%; Score 12.6; DB 1; Length 43;
Best Local Similarity 78.9%; Pred. No. 5.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCAT 21
    ||||| ||||| |||||
Db 16 TCATCTTTTCAAGAGCTT 34

RESULT 37
BZ766776/c
```

```

LOCUS      43 bp DNA linear GSS 13-MAR-2003
DEFINITION SALK_137836.19.55.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_137836.19.55.x, genomic
            survey sequence.
ACCESSION  BZ766776
VERSION     BZ766776.1 GI:28939329
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 43)
            Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gardinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmermann,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
            Location/Qualifiers
     source          1..43
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_137836.19.55.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      52.5%; Score 12.6; DB 8; Length 43;
Best Local Similarity 78.9%; Pred. No. 5.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATGTTTCCAAAGTGCATGA 23
    ||||| ||||| |||||
Db 37 ATGTAGCCAAAGTGAGTGA 19

RESULT 38
AZ388487/c
LOCUS      37 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0148F03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            Clone UUGC1M0148F03 R, genomic survey sequence.
ACCESSION  AZ388487
VERSION     AZ388487.1 GI:10502195
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 37)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```


**JOURNAL
COMMENT**

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0148 row: F column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.

FEATURES
SOURCE

Source

FEATURES	Location/Qualifiers
source	1. .41

ORIGIN

Query Match	51.7%	Score 12.4;	DB 8;	Length 41;
Best Local Similarity	72.7%;	Pred. No. 6.6e+05;		
Matches 16;	Conservative	0;	Mismatches 6;	Indels 0;
				Caps 0;

ORIGIN

```
Query Match          51.7%; Score 12.4; DB 8; Length 37;
Best Local Similarity 72.7%; Pred. No. 6.5e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

RESULT 39

Accession	LOCUS	DEFINITION	41 bp	DNA	linear	GSS	05-AUG-2002
BH856468	BH866468	SALK_101369 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 101369, genomic survey sequence.					

REFERENCE
AUTHORS

Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..42
 /organism="Trypanosoma brucei"
 FEATURES
 source

FEATURES

```
1. .42
/organism="Trypanosoma brucei"
```

LOCUS	TR232A04Q	42 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	T. brucei sheared genomic DNA clone 232a04, reverse genomic survey sequence.				

```

source
1. .42
/organism="Trypanosoma brucei"

```

```
/mol_type="genomic DNA"  
/strain="REU927"  
/db_xref="taxon:5691"  
/clone="232a04"
```

ORIGIN

```
Query Match      51.7%; Score 12.4; DB 9; Length 42;  
Best Local Similarity 72.7%; Pred. No. 6.6e+05;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      3 TCATGTTTCCAAAGTGCATGAT 24  
        |||  | |||||  |||||  
Db     23 TCACTATACCAAGGATGAT 2
```

Search completed: November 18, 2005, 21:12:43
Job time : 1150.98 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 46.6312 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-4

Perfect score: 24

Sequence: 1 CTTTCATGTTTCCAAAGTGCATGAT 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	1	US-07-989-160-4
2	16.2	67.5	34	2	US-08-577-492-21
3	16.2	67.5	34	3	US-09-079-630-21
C 4	15.6	65.0	25	4	US-09-396-196G-53744
C 5	14.8	61.7	25	4	US-09-396-196G-21176
C 6	14.8	61.7	25	4	US-09-396-196G-21177
C 7	14.8	61.7	25	4	US-09-396-196G-21178
C 8	14.6	60.8	25	4	US-09-396-196G-23224
C 9	14.6	60.8	27	3	US-08-908-643C-34
C 10	14	58.3	25	4	US-09-396-196G-59686
C 11	14	58.3	25	4	US-09-396-196G-122551
C 12	14	58.3	36	3	US-08-961-083-258
C 13	14	58.3	36	4	US-09-536-784-258
C 14	14	58.3	50	4	US-08-956-171E-1998
C 15	14	58.3	50	4	US-08-781-986A-1998
C 16	13.8	57.5	20	4	US-09-232-785-173
C 17	13.8	57.5	25	4	US-09-396-196G-21175
C 18	13.8	57.5	25	4	US-09-396-196G-109424
C 19	13.8	57.5	25	4	US-09-396-196G-109425
C 20	13.8	57.5	24	4	US-09-671-317-784
C 21	13.6	56.7	20	4	US-09-913-192A-10
C 22	13.6	56.7	25	3	US-08-544-381B-80
C 23	13.6	56.7	25	4	US-09-396-196G-41037
C 24	13.6	56.7	25	4	US-09-396-196G-59155
C 25	13.6	56.7	25	4	US-09-396-196G-122534
C 26	13.6	56.7	47	4	US-09-422-978-2662
C 27	13.4	55.8	17	3	US-08-584-040-5610

C 28	13.4	55.8	17	3	US-08-584-040-5611	Sequence 5611, Ap
C 29	13.4	55.8	17	4	US-09-371-772B-2500	Sequence 2500, Ap
C 30	13.4	55.8	17	4	US-09-371-772B-2501	Sequence 2501, Ap
C 31	13.4	55.8	17	4	US-09-685-664B-2501	Sequence 2501, Ap
C 32	13.4	55.8	17	4	US-09-685-664B-2501	Sequence 2501, Ap
C 33	13.4	55.8	18	1	US-07-768-437-10	Sequence 10, Appl
C 34	13.4	55.8	25	4	US-09-396-196G-30572	Sequence 30572, A
C 35	13.4	55.8	25	4	US-09-396-196G-33631	Sequence 33631, A
C 36	13.4	55.8	25	4	US-09-396-196G-33632	Sequence 33632, A
C 37	13.4	55.8	25	4	US-09-396-196G-45409	Sequence 45409, A
C 38	13.4	55.8	25	4	US-09-396-196G-45410	Sequence 45410, A
C 39	13.4	55.8	25	4	US-09-396-196G-70209	Sequence 70209, A
C 40	13.4	55.8	47	4	US-09-422-978-3015	Sequence 3015, Ap
C 41	13.4	55.8	47	4	US-09-422-978-3250	Sequence 3250, Ap
C 42	13.4	55.8	50	4	US-09-443-199C-835	Sequence 835, Appl
C 43	13.2	55.0	21	1	US-07-763-512-9	Sequence 9, Appl
C 44	13.2	55.0	25	4	US-09-396-196G-5610	Sequence 5610, Ap
C 45	13.2	55.0	25	4	US-09-396-196G-12297	Sequence 12297, A

ALIGNMENTS

RESULT 1
US-07-989-160-4
; Sequence 4, Application US/07989160
; Patent No. 542923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-07-989-160-4

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.07; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0

Qy 1 CTTTCATGTTTCCAAAGTGCATGAT 24
|||||

```
Db      1  CTTTCATGTTTCCAAAGTGCATG 24

RESULT 2
US-08-577-492-21
; Sequence 21, Application US/08577492
; Patent No. 5851784
; GENERAL INFORMATION:
; APPLICANT: Owens, Raymond John
; APPLICANT: Perry, Martin John
; APPLICANT: Lumb, Simon Mark
; TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
; TITLE OF INVENTION: ITS PRODUCTION AND USE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,492
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9426227.6
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9512996.1
; FILING DATE: 26-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherry, David A.
; REGISTRATION NUMBER: 35,099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-577-492-21

Query Match      67.5%; Score 16.2; DB 2; Length 34;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2  TTTTCATGTTTCCAAAGTGCATG 22
      ||| ||| ||| ||| ||| ||| ||| |||
Db      3  TTTTCATGTTTCCAAAGTGCATG 23

RESULT 3
US-08-577-630-21
; Sequence 21, Application US/09079630
; Patent No. 6291199
; GENERAL INFORMATION:
; APPLICANT: Owens, Raymond John
; APPLICANT: Perry, Martin John
; APPLICANT: Lumb, Simon Mark
; TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
; TITLE OF INVENTION: ITS PRODUCTION AND USE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6291199ris
; STREET: One Liberty Place, 46th floor

Query Match      67.5%; Score 16.2; DB 2; Length 34;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2  TTTTCATGTTTCCAAAGTGCATG 22
      ||| ||| ||| ||| ||| ||| ||| |||
Db      3  TTTTCATGTTTCCAAAGTGCATG 23

RESULT 4
US-09-396-196G-53744/c
; Sequence 53744, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53744
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-53744

Query Match      65.0%; Score 15.6; DB 4; Length 25;
Best Local Similarity 81.8%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  TTTTCATGTTTCCAAAGTGCATGA 23
      ||| ||| ||| ||| ||| ||| ||| |||
```

```
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,630
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/577,492
; FILING DATE: 22-DEC-1995
; APPLICATION NUMBER: GB 9426227.6
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9512996.1
; FILING DATE: 26-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherry, David A.
; REGISTRATION NUMBER: 35,099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-079-630-21

Query Match      67.5%; Score 16.2; DB 3; Length 34;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2  TTTTCATGTTTCCAAAGTGCATG 22
      ||| ||| ||| ||| ||| ||| ||| |||
Db      3  TTTTCATGTTTCCAAAGTGCATG 23

RESULT 4
US-09-396-196G-53744/c
; Sequence 53744, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53744
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-53744

Query Match      65.0%; Score 15.6; DB 4; Length 25;
Best Local Similarity 81.8%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  TTTTCATGTTTCCAAAGTGCATGA 23
      ||| ||| ||| ||| ||| ||| ||| |||
```

Db 25 TTCAACTTCCCAAGTGCATCA 4

RESULT 5

US-09-396-196G-21176/c

; Sequence 21176, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21176

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-21176

Query Match 61.7%; Score 14.8; DB 4; Length 25;

Best Local Similarity 88.9%; Pred. No. 1.3e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCAAGTGCATGA 23

||||| ||||| ||||| |||||

Db 23 TGTTCCTCAAGTGCATGA 6

RESULT 6

US-09-396-196G-21177/c

; Sequence 21177, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21177

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-21177

Query Match 61.7%; Score 14.8; DB 4; Length 25;

Best Local Similarity 88.9%; Pred. No. 1.3e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCAAGTGCATGA 23

||||| ||||| ||||| |||||

Db 22 TGTTCCTCAAGTGCATGA 5

RESULT 7

US-09-396-196G-21178/c

; Sequence 21178, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21178

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-21178

Query Match 61.7%; Score 14.8; DB 4; Length 25;

Best Local Similarity 88.9%; Pred. No. 1.3e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCAAGTGCATGA 23

||||| ||||| ||||| |||||

Db 20 TGTTCCTCAAGTGCATGA 3

RESULT 8

US-09-396-196G-23224/c

; Sequence 23224, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 23224

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-23224

Query Match 60.8%; Score 14.6; DB 4; Length 25;

Best Local Similarity 81.0%; Pred. No. 1.5e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22

||||| ||||| ||||| |||||

Db 24 TTCATGTTTCCAAAGTGCATG 4

RESULT 9

US-08-908-643C-34/c

; Sequence 34, Application US/08908643C

; Patent No. 6120395

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; APPLICANT: Pearlman, Joshua M.

; APPLICANT: Barber, Michael T.

; APPLICANT: Schultze, Stephanie

; APPLICANT: Parkinson, Scott J.

; TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO
COLORECTAL CANCER CELLS AND METHODS OF
USING THE SAME

; NUMBER OF SEQUENCES: 85

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA

COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,643C
FILING DATE: 07-Aug-1997
CLASSIFICATION: N/A

PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mark Deluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-2209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-08-908-643C-34
Query Match 60.8%; Score 14.6; DB 3; Length 27;
Best Local Similarity 81.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTGCATGAT 24
||| ||||| ||| |||
Db 26 CATATGTCCTCAAGAGCAGGAT 6

RESULT 10
US-09-396-196G-59686/c
Sequence 59686, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396.196G
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59686
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-59686

Query Match 58.3%; Score 14; DB 4; Length 25;
Best Local Similarity 77.3%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CTTTCATGTTTCCAAAGTGCATG 22
||| ||||| ||| |||
Db 24 CTTTCATGTTGAAAGATCCATG 3

RESULT 11
US-09-396-196G-122551
Sequence 122551, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396.196G
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 122551
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-122551

Query Match 58.3%; Score 14; DB 4; Length 25;
Best Local Similarity 77.3%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CTTTCATGTTTCCAAAGTGCATG 22
||| ||||| ||| |||
Db 1 CTTTCATGTTTCCAAAGTGCCTG 22

RESULT 12
US-08-961-083-258
Sequence 258, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

```
;
; TOPOLOGY: linear
; US-08-961-083-258
;
; Query Match 58.3%; Score 14; DB 3; Length 36;
; Best Local Similarity 77.3%; Pred. No. 3.1e+03;
; Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 3 TCATGTTTCCAAAGTGCATGAT 24
; ||| ||||| |||||
; Db 3 TCAAGCTTCCAAACTGGTTGAT 24
; ||| ||||| |||||
;
; RESULT 13
; US-09-536-784-258
; Sequence 258, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
;
; INFORMATION FOR SEQ ID NO: 258:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
;
; US-09-536-784-258
;
; Query Match 58.3%; Score 14; DB 4; Length 36;
; Best Local Similarity 77.3%; Pred. No. 3.1e+03;
; Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 3 TCATGTTTCCAAAGTGCATGAT 24
; ||| ||||| |||||
; Db 3 TCAAGCTTCCAAACTGGTTGAT 24
; ||| ||||| |||||
;
; RESULT 14
; US-08-956-171E-1998
; Sequence 1998, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; GIL H. Choi
; Patrick S. Dillon
; Craig A. Rosen
;
; Steven C. Barash
; Michael R. Fannon
;
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
;
; INFORMATION FOR SEQ ID NO: 1998:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1998:
;
; US-08-956-171E-1998
;
; Query Match 58.3%; Score 14; DB 4; Length 50;
; Best Local Similarity 73.9%; Pred. No. 3.3e+03;
; Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
; Qy 2 TTCATGTTTCCAAAGTGCATGAT 24
; ||| ||||| |||||
; Db 7 TTGATGNTCTCAAGAACATGAT 29
; ||| ||||| |||||
;
; RESULT 15
; US-08-781-986A-1998
; Sequence 1998, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
;
; US-08-781-986A-1998
```

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 1998:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-1998

Query Match      58.3%; Score 14; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2 TTTCATGTTTCCAAAGTGCATGAT 24
Db      7 TTGATGTTCTCAAGAACATGAT 29

RESULT 16
US-09-232-785-173
; Sequence 173, Application US/09232785
; Patent No. 673365
; GENERAL INFORMATION:
; APPLICANT: International Paper Co.
; APPLICANT: Echt, Craig S
; APPLICANT: Nelson, C. Dana
; TITLE OF INVENTION: MICROSATELLITE DNA MARKERS AND USES
; FILE REFERENCE: 4481/1E188US1
; CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 20;
; TYPE: DNA
; ORGANISM: Pinus taeda L.
; US-09-232-785-173

Query Match      57.5%; Score 13.8; DB 4; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TTTCATGTTTCCAAAGTG 18
Db      3 TTTCATGTTTCCAAATGTG 19

RESULT 17
US-09-396-196G-21175/c
; Sequence 21175, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109425
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-21175

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: 60/100,678
; APPLICATION NUMBER:
; FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21175
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-21175

Query Match      57.5%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GTTTCCAAAGTGCATGA 23
Db      25 GTTTCCAAAGTGCATGA 9

RESULT 18
US-09-396-196G-109424/c
; Sequence 109424, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109424
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-109424

Query Match      57.5%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTTCCAAAGTGCATGAT 24
Db      23 TTTCCTAAGTGCAGGAT 7

RESULT 19
US-09-396-196G-109425/c
; Sequence 109425, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109425
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-109425
```


Query Match 57.5%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TTCTCCAAAGTGCATGAT 24
17 TTCTCCTAAAGTGCAGGAT 1

Db

RESULT 20
US-09-671-317-784
; Sequence 784, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 784:
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-266-203 : polymorphic base C or T
US-09-671-317-784

Query Match 57.5%; Score 13.8; DB 4; Length 47;
Best Local Similarity 78.9%; Pred. No. 4e+03; 3; Indels 0; Gaps 0;

Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 TGTTCCTCAAGTGCATGAT 24
9 TGTTCCTCAAGTGCATGAT 27

Db

RESULT 21
US-09-913-192A-10
; Sequence 10, Application US/09913192A
; Patent No. 6767738
; GENERAL INFORMATION:
; APPLICANT: GAGE, FRED H.
; APPLICANT: PALMER, THEO
; APPLICANT: SAFAR, FRANCIS G.
; APPLICANT: TAKAHASHI, JUN
; APPLICANT: TAKAHASHI, MASAYO
; TITLE OF INVENTION: ISOLATION OF STEM CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: SALK2250-1
; CURRENT APPLICATION NUMBER: US/09/913,192A
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: PCT/US00/03596
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/119,642
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/155,871
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-913-192A-10

Query Match 56.7%; Score 13.6; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 4.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CATGTTTCCAAAGTGCATGA 23
1 CATGTAATTCAAAGACCATGA 20

Db

RESULT 22
US-08-544-381B-80
; Sequence 80, Application US/08544381B
; Patent No. 6027880
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; TITLE OF INVENTION: Detecting Cystic Fibrosis
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,381B
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:

```
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-544-381B-80

Query Match          56.7%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  4 CATGTTTCCAAAGTGCATGA 23
Db  4 CATTTTGCAAAGTTCATTA 23

RESULT 23
US-09-396-196G-41037/c
; Sequence 41037, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41037
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-41037

Query Match          56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  1 CTTCATGTTTCCAAAGTGCA 20
Db  24 CTACAGATTTCAAAAGTGCA 5

RESULT 24
US-09-396-196G-59155
; Sequence 59155, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59155
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-59155

Query Match          56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
```

```
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  1 CTTCATGTTTCCAAAGTGCA 20
Db  2 CTTGCTGTTTCCAAATTCCA 21

RESULT 25
US-09-396-196G-122534
; Sequence 122534, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122534
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-122534

Query Match          56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  3 TCATGTTTCCAAAGTGCATG 22
Db  1 TCATTCTTCAAGTGCTTG 20

RESULT 26
US-09-422-978-2662/c
; Sequence 2662, Application US/09422978
; Patent No. 8537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2662
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-13113-234 : polymorphic base G or A
US-09-422-978-2662

Query Match          56.7%; Score 13.6; DB 4; Length 47;
Best Local Similarity 72.7%; Pred. No. 5e+03;
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy  3 TCATGTTTCCAAAGTGCATGAT 24
```

Db 33 TCATGAATTAAATTCATGAT 12
||||| | : ||| | |||||

RESULT 27
US-08-584-040-5610/c
; Sequence 5610, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5610:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-5610

Query Match 55.8%; Score 13.4; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCAAAGTGCAT 21
Db 16 GTTTCCAAAGAGCAT 2
||||| | : ||| | |||||

RESULT 28
US-08-584-040-5611/c
; Sequence 5611, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-5611

Query Match 55.8%; Score 13.4; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCAAAGTGCAT 21
Db 15 GTTTCCAAAGAGCAT 1
||||| | : ||| | |||||

RESULT 29
US-09-371-772B-2500/c
; Sequence 2500, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2500
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2500

Query Match 55.8%; Score 13.4; DB 4; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCTCAAGTGCAT 21
|||||
Db 16 GTTTCCTCAAGAGCAT 2

RESULT 30

US-09-371-772B-2501/c
; Sequence 2501, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2501
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2501

Query Match 55.8%; Score 13.4; DB 4; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCTCAAGTGCAT 21
|||||
Db 15 GTTTCCTCAAGAGCAT 1

RESULT 31

US-09-685-664B-2500/c
; Sequence 2500, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10

; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2500
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2500

Query Match 55.8%; Score 13.4; DB 4; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCTCAAGTGCAT 21
|||||
Db 16 GTTTCCTCAAGAGCAT 2

RESULT 32

US-09-685-664B-2501/c
; Sequence 2501, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2501
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2501

Query Match 55.8%; Score 13.4; DB 4; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCTCAAGTGCAT 21
|||||
Db 15 GTTTCCTCAAGAGCAT 1

RESULT 33

US-07-768-437-10
; Sequence 10, Application US/07768437
; Patent No. 5371009
; GENERAL INFORMATION:
; APPLICANT: NEUBERGER, MICHAEL S.
; APPLICANT: MEYER, KERSTIN B.
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO ENHANCERS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON, D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/768,437
FILING DATE: 19910925
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 92374/HCM/JNF/C6734M
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-768-437-10

Query Match 55.8%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAG 16
Db 3 TTCAAGTTTCCAAAG 17
|||||

RESULT 34
US-09-396-196G-30572/c
Sequence 30572, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30572
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-30572

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 5.6e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTCATGAT 24
Db 25 TGCCTTCTTCCAAAGTCATGAT 3
|||||

RESULT 35
US-09-396-196G-33631/c
Sequence 33631, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33631
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-33631

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TCCAAAGTGCATGAT 24
Db 18 TCCAAAGTGCATCAT 4
|||||

RESULT 36
US-09-396-196G-33632/c
Sequence 33632, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33632
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-33632

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TCCAAAGTGCATGAT 24
Db 15 TCCAAAGTGCATCAT 1
|||||

RESULT 37
US-09-396-196G-45409
Sequence 45409, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45409

; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-45409

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAA 15
Db 11 CTTTCATGTTTACAAA 25

RESULT 38
US-09-396-196G-45410
; Sequence 45410, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45410
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-45410

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAA 15
Db 5 CTTTCATGTTTACAAA 19

RESULT 39
US-09-396-196G-70209/c
; Sequence 70209, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70209
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-70209

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 5.6e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATGA 23
Db 24 CTTTCATGTTTATAAAGAACATGA 2

RESULT 40
US-09-422-978-3015/c
; Sequence 3015, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3015
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-21687-313 : polymorphic base G or A
US-09-422-978-3015

Query Match 55.8%; Score 13.4; DB 4; Length 47;
Best Local Similarity 73.9%; Pred. No. 6.2e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATGA 23
Db 23 CTTTCATCTTTCACAGACTAAGA 1

Search completed: November 18, 2005, 11:21:59
Job time : 47.6312 Secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 322.586 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-4

Perfect score: 24

Sequence: 1 CTTTCATGTTTCCAAAGTCATGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:**

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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:

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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:

13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:

14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:

15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:

16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:

17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:

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19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:

20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:

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23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:

24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:

25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:

26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:

27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	8	US-08-469-172-4
2	24	100.0	24	20	US-10-788-779-4
3	18.2	75.8	25	22	US-10-956-157-125280
4	16.8	70.0	25	26	US-11-036-317-256437
5	15.8	65.8	25	24	US-10-719-956-403636

6	15.8	65.8	25	26	US-11-036-317-363552	Sequence 363552,
7	15.8	65.8	25	26	US-11-036-317-478233	Sequence 478233,
8	15.8	65.8	25	26	US-11-060-756-27538	Sequence 27538, A
9	15.8	65.8	25	26	US-11-060-756-27539	Sequence 27539, A
10	15.8	65.8	25	26	US-11-060-756-27549	Sequence 27549, A
11	15.8	65.8	25	26	US-11-060-756-170463	Sequence 170463,
12	15.8	65.8	25	26	US-11-060-756-180820	Sequence 180820,
13	15.6	65.0	25	22	US-10-719-900-394513	Sequence 394513,
14	15.6	65.0	25	22	US-10-809-189-53744	Sequence 53744, A
15	15.6	65.0	25	22	US-10-719-956-219368	Sequence 219368,
16	15.6	65.0	25	26	US-11-036-317-606061	Sequence 606061,
17	15.4	64.2	48	24	US-10-973-783-180	Sequence 180, Appl
18	15.2	63.3	25	21	US-10-882-761-37	Sequence 37, Appl
19	15.2	63.3	25	22	US-10-719-900-199176	Sequence 199176,
20	15.2	63.3	25	22	US-10-719-900-413418	Sequence 413418,
21	15.2	63.3	25	22	US-10-956-157-132433	Sequence 132433,
22	15.2	63.3	25	24	US-10-843-527-50302	Sequence 50302, A
23	15.2	63.3	25	24	US-10-843-527-51276	Sequence 51276, A
24	15.2	63.3	25	24	US-10-843-527-51277	Sequence 51277, A
25	15.2	63.3	25	24	US-10-843-527-185436	Sequence 185436,
26	15.2	63.3	25	24	US-10-843-527-185437	Sequence 185437,
27	15.2	63.3	25	24	US-10-843-527-186411	Sequence 186411,
28	15.2	63.3	25	26	US-11-036-317-81554	Sequence 81554, A
29	15.2	63.3	25	26	US-11-036-317-472576	Sequence 472576,
30	15.2	63.3	25	26	US-11-036-317-472576	Sequence 472576,
31	15.2	63.3	25	26	US-11-036-317-551468	Sequence 551468,
32	15.2	63.3	25	26	US-11-036-317-771700	Sequence 771700,
33	15	62.5	25	22	US-10-719-900-247281	Sequence 247281,
34	15	62.5	25	24	US-10-681-773-115420	Sequence 115420,
35	15	62.5	25	24	US-10-681-773-120711	Sequence 120711,
36	15	62.5	25	26	US-11-036-317-989895	Sequence 989895,
37	14.8	61.7	20	20	US-10-316-244-31	Sequence 31, Appl
38	14.8	61.7	20	20	US-10-316-244-136	Sequence 136, Appl
39	14.8	61.7	25	22	US-10-719-900-48069	Sequence 48069, A
40	14.8	61.7	25	22	US-10-719-900-262242	Sequence 262242,
41	14.8	61.7	25	22	US-10-719-900-827966	Sequence 827966,
42	14.8	61.7	25	22	US-10-719-900-838178	Sequence 838178,
43	14.8	61.7	25	22	US-10-809-189-211176	Sequence 211176, A
44	14.8	61.7	25	22	US-10-809-189-211177	Sequence 211177, A
45	14.8	61.7	25	22	US-10-809-189-211178	Sequence 211178, A

ALIGNMENTS

RESULT 1
US-08-469-172-4
; Sequence 4, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-469-172-4

Query Match 100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. NO. 0.32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCATGTTTCCAAAGTGCATGAT 24
Db 1 CTTCATGTTTCCAAAGTGCATGAT 24

RESULT 2
US-10-788-779-4
; Sequence 4, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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RESULT 5
US-10-719-956-403636
; Sequence 403636, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403636
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-403636
Query Match      65.8%; Score 15.8; DB 24; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCAT 21
||||| |||||||
Db 5 TCATGTTACCAAGTGCCT 23

RESULT 6
US-11-036-317-363552
; Sequence 363552, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 363552
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-363552
Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCAT 21
||||| |||||||
Db 7 TCATGTTACCGAAGTGCAT 25

RESULT 7
US-11-036-317-478233
; Sequence 478233, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 478233
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-478233
Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCCAAAGTGCATGAT 24
||||| |||||||
Db 3 TGTGTCCTCCAAAGTGCATGTT 21

RESULT 8
US-11-060-756-27538
; Sequence 27538, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27538
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-27538
Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCCAAAGTGCATGAT 24
||||| |||||||
Db 6 TGTTCCTCCAAAGTGCATGAT 24

RESULT 9
US-11-060-756-27539
; Sequence 27539, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27539
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-27539
Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCCAAAGTGCATGAT 24
||||| |||||||
Db 7 TGTTCCTCCAAAGTGCATGAT 25
```

```
RESULT 10
US-11-060-756-27549
; Sequence 27549, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-27549

Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 TGTTCCTCCAAAGTCATGAT 24
      ||||| ||||| ||||| |||||
Db      5 TGTTCCTCCAAAGTCATGAT 23

RESULT 11
US-11-060-756-170463
; Sequence 170463, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170463
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-170463

Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 TGTTCCTCCAAAGTCATGAT 24
      ||||| ||||| ||||| |||||
Db      5 TGTTCCTCCAAAGTCATGAT 23

RESULT 12
US-11-060-756-180820
; Sequence 180820, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180820
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-180820

Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 TGTTCCTCCAAAGTCATGAT 24
      ||||| ||||| ||||| |||||
Db      7 TGTTCCTCCAAAGTCATGAT 25
```

```
RESULT 13
US-10-719-900-394513
; Sequence 394513, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 394513
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-394513

Query Match      65.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CTTTCATGTTTCCAAAGTCATG 22
      ||||| ||||| ||||| |||||
Db      1 CTTTCATGTTTTCATTTGTGCAAG 22

RESULT 14
US-10-809-189-53744/c
; Sequence 53744, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53744
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-53744

Query Match      65.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 2 TTTCATGTTTCCAAAGTGCATGA 23
|||||
Db 25 TTCAACTTCCCAAGTGCATCA 4

RESULT 15

US-10-719-956-219368/c
; Sequence 219368, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-219368

Query Match 65.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATG 22
|||||
Db 22 CTGCTGTGTCCAAAGTGCCTTG 1

RESULT 16

US-11-036-317-606061/c
; Sequence 606061, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 606061
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-606061

Query Match 65.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATG 22
|||||
Db 24 CTTTCATCTGTACAAAGTGCCTTG 3

RESULT 17

US-10-973-783-180
; Sequence 180, Application US/10973783
; Publication No. US20050164246A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Bibikova, Marina
; TITLE OF INVENTION: Methods and Compositions For Diagnosing
; TITLE OF INVENTION: Lung Cancer with Specific DNA Methylation Patterns

; FILE REFERENCE: 67234-100
; CURRENT APPLICATION NUMBER: US/10/973,783
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: US 10/845,667
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/471,488
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 1513
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-973-783-180

Query Match 64.2%; Score 15.4; DB 24; Length 48;
Best Local Similarity 94.1%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGC 19
|||||
Db 5 TCAIGTTTCCAAAGTCC 21

RESULT 18

US-10-882-761-37/c
; Sequence 37, Application US/10882761
; Publication No. US20040265890A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
; TITLE OF INVENTION: PREDOMINATELY IN SMALL INTESTINE, HLRRS11
; FILE REFERENCE: D0066DIV
; CURRENT APPLICATION NUMBER: US/10/882,761
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US 10/029,347
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 25
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthesized oligonucleotide.
US-10-882-761-37

Query Match 63.3%; Score 15.2; DB 21; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGC 20
|||||
Db 23 CTTGCTGCTCCAAAGTGC 4

RESULT 19

US-10-719-900-199176/c
; Sequence 199176, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 199176
; LENGTH: 25
; TYPE: DNA

```

; ORGANISM: Mus musculus
US-10-719-900-199176

Query Match      63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TCATGTTTCCAAAGTGCATG 22
   ||||| ||||| ||||| ||
Db 24 TAATGTTTACAAAGTGCCTG 5
   ||||| ||||| ||||| ||

RESULT 20
US-10-719-900-413418/c
; Sequence 413418, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 413418
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-413418

Query Match      63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ATGTTTCCAAAGTGCATGAT 24
   ||| ||||| ||||| |||
Db 21 ATGCTTCCAAAGTCTTGTT 2
   ||||| ||||| ||||| ||

RESULT 21
US-10-956-157-132433
; Sequence 132433, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132433
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-132433

Query Match      63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ATGTTTCCAAAGTGCATGAT 24
   ||||| ||||| ||||| ||
Db 1 ATGTTTCCAAATGTACCTGAT 20
   ||||| ||||| ||||| ||

RESULT 22
US-10-843-527-50302/c
; Sequence 50302, Application US/10843527

```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-51277

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CTTTCATGTTTCCAAAGTGCA 20
         ||||| ||||| ||||| |||||
Db      23  CTTTCATGTTTCCAAAGTGAA 4

RESULT 25
US-10-843-527-185436
; Sequence 185436, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 185436
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-185436

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CTTTCATGTTTCCAAAGTGCA 20
         ||||| ||||| ||||| |||||
Db      3  CTTTCATGTTTCCAAAGTGAA 22

RESULT 26
US-10-843-527-185437
; Sequence 185437, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 185437
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-185437

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CTTTCATGTTTCCAAAGTGCA 20
         ||||| ||||| ||||| |||||
Db      2  CTTTCATGTTTCCAAAGTGAA 21

RESULT 27
US-10-843-527-186411
; Sequence 186411, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 186411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-186411

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CTTTCATGTTTCCAAAGTGCA 20
         ||||| ||||| ||||| |||||
Db      4  CTTTCATGTTTATTAAGTGAA 23

RESULT 28
US-11-036-317-81554/c
; Sequence 81554, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-81554

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  TCATGTTTCCAAAGTGCA 22
         ||||| ||||| ||||| |||||
Db      20  TCAGTTTCCAAAGCGTTG 1

RESULT 29
US-11-036-317-147524/c
; Sequence 147524, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
```

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; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 147524
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-147524

```

Query Match 63.3%; Score 15.2; DB 26;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels

Qy 1 CTTTCATGTTTCCAAAGTGCA 20
|||
Db 20 CTTTCAGGTTTCCCAAGTCCA 1

```

RESULT 30
US-11-036-317-472576/c
, Sequence 472576, Application US/11036317
, Publication No. US20050214823A1
GENERAL INFORMATION:
, APPLICANT: Williams, Alan
, APPLICANT: Blume, John
, TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
, FILE REFERENCE: 3654.1
, CURRENT APPLICATION NUMBER: US/11/036,317
, CURRENT FILING DATE: 2005-01-13
, PRIOR APPLICATION NUMBER: US 60/536,639
, PRIOR FILING DATE: 2004-01-13
, NUMBER OF SEQ ID NOS: 991174
, SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
, SEQ ID NO 472576
, LENGTH: 25
, TYPE: DNA
, ORGANISM: Mus musculus
US-11-036-317-472576

```

```
Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 CTTCATGTTTCCAAAGTGCA 20
|||
Db 20 CTTCATGTTTCCAAAGTGGA 1

```

RESULT 31
US-11-036-317-551468/c
; Sequence 551468, Application US/11036317
; Publication No. US20050214823A1
GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 551468
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-551468

```

```
Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

Qy      3  TCATGTTTCAAAGTGCATG  22
      ||| ||| ||| ||| ||| |||
Db      20  TCAGGTTTCCAAAGCGCTG  1

```

```

/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 771700
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
/
US-11-036-317-771700

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Query Match	62.5%	Score 15	DB 22	Length 25
Best Local Similarity	78.3%	Pred. No. 5.5e+03		
Matches 18	Conservative	0	Mismatches 5	Indels 0
			Gaps	0

Qy 1 CTTCATGTTTCCAAAGTCATGA 23
||| ||| ||| ||| ||| ||| ||| |||
Db 3 CTACATGGTTCAAAAGTCCGTA 25

RESULT 34
US-10-681-773-115420/c
; Sequence 115420, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia

```
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 115420
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-115420
```

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Query Match 62.5%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 CTTTCATGTTTCCAAAGTGCATCA 23
Db 24 CTTTCATGTTTCCAGAGTGACGA 2
```

```
RESULT 35
US-10-681-773-120711/c
; Sequence 120711, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 120711
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-120711
```

```
Query Match 62.5%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 CTTTCATGTTTCCAAAGTGCATCA 23
Db 25 CTTTCATGTTTCCAGAGTGACGA 3
```

```
RESULT 36
US-11-036-317-989895
; Sequence 989895, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 989895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-989895
```

```
Query Match 62.5%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 2 TTCATGTTTCCAAAGTGCATCAT 24
Db 2 TTCATCCTTCAGAAAGTACATCAT 24
```

```
RESULT 37
US-10-316-244-31
; Sequence 31, Application US/10316244
; Publication No. US20040110148A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF ORNITHINE DECARBOXYLASE 1 EXPRESSION
; FILE REFERENCE: HTS-0096
; CURRENT APPLICATION NUMBER: US/10/316,244
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 219
; SEQ ID NO: 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-316-244-31
```

```
Query Match 61.7%; Score 14.8; DB 20; Length 20;
Best Local Similarity 88.9%; Pred. No. 6.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 CATGTTTCCAAAGTGCAT 21
Db 1 CATGTTTCCAAAGAGCAT 18
```

```
RESULT 38
US-10-316-244-136/c
; Sequence 136, Application US/10316244
; Publication No. US20040110148A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF ORNITHINE DECARBOXYLASE 1 EXPRESSION
; FILE REFERENCE: HTS-0096
; CURRENT APPLICATION NUMBER: US/10/316,244
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 219
; SEQ ID NO: 136
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-316-244-136
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```
Query Match 61.7%; Score 14.8; DB 20; Length 20;
Best Local Similarity 88.9%; Pred. No. 6.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 CATGTTTCCAAAGTGCAT 21
Db 20 CATGTTTCCAAAGAGCAT 3
```

```

RESULT 39
US-10-719-900-48069
; Sequence 48069, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48069
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-48069

```

```

Query Match      61.7%; Score 14.8; DB 22; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      7 GTTTCCAAAGTGCATGAT 24
        ||||| ||||| |||||
Db      7 GTTTCAGAGTGCATGAT 24

```

```

RESULT 40
US-10-719-900-262242
; Sequence 262242, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 262242
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-262242

```

```

Query Match      61.7%; Score 14.8; DB 22; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 CTTTCATGTTTCCAAAGTG 18
        ||||| ||||| |||||
Db      4 CTTTCATGTTTCTGAGTG 21

```

Search completed: November 18, 2005, 15:41:05
Job time : 323.586 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 693.631 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-5
Perfect score: 25
Sequence: 1 CTGGGCTTCACTTCAGAGGAGAAAA 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	I12898 Sequence 5
2	14.6	58.4	21	6	E25007 Oligonucleo
3	14.4	57.6	30	6	A19073 oligonucleo
4	14.4	57.6	30	6	AR059408 Sequence
5	14.4	57.6	30	6	ARI78489 Sequence
6	14.4	57.6	37	6	CQ826719 Sequence
7	14.4	57.6	37	6	CQ826720 Sequence
8	14.2	56.8	47	6	A94788 Sequence 32
9	14	56.0	29	6	BD258702 Regulation
10	14	56.0	30	6	AX406739 Sequence
11	14	56.0	40	6	BD180726 Array of
12	14	56.0	49	6	AR098688 Sequence
13	14	56.0	49	6	AR098689 Sequence
14	14	56.0	49	6	AR098690 Sequence
15	14	56.0	49	6	AR098692 Sequence
16	14	56.0	49	6	AR204762 Sequence
17	14	56.0	49	6	AR204763 Sequence
18	14	56.0	49	6	AR204764 Sequence
19	14	56.0	49	6	AR204766 Sequence

20	14	56.0	50	6	CQ008790	Sequence
21	13.8	55.2	29	6	BD138865	Secreted
22	13.8	55.2	38	6	AX573495	Sequence
23	13.8	55.2	48	6	BD081415	Fused pro
24	13.8	55.2	50	6	ARI07707	Sequence
25	13.6	54.4	25	6	ARI53673	Sequence
26	13.6	54.4	25	6	CQ862312	Sequence
27	13.6	54.4	29	6	BD197942	Method an
28	13.6	54.4	31	6	AX801708	Sequence
29	13.6	54.4	33	6	CQ867997	Sequence
30	13.6	54.4	36	6	AR366334	Sequence
31	13.6	54.4	36	6	AX030985	Sequence
32	13.6	54.4	42	6	AX767197	Sequence
33	13.6	54.4	50	6	AX157872	Sequence
34	13.4	53.6	19	6	AX671483	Sequence
35	13.4	53.6	19	6	AX675004	Sequence
36	13.4	53.6	25	6	AX043509	Sequence
37	13.4	53.6	27	6	AX817756	Sequence
38	13.4	53.6	30	6	AX115007	Sequence
39	13.4	53.6	36	6	AX026972	Sequence
40	13.4	53.6	36	6	AX035992	Sequence
41	13.4	53.6	36	6	AX093461	Sequence
42	13.4	53.6	38	6	BD137046	Method of
43	13.4	53.6	38	6	AX080051	Sequence
44	13.4	53.6	42	6	ARI03109	Sequence
45	13.4	53.6	42	6	ARI39725	Sequence

ALIGNMENTS

RESULT 1
LOCUS I12898 25 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 5 from patent US 5429923.
ACCESSION I12898
VERSION I12898.1 GI:910875
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 5 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACTTCAGAGGAGAAAA 25
Db 1 CTGGGCTTCACTTCAGAGGAGAAAA 25
RESULT 2
LOCUS E25007 21 bp DNA linear PAT 18-JUN-2001
DEFINITION Oligonucleotide probe species-specific to bacterium of Bacteroides group.
ACCESSION E25007
VERSION E25007.1 GI:13024705
KEYWORDS JP 1999127899-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 21)

AUTHORS Yukiko, T. and Kikui, I.
 TITLE Oligonucleotide probe species-specific to bacterium of Bacteroides
 JOURNAL Patent: JP 199127899-A 7 18-MAY-1999;
 YAKULT BIOSCIENCE KENKYU ZAIDAN
 COMMENT OS Unidentified
 PN JP 199127899-A/7
 PD 18-MAY-1999
 PF 29-OCT-1997 JP 1997297085
 PR YUKIKO TOMA, KIKUI ITO
 PC C12Q1/68, C12N15/09/(C12Q1/68, C12R1:01), (C12N15/09, C12R1:01),
 PC C12N15/00,
 PC (C12N15/00, C12R1:01)
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..21 /organism='Unidentified'.
 FT Location/Qualifiers
 FT 1..21 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'
 ORIGIN
 Query Match 58.4%; Score 14.6; DB 6; Length 21;
 Best Local Similarity 81.0%; Pred. No. 4.2e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 CTGGGCTTCACTTCAGAGGAG 21
 ||||| ||||| ||||| ||||| |||||
 Db 21 CCGGGCTTGACTTCAGTGGCG 1
 RESULT 3
 A19073
 LOCUS A19073 oligonucleotide. 30 bp RNA linear PAT 26-APR-1994
 DEFINITION A19073
 ACCESSION A19073
 VERSION A19073.1 GI:513993
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Little, M., Breitling, F.B., Seehaus, T., Duebel, S. and Klewinghaus, I.
 TITLE Preparation and use of a human antibody gene bank (human antibody libraries)
 JOURNAL Patent: EP 0440147-A 19 07-AUG-1991;
 BEHRINGERWERKE Aktiengesellschaft
 FEATURES source 1..30
 Location/Qualifiers
 1..30 /organism='unidentified'
 /mol_type='unassigned RNA'
 /db_xref='taxon:32644'
 ORIGIN
 Query Match 57.6%; Score 14.4; DB 6; Length 30;
 Best Local Similarity 75.0%; Pred. No. 5.3e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CTGGGCTTCACTTCAGAGGAGAA 24
 ||||| ||||| ||||| ||||| |||||
 Db 7 CTTGAATTCATTAAAGAGGAGAA 30
 RESULT 4
 AR059408
 LOCUS AR059408 Sequence 28 from patent US 5840479. 30 bp DNA linear PAT 29-SEP-1999
 DEFINITION AR059408
 ACCESSION AR059408
 VERSION AR059408.1 GI:598588
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Little, M., Breitling, F.Berthold., Seehaus, T., Dubel, S. and Klewinghaus, I.
 TITLE Preparation and use of gene banks of synthetic human antibodies ('synthetic human-antibody libraries')
 JOURNAL Patent: US 5840479-A 28 24-NOV-1998;
 FEATURES source 1..30
 Location/Qualifiers
 1..30 /organism='unknown'
 /mol_type='unassigned DNA'
 ORIGIN
 Query Match 57.6%; Score 14.4; DB 6; Length 30;
 Best Local Similarity 75.0%; Pred. No. 5.3e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CTGGGCTTCACTTCAGAGGAGAA 24
 ||||| ||||| ||||| ||||| |||||
 Db 7 CTTGAATTCATTAAAGAGGAGAA 30
 RESULT 5
 AR178489
 LOCUS AR178489 Sequence 19 from patent US 6319690. 30 bp DNA linear PAT 20-APR-2002
 DEFINITION AR178489
 ACCESSION AR178489
 VERSION AR178489.1 GI:20219627
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Little, M., Breitling, F.Berthold., Seehaus, T., Dubel, S. and Klewinghaus, I.
 TITLE Preparation and use of gene banks of human antibodies ('human-antibody libraries')
 JOURNAL Patent: US 6319690-A 19 20-NOV-2001;
 FEATURES source 1..30
 Location/Qualifiers
 1..30 /organism='unknown'
 /mol_type='unassigned DNA'
 ORIGIN
 Query Match 57.6%; Score 14.4; DB 6; Length 30;
 Best Local Similarity 75.0%; Pred. No. 5.3e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CTGGGCTTCACTTCAGAGGAGAA 24
 ||||| ||||| ||||| ||||| |||||
 Db 7 CTTGAATTCATTAAAGAGGAGAA 30
 RESULT 6
 CQ826719
 LOCUS CQ826719 Sequence 22 from Patent EP1431387. 37 bp DNA linear PAT 29-JUN-2004
 DEFINITION CQ826719
 ACCESSION CQ826719
 VERSION CQ826719.1 GI:49455447
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Mueller, R., Kirschbaum, T., Suppmann, B., Schoen, H., Engh, R., Hoffmann, A., Thalhofer, J.P., Siedel, J. and Engel, W.D.
 TITLE Heat-labile desoxyribonuclease I variants
 JOURNAL Patent: EP 1431387-A 22 23-JUN-2004;
 Roche Diagnostics GmbH (DE); F. HOFFMANN-LA ROCHE AG (CH)
 FEATURES source 1..37
 Location/Qualifiers

Query Match 56.8%; Score 14.2; DB 6;
Best Local Similarity 84.2%; Pred. No. 6.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels

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ORIGIN
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

Query Match      56.0%; Score 14; DB 6; Length 30;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GGCCTCACTTCAGAGGAGAAA 25
    ||| ||||| ||||| |||
Db 29 GACTCCACTTCAGAGCGAGAA 8

RESULT 11
BD180726/c
LOCUS BD180726 40 bp DNA linear PAT 15-MAY-2003
DEFINITION Array of nucleic acid.
ACCESSION BD180726
VERSION BD180726.1 GI:30791644
KEYWORDS JP 2002330767-A/18.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mineno,J., Rokushima,M., Sotozono,N., Asada,K. and Kato,I.
TITLE Array of nucleic acid
JOURNAL Takara Bio Inc
COMMENT Patent: JP 2002330767-A 18 19-NOV-2002;
OS Artificial Sequence
PN JP 2002330767-A/18
PD 19-NOV-2002
PF 11-MAY-2001 JP 2001142082
PI JUNICHI MINENO,MASATOMO ROKUSHIMA,NARIKAZU SOTOZONO,KIYOZO
PI ASADA,
PI IKUNOSHIN KATO
PC C12N15/09,C12M1/00,C12O1/68,G01N33/53,G01N37/00,C12N15/00 CC
Designed oligonucleotide probe for detecting in vitro CC
transcribed RNA of
CC lamda DNA fragment 1
FH Key Location/Qualifiers
FT source 1..40
FT Location/Qualifiers
FEATURES
source 1..40
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      56.0%; Score 14; DB 6; Length 40;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGGCTTCACTTCAGAGGAGA 22
    ||| ||| ||| ||| |||
Db 39 CTGGCAATCGCATCAAGGAGA 18

RESULT 12
AR098688/c
LOCUS AR098688 49 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 46 from patent US 6077668.
ACCESSION AR098688
VERSION AR098688.1 GI:12808454
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 46 20-JUN-2000;
FEATURES Location/Qualifiers

ORIGIN
/mol_type="unassigned DNA"

Query Match      56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGCCTTCACTTCAGAGGAGAAA 24
    ||||| || ||||| ||||
Db 43 GGCCTTTTCTGAAGAGCGGAAA 22

RESULT 13
AR098689
LOCUS AR098689 49 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 47 from patent US 6077668.
ACCESSION AR098689
VERSION AR098689.1 GI:12808455
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 47 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGCCTTCACTTCAGAGGAGAAA 24
    ||||| || ||||| ||||
Db 3 GGCCTTTTCTGAAGAGCGGAAA 24

RESULT 14
AR098690
LOCUS AR098690 49 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 48 from patent US 6077668.
ACCESSION AR098690
VERSION AR098690.1 GI:12808456
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 48 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGCCTTCACTTCAGAGGAGAAA 24
    ||||| || ||||| ||||
Db 11 GGCCTTTTCTGAAGAGCGGAAA 32

RESULT 15
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source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGCCTTCACTTCAGAGGAGAAA 24
    ||||| || ||||| ||||
Db 43 GGCCTTTTCTGAAGAGCGGAAA 22
```

```
RESULT 13
AR098689
LOCUS AR098689 49 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 47 from patent US 6077668.
ACCESSION AR098689
VERSION AR098689.1 GI:12808455
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 47 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGCCTTCACTTCAGAGGAGAAA 24
    ||||| || ||||| ||||
Db 3 GGCCTTTTCTGAAGAGCGGAAA 24
```

```
RESULT 14
AR098690
LOCUS AR098690 49 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 48 from patent US 6077668.
ACCESSION AR098690
VERSION AR098690.1 GI:12808456
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 48 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGCCTTCACTTCAGAGGAGAAA 24
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Db 11 GGCCTTTTCTGAAGAGCGGAAA 32
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RESULT 15
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AR098692
LOCUS AR098692 49 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 50 from patent US 6077668.
ACCESSION AR098692
VERSION AR098692.1 GI:12808458
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 50 20-JUN-2000;
FEATURES
    Location/Qualifiers
        source
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ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
    ||||| || ||||| |||||
Db 11 GGGCTTTTCTGAAGAGCGGAAA 32

RESULT 16
AR204762/c
LOCUS AR204762 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 46 from patent US 6368802.
ACCESSION AR204762
VERSION AR204762.1 GI:21502171
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 46 09-APR-2002;
FEATURES
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                /mol_type="unassigned DNA"
ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
    ||||| || ||||| |||||
Db 11 GGGCTTTTCTGAAGAGCGGAAA 32

RESULT 17
AR204763
LOCUS AR204763 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 47 from patent US 6368802.
ACCESSION AR204763
VERSION AR204763.1 GI:21502172
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 47 09-APR-2002;
FEATURES
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                /mol_type="unassigned DNA"
ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
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Db 43 GGGCTTTTCTGAAGAGCGGAAA 22

RESULT 18
AR204764
LOCUS AR204764 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 48 from patent US 6368802.
ACCESSION AR204764
VERSION AR204764.1 GI:21502174
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 48 09-APR-2002;
FEATURES
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        source
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                /mol_type="unassigned DNA"
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Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
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Db 3 GGGCTTTTCTGAAGAGCGGAAA 24

RESULT 19
AR204766
LOCUS AR204766 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 50 from patent US 6368802.
ACCESSION AR204766
VERSION AR204766.1 GI:21502176
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 50 09-APR-2002;
FEATURES
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        source
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Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
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Db 11 GGGCTTTTCTGAAGAGCGGAAA 32

RESULT 20
CQ008790
LOCUS CQ008790 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 49 from patent US 6368802.
ACCESSION CQ008790
VERSION CQ008790.1 GI:12808459
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 49 09-APR-2002;
FEATURES
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        source
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                /mol_type="unassigned DNA"
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Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
    ||||| || ||||| |||||
Db 11 GGGCTTTTCTGAAGAGCGGAAA 32
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LOCUS	CQ008790	50 bp	DNA	linear	PAT 16-JAN-2004
DEFINITION	Sequence 7430 from Patent WO0147944.				
ACCESSION	CQ008790				
VERSION	CQ008790.1	GI:41015507			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Shimkets, R.A. and Leach, M.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
JOURNAL	Patent: WO 0147944-A 7430 05-JUL-2001;				
	Curagen Corporation (US)				
FEATURES	Location/Qualifiers				
source	1..50				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
misc_feature	25..26				
	/note="Nucleotide deleted between bases 25 and 26				
	Accession number CG43994815"				
ORIGIN					
Query Match	56.0%;	Score 14;	DB 6;	Length 50;	
Best Local Similarity	77.3%;	Pred. No. 8.5e+04;			
Matches	17;	Conservative	0;	Mismatches	5;
				Indels	0;
				Gaps	0;
Qy	3	GGGCTTCACCTCAGAGGAGAA	24		
Db	18	GAGCTTCACACAGGGGACA	39		
RESULT 21					
BD138865/c					
LOCUS	BD138865	29 bp	DNA	linear	PAT 18-SEP-2002
DEFINITION	Secreted proteins and polynucleotides encoding them.				
ACCESSION	BD138865				
VERSION	BD138865.1	GI:23233810			
KEYWORDS	JP 2002505074-A/10.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 29)				
AUTHORS	Jacobs, D., Mccoy, J.M., Lavallie, E.R., Racie, L.A.C., Evans, C., Merberg, K., Treacy, M. and Spaulding, V.				
TITLE	Secreted proteins and polynucleotides encoding them				
JOURNAL	Patent: JP 2002505074-A 10 19-FEB-2002;				
	GENETICS INSTITUTE INC				
COMMENT	OS Artificial Sequence				
	PN JP 2002505074-A/10				
	PD 19-FEB-2002				
	PF 20-NOV-1998				
	PR 21-NOV-1997 US 08/975936, 26-OCT-1998 US 09/179034 PI				
	KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A COLLINS PI				
	RACIE,				
	PI CHERYL EVANS, DAVID MERBERG, MAURICE TREACY, VIKKI SPAULDING PC				
	C12N15/09, C07K14/47, C12N5/10, C12N15/00, C12N5/00 CC				
	oligonucleotide				
	CC biotinylated phosphoramidite residue				
FH	Key	Location/Qualifiers			
FT	misc_feature (2):				
	Location/Qualifiers				
source	1..29				
	/organism="synthetic construct"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:32630"				
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Best Local Similarity	88.2%;	Pred. No. 1.1e+05;			
Matches	15;	Conservative	0;	Mismatches	2;
				Indels	0;
				Gaps	0;

[illegible]

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FEATURES
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        /mol_type="genomic RNA"
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  Best Local Similarity
    76.2%; Pred. No. 1.4e+05;
  Matches
    16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy
  4 GGCTTCACCTTCAGAGAGAAA 24
  |||||
  2 GGCTTCACCTGATGAGCGAAA 22
  |||||
RESULT 28
AX801708/c
LOCUS
  AX801708 31 bp DNA linear PAT 24-NOV-2003
DEFINITION
  Sequence 7 from Patent WO03057730.
ACCESSION
  AX801708
VERSION
  AX801708.1 GI:38500660
KEYWORDS
  .
SOURCE
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
  AUTHORS
    le Poul,E., Dethieux,M., Brezillon,S., Lannoy,V. and Parmentier,M.
  TITLE
    Ligand for G-protein coupled receptor gpr43 and uses thereof
  JOURNAL
    Patent: WO 03057730-A 7 17-JUL-2003;
    Euroscreen S.A. (BE)
FEATURES
  source
    Location/Qualifiers
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        /db_xref="taxon:32630"
        /note="Oligonucleotide"
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  Matches
    16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy
  4 GGCTTCACCTTCAGAGAGAA 23
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  31 GACTTCACACAGAGTAGCA 12
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RESULT 29
CQ867997
LOCUS
  CQ867997 33 bp DNA linear PAT 13-SEP-2004
DEFINITION
  Sequence 214 from Patent WO2004074318.
ACCESSION
  CQ867997
VERSION
  CQ867997.1 GI:51998049
KEYWORDS
  .
SOURCE
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
  AUTHORS
    Dautry-Varsat,A. and Subtil-Sands,A.
  TITLE
    Secreted chlamydia polypeptides, polynucleotides coding
    therefor,therapeutic and diagnostic uses thereof
  JOURNAL
    Patent: WO 2004074318-A 214 02-SEP-2004;
    INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
    (CNRS) (FR)
FEATURES
  source
    Location/Qualifiers
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        /db_xref="taxon:32630"
        /note="Synthetic DNA"
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  34 CGGCGTTTCACCTTCAGGA 15
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RESULT 30
AR366334/c
LOCUS
  AR366334 36 bp mRNA linear PAT 12-SEP-2003
DEFINITION
  Sequence 5 from patent US 6329160.
ACCESSION
  AR366334
VERSION
  AR366334.1 GI:34598751
KEYWORDS
  .
SOURCE
  Unknown.
  ORGANISM
    Unclassified.
REFERENCE
  1 (bases 1 to 36)
  AUTHORS
    Schneider,R., Vancov,T. and Jury,K.
  TITLE
    Biosensors
  JOURNAL
    Patent: US 6329160-A 5 11-DEC-2001;
  FEATURES
    Location/Qualifiers
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  34 CGGCGTTTCACCTTCAGGA 15
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RESULT 31
AX030985/c
LOCUS
  AX030985 36 bp DNA linear PAT 20-SEP-2000
DEFINITION
  Sequence 5 from Patent WO9804716.
ACCESSION
  AX030985
VERSION
  AX030985.1 GI:10278382
KEYWORDS
  .
SOURCE
  unidentified
  ORGANISM
    unidentified
    unclassified.
REFERENCE
  1
  AUTHORS
    Vancov,T., Schneider,R. and Jury,K.
  TITLE
    Biosensors
  JOURNAL
    Patent: WO 9804716-A 5 05-FEB-1998;
    VANCOV TONY (AU); SCHNEIDER RENE (AU); CRC WASTE MAN & POLL CONTR
    LTD (AU); JURY KAREN (GB)
FEATURES
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        /db_xref="taxon:32644"
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  Best Local Similarity
    80.0%; Pred. No. 1.4e+05;
  Matches
    16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy
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  34 CGGCGTTTCACCTTCAGGA 15
  |||||
RESULT 32
AX767197
LOCUS
  AX767197 42 bp DNA linear PAT 25-JUN-2003
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KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Macdonald,M.L., Goldberg,Y.P. and Hayden,M.R.	
TITLE	Methods for identifying therapeutic agents for treating diseases involving wnt polypeptides and wnt receptors	
JOURNAL	Patent: WO 0304045-A 7 16-JAN-2003;	
FEATURES	Xenon Genetics, Inc. (CA) ; The University of British Columbia (CA) Location/Qualifiers	
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	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
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Best Local Similarity	93.3%; Pred. No. 1.7e+05;	
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2 TGGGCTTCACTTCAG 16	
Db		
	4 TGGGCATCACTTCAG 18	
RESULT 35		
AX675004		
LOCUS	AX675004 19 bp DNA linear PAT 27-MAR-2003	
DEFINITION	Sequence 131 from Patent WO03005034.	
ACCESSION	AX675004	
VERSION	AX675004.1 GI:293333337	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Macdonald,M.L., Zeisler,J.M., Samuels,M., Goldberg,Y.P., Robataille,J.M. and Hayden,M.R.	
TITLE	Processes for identifying therapeutic agents useful in treating diseases involving fz4 gene	
JOURNAL	Patent: WO 03005034-A 131 16-JAN-2003;	
	Xenon Genetics, Inc. (CA) ; The University of British Columbia (CA) Location/Qualifiers	
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Best Local Similarity	93.3%; Pred. No. 1.7e+05;	
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2 TGGGCTTCACTTCAG 16	
Db		
	4 TGGGCATCACTTCAG 18	
RESULT 36		
AX043509/c		
LOCUS	AX043509 25 bp DNA linear PAT 23-NOV-2000	
DEFINITION	Sequence 1075 from Patent WO0065088.	
ACCESSION	AX043509	
VERSION	AX043509.1 GI:11342117	
KEYWORDS		
SOURCE	synthetic construct	
ORGANISM	synthetic construct	
	other sequences; artificial sequences.	
REFERENCE	1	
AUTHORS	Ulfendahl,P.J. and Wong,K.C.	

Query Match 53.6%; Score 13.4; DB 6; Length 36;
Best Local Similarity 73.9%; Pred. No. 1.7e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TCGGCTTCACCTCAGAGGAGAAA 24
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Db 5 TAGAATTCATTAAAGAGGAGAAA 27

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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 172.148 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-5

Perfect score: 25

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167236

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
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- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	2	AaQ91125 Beta-card
2	25	100.0	25	9	ACA63115 Human bet
3	25	100.0	25	13	ADR05301 Human bet
4	16	64.0	41	6	ABA02364 Human nuc
5	15.4	61.6	30	12	ADH43094 CRAM prot
6	15.2	60.8	30	10	ACC58874
7	15.2	60.8	31	10	ACC58875 Doubly la
8	14.8	59.2	25	9	ACI46238 Human mic
9	14.8	59.2	33	8	ABX12624 Human zin
10	14.8	59.2	41	8	ABX12626 Human zin
11	14.8	59.2	41	8	ABX12627 Human zin
12	14.6	58.4	21	2	AAX59982 Oligonucl
13	14.6	58.4	34	12	ADQ28791 PCR prime
14	14.6	58.4	41	9	ACC42057 Human SCN
15	14.4	57.6	25	10	ABZ84436 Toxicolog
16	14.4	57.6	37	12	ADP88540 Bovine pa
17	14.4	57.6	37	12	ADP88541 Bovine pa
18	14.4	57.6	41	6	ABA02365 Human nuc
19	14.2	56.8	25	9	ACI31972 Human mic
20	14.2	56.8	25	12	ADP14058 Renal cel

c	21	14.2	56.8	25	12	ADP14057
c	22	14.2	56.8	33	2	AAT31079
c	23	14.2	56.8	39	10	ADF50502
c	24	14.2	56.8	41	6	ABZ24931
c	25	14.2	56.8	47	2	AAX78849
c	26	14.2	56.8	48	10	ADB73490
c	27	14.2	56.8	50	6	ABZ02803
c	28	14	56.0	29	3	AAF06504
c	29	14	56.0	30	6	ABA99901
c	30	14	56.0	40	10	ADH10991
c	31	14	56.0	49	2	AAV12937
c	32	14	56.0	49	2	AAV12941
c	33	14	56.0	49	2	AAV12938
c	34	14	56.0	49	2	AAV12939
c	35	14	56.0	49	2	AAV59251
c	36	14	56.0	49	2	AAV59252
c	37	14	56.0	49	2	AAV59253
c	38	14	56.0	49	2	AAV30039
c	39	14	56.0	49	10	ADC65914
c	40	14	56.0	49	10	ADC65915
c	41	14	56.0	49	10	ADC65913
c	42	14	56.0	49	10	ADC65917
c	43	14	56.0	50	4	AAL34222
c	44	13.8	55.2	24	8	ACC70890
c	45	13.8	55.2	25	9	ACI10278

ALIGNMENTS

RESULT 1

AAQ91125

ID AAQ91125 standard; cDNA; 25 BP.

XX AAQ91125;

AC AAQ91125;

DT 19-FEB-1996 (first entry)

XX Beta-cardiac myosin heavy chain PCR primer C.

DE Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;

XX diagnosis; primer; mutation; detection; ss.

KW Synthetic.

OS US5429923-A.

PN 04-JUL-1995.

XX 11-DEC-1992; 92US-00989160.

XX 11-DEC-1992; 92US-00989160.

XX (HARD) HARVARD COLLEGE.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX (GCHO-) GEN HOSPITAL SHENYANG MILITARY AREA.

XX Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX WPI; 1995-245715/32.

XX Non-invasive method for diagnosis of hypertrophic cardio-myopathy -

XX useful for testing asymptomatic individual(s).

XX Example 1; Col 10; 22pp; English.

XX AAQ91121-Q91130 are nested PCR primers used for the amplification and

XX identification of beta-cardiac myosin heavy-chain RNA. They are used in a

XX new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),

XX the method involves detecting the presence or absence of specific HC-

XX associated mutations in the beta-cardiac myosin heavy-chain obtained from

XX a blood sample. The method may be used to diagnose familial or sporadic

XX HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 25 BP; 8 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTCAGAGGAGAAA 25

Db 1 CTGGGCTTCACCTCAGAGGAGAAA 25

RESULT 2

ACA63115

ID ACA63115 standard; DNA; 25 BP.

XX AC ACA63115;

XX DT 28-AUG-2003 (first entry)

XX DE Human beta cardiac myosin heavy chain PCR primer C.

XX KW Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;

XX KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;

XX KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;

XX KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;

XX KW phenylketonuria; cystic fibrosis.

XX OS Homo sapiens.

XX XX US2003054343-A1.

XX XX 20-MAR-2003.

XX XX 06-JUN-1995; 95US-00469172.

XX XX 11-DEC-1992; 92US-00989160.

XX XX (SEID/) SEIDMAN C.

XX XX (SEID/) SEIDMAN J.

XX XX (WATK/) WATKINS H.

XX XX (ROSE/) ROSENZWEIG A.

XX XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX XX WPI; 2003-512374/48.

XX XX Detecting a presence or absence of a mutation associated with

XX XX hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or

XX XX hemophilia, by detecting a mutation in an amplified product of a beta

XX XX cardiac myosin heavy-chain DNA.

XX XX Example 1; Page 5; 22pp; English.

XX XX The invention relates to detecting the presence or absence of a mutation

XX XX associated with hypertrophic cardiomyopathy (sporadic or familial, SHC

XX XX and FHC) comprises detecting a mutation associated with hypertrophic

XX XX cardiomyopathy in an amplified product of a beta cardiac myosin heavy

XX XX chain DNA. The mutations associated with SHC/FHC are detected in the

XX XX myosin gene isolated from blood, by detecting mis-matched areas in RNA-

XX XX DNA hybrid double strands (RNA from the normal gene, DNA from the suspect

XX XX sample). FHC associated point mutation can be classified and used to

XX XX determine life expectancy in affected individuals e.g. using a Kaplan-

XX XX Meier curve for the classified type of FHC causing point mutation. Also

XX XX included are an RNA probe comprising ribonucleotides arranged in a

XX XX sequence which is complementary to at least a portion of beta-cardiac

XX XX myosin heavy-chain DNA and a set of DNA oligonucleotide primers for

XX XX amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
 CC chain cDNA containing an FHC-associated mutation

XX Sequence 25 BP; 8 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTCAGAGGAGAAA 25

Db 1 CTGGGCTTCACCTCAGAGGAGAAA 25

RESULT 3

ADRO5301

ID ADRO5301 standard; DNA; 25 BP.

XX AC ADRO5301;

XX DT 21-OCT-2004 (first entry)

XX DE Human beta cardiac myosin heavy chain mutation detection primer C.

XX KW Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;

XX KW familial hypertrophic cardiomyopathy;

XX KW sporadic hypertrophic cardiomyopathy.

XX OS Homo sapiens.

XX XX US2004152121-A1.

XX XX 05-AUG-2004.

XX XX 27-FEB-2004; 2004US-00788779.

XX XX 11-DEC-1992; 92US-00989160.

XX XX 06-JUN-1995; 95US-00469172.

XX XX (SEID/) SEIDMAN C.

XX XX (SEID/) SEIDMAN J.

XX XX (WATK/) WATKINS H.

XX XX (ROSE/) ROSENZWEIG A.

XX XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX XX WPI; 2004-592586/57.

XX XX Detecting mutations associated with hypertrophic cardiomyopathy to

XX XX diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac

XX XX myosin heavy-chain DNA and detecting the mutation in the amplified

XX XX product.

XX XX Claim 18; SEQ ID NO 5; 22pp; English.

XX XX The invention relates to detecting the presence or absence of a mutation

XX XX associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,

XX XX SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,

XX XX comprising amplifying beta-cardiac myosin heavy-chain DNA forming an

XX XX amplified product, and detecting the presence or absence of a mutation

XX XX associated with hypertrophic cardiomyopathy in the amplified product,

XX XX thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also

XX XX included are a set of DNA oligonucleotide primers for amplifying beta-

XX XX cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
 CC oligonucleotide primers being useful for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
 CC cardiomyopathy-associated mutation) and a kit for facilitating the
 CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
 CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
 CC heavy chain DNA, where the RNA probe is capable of detecting a
 CC hypertrophic cardiomyopathy-associated mutation, a second container
 CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
 CC instructions for using the components of the kit to detect the presence
 CC or absence of a hypertrophic cardiomyopathy-associated mutation in
 CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
 CC detecting the presence or absence of a mutation associated with
 CC hypertrophic cardiomyopathy for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
 CC having hypertrophic cardiomyopathy relies on the presence of typical
 CC clinical symptoms and the demonstration of unexplained ventricular
 CC hypertrophy. The present invention is non-invasive and based, at least in
 CC part, on the discovery that hypertrophic cardiomyopathy is caused by
 CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
 CC reveals that there are no extensive studies involving a large number of
 CC families which established that this particular disease or disorder was
 CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
 CC The present sequence is a PCR primer used to amplify a region of the beta
 CC cardiac myosin heavy chain having a disease-related point mutation.

SQ Sequence 25 BP; 8 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 13; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCTTCACCTTCAGAGGAGAAA 25
 |||||
 DB 1 CTGGCTTCACCTTCAGAGGAGAAA 25

RESULT 4
 ABA02364
 ID ABA02364 standard; DNA; 41 BP.

XX AC ABA02364;

XX DT 22-FEB-2002 (first entry)

XX DE Human nucleotide reductase 9 probe, SEQ ID NO:8.

XX Human; nucleotide reductase 9; recombinant production; malignant tumour;
 KW cancer; blood disease; HIV infection; human immunodeficiency virus;
 KW immune disorder; inflammatory condition; purine; pyrimidine;
 KW metabolism-disorder; embryonic disorder; growth disorder; gene therapy;
 KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.

XX OS Homo sapiens.

XX PN WO200181385-A1.

XX PD 01-NOV-2001.

XX PP 23-APR-2001; 2001WO-CN000591.

XX PR 27-APR-2000; 2000CN-00115483.

XX PA (BTOW-) BLOWNDOW GENE DEV INC SHANGHAI.

XX PI Mao Y, Xie Y;

XX DR WPI; 2002-026142/03.

XX Human reductase nucleotide 9 and encoded polynucleotide, used in
 PT diagnosis and treatment of malignant tumors, hemopathy, human
 PT immunodeficiency virus infection, immunological diseases and
 PT inflammation.

XX

PS Example 7; Page 15; 35pp; Chinese.

XX The invention relates to human nucleotide reductase 9 (AAM52683), nucleic
 CC acids encoding it (ABA02359), and a method for the recombinant production
 CC of nucleotide reductase 9. The protein has a molecular weight of 9 kD.
 CC The present invention additionally discloses an antagonist of nucleotide
 CC reductase 9 for therapeutic use, and an antibody which specifically binds
 CC to nucleotide reductase 9. Nucleotide reductase 9, and nucleotides which
 CC encode it may be used for treating a variety of diseases, such as
 CC malignant tumours, blood diseases, HIV (human immunodeficiency virus)
 CC infection, immune disorders, inflammatory conditions, disorders of purine
 CC and pyrimidine metabolism, and embryonic and growth disorders. The
 CC protein may also be used to screen for modulators of its activity or for
 CC peptide fingerprinting identification. The polynucleotide can be used as
 CC a primer for nucleic acid amplification reactions or as a probe for
 CC hybridisation reactions, or in producing gene chips or microarrays.
 CC Sequences ABA02364-ABA02365 represent human nucleotide reductase 9 probes
 CC used in an exemplification of the invention

SQ Sequence 41 BP; 10 A; 5 C; 9 G; 17 T; 0 U; 0 Other;

Query Match 64.0%; Score 16; DB 6; Length 41;

Best Local Similarity 79.2%; Pred. No. 1.7e+03;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 TGGGCTTCACCTTCAGAGGAGAAA 25

|||||

DB 15 TGGGTTTCACCTTCAGTTGAAACAA 38

RESULT 5

ADH43094

ID ADH43094 standard; DNA; 30 BP.

XX AC ADH43094;

XX DT 25-MAR-2004 (first entry)

XX DE CRAM protein related primer sequence #SEQ ID 6.

XX Neuroprotective; neutralisation; CRAM;
 KW collapsing-response mediator protein-associated molecule; gene therapy;
 KW mitochondria; drug development; neural disease; pathosis; PCR; primer;
 KW ss.

XX OS Synthetic.

XX PN WO2004001038-A1.

XX PD 31-DEC-2003.

XX PF 19-JUN-2003; 2003WO-JP0007766.

XX PR 19-JUN-2002; 2002JP-00179105.

XX PA (NEWI-) NEW IND RES ORG.

XX PI Yanagi S;

XX DR WPI; 2004-099123/10.

XX Genes and proteins participating in neutralization of cells or tissues,
 PT useful in gene therapy and regeneration medicine, applicable in
 PT diagnosis, drug development for neural diseases and study of mechanism of
 PT pathosis.

XX Example 1; SEQ ID NO 6; 101pp; Japanese.

XX The invention relates to a method for inducing neutralisation of cells or
 CC tissues by using a protein binding to CRAM (collapsing-response mediator
 CC protein-associated molecule) protein or its encoded gene. The proteins
 CC and their encoded genes are useful in gene therapy and regenerative

CC medicine, e.g. by inducing neutralisation of mitochondria. They are also
CC applicable in diagnosis, drug development for neural diseases and
CC studying the mechanism of pathosis. The current sequence represents CRAM
CC protein related PCR primer sequence.

XX SQ Sequence 30 BP; 5 A; 8 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 61.6%; Score 15.4; DB 12; Length 30;

Best Local Similarity 94.1%; Pred. No. 3.1e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAG 18

Db 8 TGGGCTTCCTCAGAG 24

RESULT 6

ACC58874/c

ID ACC58874 standard; DNA; 30 BP.

XX AC ACC58874;

XX DT 08-SEP-2003 (first entry)

XX DE Doubly labelled DNA probe.

XX KW Probe; nucleic acid detection; ss.

XX OS Synthetic.

XX PN WO2003043402-A2.

XX PD 30-MAY-2003.

XX PF 21-OCT-2002; 2002WO-US033699.

XX PR 19-OCT-2001; 2001US-0336432P.

XX PA (PROL-) PROLIGO LLC.

XX PI Bruce I, Davies M, Wolter A;

XX PI WPI; 2003-505122/47.

XX DR Detection or quantification of nucleic acid analyte, by hybridizing a

XX PT nucleic acid probe having non-identical covalently attached dyes, with

XX PT nucleic acid analyte, and measuring change in fluorescence of the probes.

XX PS Example 9; Page 33; 110pp; English.

XX CC The present sequence is an example of nucleic acid probes of the

XX CC invention. The probe may be doubly labelled with non-identical covalently

XX CC attached dyes, i.e. thiazole orange and MDCC. A bifunctional branched

XX CC linker is used to attach the dyes to the oligonucleotide. The probe

XX CC generates a fluorescent signal upon hybridisation to a complementary

XX CC nucleic acid based on the interaction of an intercalator or DNA groove

XX CC binder with the formed double-stranded DNA. Nucleic acid probes of the

XX CC invention can be used in homogeneous assays, real-time PCR monitoring,

XX CC transcription assays, expression analysis on nucleic acid microarrays and

XX CC other microarray applications such as genotyping

XX SQ Sequence 30 BP; 7 A; 11 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 60.8%; Score 15.2; DB 10; Length 30;

Best Local Similarity 85.0%; Pred. No. 3.8e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAG 21

Db 22 TGGGCTTTACTGAAGAGGAG 3

RESULT 7

ACC58875/c

ID ACC58875 standard; DNA; 31 BP.

XX AC ACC58875;

XX DT 08-SEP-2003 (first entry)

XX DE Doubly labelled DNA probe.

XX KW Probe; nucleic acid detection; ss.

XX OS Synthetic.

XX PN WO2003043402-A2.

XX PD 30-MAY-2003.

XX PF 21-OCT-2002; 2002WO-US033699.

XX PR 19-OCT-2001; 2001US-0336432P.

XX PA (PROL-) PROLIGO LLC.

XX PI Bruce I, Davies M, Wolter A;

XX PI WPI; 2003-505122/47.

XX DR Detection or quantification of nucleic acid analyte, by hybridizing a

XX PT nucleic acid probe having non-identical covalently attached dyes, with

XX PT nucleic acid analyte, and measuring change in fluorescence of the probes.

XX PS Example 9; Page 33; 110pp; English.

XX CC The present sequence is an example of nucleic acid probes of the

XX CC invention. The probe may be doubly labelled with non-identical covalently

XX CC attached dyes, i.e. thiazole orange and MDCC. A bifunctional branched

XX CC linker is used to attach the dyes to the oligonucleotide. The probe

XX CC generates a fluorescent signal upon hybridisation to a complementary

XX CC nucleic acid based on the interaction of an intercalator or DNA groove

XX CC binder with the formed double-stranded DNA. Nucleic acid probes of the

XX CC invention can be used in homogeneous assays, real-time PCR monitoring,

XX CC transcription assays, expression analysis on nucleic acid microarrays and

XX CC other microarray applications such as genotyping

XX SQ Sequence 31 BP; 8 A; 11 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 60.8%; Score 15.2; DB 10; Length 31;

Best Local Similarity 85.0%; Pred. No. 3.8e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGGAG 21

Db 23 TGGGCTTTACTGAAGAGGAG 4

RESULT 8

ACI46238

ID ACI46238 standard; DNA; 25 BP.

XX AC ACI46238;

XX DT 13-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 46229.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;

XX KW genetic variation; biallelic marker; polymorphism; human;

XX KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX

PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
PR
XX (AFFY-) AFFYMETRIX INC.
PA
XX Mittmann MP;
PI
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 46229; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX SQ Sequence 25 BP; 8 A; 4 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 6 CTTCACTTCAGAGGAGAA 23
Db 2 CTTAATTTCAAGAGGAGAA 19
RESULT 9
ABX12624
ID ABX12624 standard; DNA; 33 BP.
AC ABX12624;
XX
XX 13-MAY-2003 (first entry)
DT
XX Human zinc finger protein 33.22, PCR primer #1.
DE
XX Human; zinc finger protein 33.22; PCR; primer; ss.
KW
XX Homo sapiens.
OS
XX CN1376683-A.
PN
XX 30-OCT-2002.
PD
XX 22-MAR-2001; 2001CN-00105731.
PF
XX 22-MAR-2001; 2001CN-00105731.
PR
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2003-176047/18.
DR
XX Human zinc finger protein 33.22, encoding polynucleotide, antagonist and
PT recombinant preparation, useful for treating tumors and diabetes.
PT
XX Example 7; Page 20 (Disclosure); 32pp; Chinese.
PS
XX The invention describes a human zinc finger protein -33.22, encoding
CC polynucleotide, antagonist, and recombinant preparation. This sequence
CC represents a probe used to detect DNA encoding the human zinc finger
CC protein 33.22
XX
XX SQ Sequence 41 BP; 20 A; 6 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.8; DB 8; Length 41;
Best Local Similarity 88.9%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PR 22-MAR-2001; 2001CN-00105731.
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2003-176047/18.
DR
XX Human zinc finger protein 33.22, encoding polynucleotide, antagonist and
PT recombinant preparation, useful for treating tumors and diabetes.
PT
XX Example 5; Page 18 (Disclosure); 32pp; Chinese.
PS
XX The invention describes a human zinc finger protein -33.22, encoding
CC polynucleotide, antagonist, and recombinant preparation. This sequence
CC represents a PCR primer used to amplify DNA encoding the human zinc
CC finger protein 33.22
XX
XX SQ Sequence 33 BP; 12 A; 6 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.8; DB 8; Length 33;
Best Local Similarity 88.9%; Pred. No. 5.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 7 TTCACTTCAGAGGAGAAA 24
Db 13 TACACTTCAGAGAGAAA 30
RESULT 10
ABX12626
ID ABX12626 standard; DNA; 41 BP.
XX
XX AC ABX12626;
XX
XX 13-MAY-2003 (first entry)
DT
XX Human zinc finger protein 33.22, probe #1.
DE
XX Human; zinc finger protein 33.22; probe; ss.
KW
XX Homo sapiens.
OS
XX CN1376683-A.
PN
XX 30-OCT-2002.
PD
XX 22-MAR-2001; 2001CN-00105731.
PF
XX 22-MAR-2001; 2001CN-00105731.
PR
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2003-176047/18.
DR
XX Human zinc finger protein 33.22, encoding polynucleotide, antagonist and
PT recombinant preparation, useful for treating tumors and diabetes.
PT
XX Example 7; Page 20 (Disclosure); 32pp; Chinese.
PS
XX The invention describes a human zinc finger protein -33.22, encoding
CC polynucleotide, antagonist, and recombinant preparation. This sequence
CC represents a probe used to detect DNA encoding the human zinc finger
CC protein 33.22
XX
XX SQ Sequence 41 BP; 20 A; 6 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.8; DB 8; Length 41;
Best Local Similarity 88.9%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 7 TTCACCTTCAGAGGAGAAA 24
XX | | | | | | | | | | | | | | | |
Db 3 TACACTTCAGAGAGAAA 20

RESULT 11
ABX12627
ID ABX12627 standard; DNA; 41 BP.
XX
XX AC ABX12627;
XX
XX DT 13-MAY-2003 (first entry)
XX
DE Human zinc finger protein 33.22, probe #2.
XX
XX KW Human; zinc finger protein 33.22; probe; ss.
XX
XX OS Homo sapiens.
XX
XX PN CN1376683-A.
XX
XX PD 30-OCT-2002.
XX
XX PF 22-MAR-2001; 2001CN-00105731.
XX
XX PR 22-MAR-2001; 2001CN-00105731.
XX
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX PI Mao Y, Xie Y;
XX
XX DR WPI; 2003-176047/18.
XX
XX PT Human zinc finger protein 33.22, encoding polynucleotide, antagonist and
XX recombinant preparation, useful for treating tumors and diabetes.
XX
XX PS Example 7; Page 20 (Disclosure); 32pp; Chinese.
XX
XX CC The invention describes a human zinc finger protein -33.22, encoding
XX polynucleotide, antagonist, and recombinant preparation. This sequence
XX CC represents a probe used to detect DNA encoding the human zinc finger
XX protein 33.22
XX
XX SQ Sequence 41 BP; 20 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.8; DB 8; Length 41;
Best Local Similarity 88.9%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTCACCTTCAGAGGAGAAA 24
XX | | | | | | | | | | | | | | | |
Db 3 TACACTTCAGAGAGAAA 20

RESULT 12
AA59982/C
ID AA59982 standard; DNA; 21 BP.
XX
XX AC AA59982;
XX
XX DT 04-AUG-1999 (first entry)
XX
XX DE Oligonucleotide probe specific for Porphyromonas gingivalis.
XX
XX KW Species-specific; Bacteroides; microbe; identification; Rikenella;
XX Porphyromonas; Prevotella; probe; ss.
XX
XX OS Synthetic.
XX
XX PN JP11127899-A.
XX
XX PD 18-MAY-1999.
XX

QY 29-OCT-1997; 97JP-00297085.
XX
XX PR 29-OCT-1997; 97JP-00297085.
XX
XX PA (YAKU-) ZH YAKULT BIOSCIENCE KENKYU ZAIDAN.
XX
XX DR WPI; 1999-350346/30.
XX
XX PT New oligonucleotide probe species-specific to a Bacteroides group microbe
XX - useful for identification of the microbe.
XX
XX PS Claim 1; Page 7; 9pp; Japanese.
XX
XX CC AAX59976-93 represents oligonucleotide probes that are species-specific
XX Bacteroides group microbes. The probes are useful for species-specific
XX CC identification of a Bacteroides group microbe
XX
XX SQ Sequence 21 BP; 5 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 58.4%; Score 14.6; DB 2; Length 21;
Best Local Similarity 81.0%; Pred. No. 6.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTTCAGAGGAG 21
XX | | | | | | | | | | | | | | | |
Db 21 CCGGGCTTGACTTCAGTGGCG 1

RESULT 13
ADQ28791
ID ADQ28791 standard; DNA; 34 BP.
XX
XX AC ADQ28791;
XX
XX DT 07-OCT-2004 (first entry)
XX
XX DE PCR primer SP-23 to amplify B-IV group phage bacteriolytic gene Seq 11.
XX
XX KW bacteriophage; infectious disease; pathogenic; bacteriolysis; ss;
XX antimicrobial; bacteriolytic; PCR; primer.
XX
XX OS Synthetic.
XX
XX PN JP2004194654-A.
XX
XX PD 15-JUL-2004.
XX
XX PF 03-DEC-2003; 2003JP-00404062.
XX
XX PR 04-DEC-2002; 2002JP-00352523.
XX
XX PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
XX
XX DR WPI; 2004-503333/48.
XX
XX PT Pharmaceutical composition useful for treating infectious diseases,
XX comprises gene construct containing bacteriolytic gene of bacteriophage,
XX and carrier.
XX
XX PS Example 7; SEQ ID NO 11; 25pp; Japanese.
XX
XX CC This invention relates to a novel pharmaceutical composition that
XX comprises a bacteriolytic gene derived from a bacteriophage.
XX Specifically, it refers to a bacteriophage chosen from a levi virus of
XX the Leviviridae family, which is a small globular form RNA phage or a
XX micro virus of the Microviridae family, which is a small globular form
XX DNA phage. The bacteriolytic gene in the construct is under the control
XX of a phage lambda lactose promoter, and further contains a gene encoding
XX a coat protein as well as an inducer of gene expression i.e. isopropyl
XX beta-D-1 thio-galactopyranoside (IPTG). The present invention describes a
XX composition useful for treating infectious disease through the
XX bacteriolysis of bacteria such as Escherichia coli infections occurring
XX in both humans and animals. Furthermore, it is a highly reliable, safe
```

CC and specific antimicrobial method for targeting pathogenic bacteria and
 CC because it does not comprise a medical agent it also prevents the risk of
 CC generating drug-resistant microbes. This oligonucleotide sequence is a
 CC PCR primer given in an exemplification of the invention.

XX Sequence 34 BP; 9 A; 9 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 58.4%; Score 14.6; DB 12; Length 34;
 Best Local Similarity 81.0%; Pred. No. 7.4e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 GGGCTTCACTTCAGAGGAA 23
 |||||
 Db 7 GCGCGCACTACAGAGGAA 27

RESULT 14
 ACC42057/c
 ID ACC42057 standard; DNA; 41 BP.
 XX
 AC ACC42057;
 XX
 DT 21-MAY-2003 (first entry)
 XX
 DE Human SCN5A gene related polymorphism oligonucleotide SEQ ID NO:86.

XX Human; KCNQ1; KCNE1; HERG; SCN5A; KCNE2; ion channel disease; epilepsy;
 KW polymorphism; genetic abnormality; genotype; mutation; long QT syndrome;
 KW cardiac arrhythmia; hearing loss; sudden infant death syndrome; SIDS;
 KW sudden unexpected death in epilepsy; acquired sudden death syndrome;
 KW post-myocardial infarction complication; SUDEP; SIDS; ss;
 KW sudden unexpected death in sleep.

XX Homo sapiens.
 OS Synthetic.

XX WO2003016504-A2.
 XX
 PD 27-FEB-2003.

XX 20-AUG-2002; 2002WO-US026708.

XX 20-AUG-2002; 2001US-0314331P.
 PR 06-MAY-2002; 2002US-0378521P.

XX (DNAS-) DNA SCI INC.

XX Sotos JG, Curran ME, Guida M, Rienhoff HY;
 XX WPI; 2003-268324/26.

XX Determining ion channel disease genotype of an individual, by analyzing

PT nucleic acid sample of individual for a mutation indicating decreased ion
 PT channel conductivity resulting in amino acid change of KCNQ1 protein.

XX Claim 15; Page 19; 75pp; English.

XX The present invention describes a method (M) for determining the ion
 CC channel disease genotype of an individual. Also described: (1) an
 CC isolated KCNQ1 nucleic acid molecule (I) comprising a sequence (S1, see
 CC ACC41977 to ACC41980), or a nucleic acid sequence that is fully
 CC complementary to S1, where the isolated nucleic acid molecule is less
 CC than 5 kilobases in length; (2) an array of oligonucleotides comprising
 CC (I); and (3) an isolated nucleic acid molecule (II) comprising at least
 CC one base variation from that of an ion channel associated gene sequence
 CC comprising a polymorphic nucleotide identified in Tables 4 and 5 in the
 CC specification (see ACC41982 to ACC42156), and at least 20 other bases of
 CC the ion channel associated gene identified in tables 4 and 5 in the
 CC specification, with the polymorphic nucleotide, where the isolated
 CC nucleic acid molecule is less than about 5 kilobases in length. (M) is
 CC useful for determining ion channel disease genotype of an individual,
 CC where the individual has or is suspected of having an ion channel disease
 CC selected from long QT syndrome, cardiac arrhythmias, epilepsy, hearing

CC loss, sudden infant death syndrome (SIDS), sudden unexpected death in
 CC epilepsy (SUDEP), sudden unexpected death in sleep (SUDS), post-
 CC myocardial infarction complications, and acquired sudden death syndrome,
 CC or the individual is a lineal descendant of an individual who has or is
 CC suspected of having the above diseases. (II) is useful for conducting
 CC clinical trials of drug candidates for ion channel diseases, for
 CC preparing probes or primers for detection of the presence of long QT
 CC genes, and for establishing physical linkage between a genetic locus
 CC associated with a trait of interest and polymorphic markers that are not
 CC associated with the trait but are in physical proximity with the genetic
 CC locus responsible for the trait and co-segregate with it. ACC41977 to
 CC ACC42159, ABP96320 and ABP96321 represent sequences used in the
 CC exemplification of the present invention

SQ Sequence 41 BP; 7 A; 16 C; 11 G; 7 T; 0 U; 0 Other;

Query Match 58.4%; Score 14.6; DB 9; Length 41;
 Best Local Similarity 81.0%; Pred. No. 7.6e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACTTCAGAGGAG 21
 |||||
 Db 28 CTGGCCTTGGCCTCAGAGGAG 8

RESULT 15

ID ABZ84436 standard; DNA; 25 BP.

XX ABZ84436;

DT 14-MAY-2003 (first entry)

XX Toxicologically relevant human PCR primer #1595.

XX Toxicologically relevant gene; toxicological response; PCR primer; ss.

OS Homo sapiens.

OS Synthetic.

XX WO2003016500-A2.

XX 27-FEB-2003.

XX 16-AUG-2002; 2002WO-US026514.

XX 16-AUG-2001; 2001US-0313080P.

XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweiser K;
 PI Alen P;

XX WPI; 2003-268322/26.

XX Determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.

XX Claim 1; Page 351; 455pp; English.

XX The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in ABZ82842
 CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
 CC ; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject

CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals
 XX
 XX
 SQ Sequence 25 BP; 9 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 57.6%; Score 14.4; DB 10; Length 25;
 Best Local Similarity 75.0%; Pred. No. 8.7e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 CTGGGCTTCACCTTCAGAGGAGAAA 24
 Db 2 CAGCGTTGAACCTCAGAGGAGAAA 25

RESULT 16
 ADP88540
 ID ADP88540 standard; DNA; 37 BP.
 XX
 AC ADP88540;
 XX
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Bovine pancreatic DNase I mutagenic PCR primer SEQ ID NO: 22.

ss; PCR; cow; bovine pancreatic DNase I;
 KW bovine pancreatic desoxyribonuclease I; DNA hydrolysis; primer;
 KW mutagenic.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 PN EP1431387-A1.
 XX

PD 23-JUN-2004.

PF 16-DEC-2003; 2003EP-00028861.

XX 20-DEC-2002; 2002EP-00028558.

PR 20-JAN-2003; 2003EP-00001214.

PR 21-JAN-2003; 2003US-0441550P.

XX (HOFF) ROCHE DIAGNOSTICS GMBH.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Mueller R, Kirschbaum T, Suppmann B, Schoen H, Engh R;

PI Hoffmann A, Thalhofer J, Siedel J, Engel W;

XX WPI; 2004-452511/43.

DR Variant of bovine pancreatic desoxyribonuclease I produced by specific
 XX amino acid substitutions in bovine pancreatic desoxyribonuclease I, has
 XX increased thermolability and is useful for hydrolyzing DNA.

PS Example 2; SEQ ID NO 22; 46pp; English.

XX The present invention relates to a variant of bovine pancreatic
 CC desoxyribonuclease I (pancreatic DNase I), by way of amino acid
 CC substitution, where at least one different amino acid substitutes for an
 CC amino acid residue chosen from Cys173, Cys101, Cys104, Lys117, Arg185,
 CC Arg187, Ile3, Phe82, and Phe128. Bovine pancreatic DNase I is useful for
 CC hydrolyzing DNA and subsequently reducing the specific desoxyribonuclease
 CC activity of the variant of the enzyme to approximately zero units per mg
 CC of protein. The present sequence is a mutagenic primer used to alter the
 CC wild-type bovine pancreatic DNase I coding sequence.

XX
 SQ Sequence 37 BP; 11 A; 10 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 57.6%; Score 14.4; DB 12; Length 37;
 Best Local Similarity 75.0%; Pred. No. 9.2e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 2 TGGGCTTCACCTTCAGAGGAGAAA 25
 Db 6 TGGCTTCACCTTCAGAGGAGAAA 29

RESULT 17

ADP88541/C

ID ADP88541 standard; DNA; 37 BP.

XX AC ADP88541;

XX DT 09-SEP-2004 (first entry)

XX DE Bovine pancreatic DNase I mutagenic PCR primer SEQ ID NO: 23.

ss; PCR; cow; bovine pancreatic DNase I;
 KW bovine pancreatic desoxyribonuclease I; DNA hydrolysis; primer;
 KW mutagenic.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 PN EP1431387-A1.

XX PD 23-JUN-2004.

XX PF 16-DEC-2003; 2003EP-00028861.

XX PR 20-DEC-2002; 2002EP-00028558.

PR 20-JAN-2003; 2003EP-00001214.

PR 21-JAN-2003; 2003US-0441550P.

XX (HOFF) ROCHE DIAGNOSTICS GMBH.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Mueller R, Kirschbaum T, Suppmann B, Schoen H, Engh R;

PI Hoffmann A, Thalhofer J, Siedel J, Engel W;

XX WPI; 2004-452511/43.

XX Variant of bovine pancreatic desoxyribonuclease I produced by specific
 XX amino acid substitutions in bovine pancreatic desoxyribonuclease I, has
 XX increased thermolability and is useful for hydrolyzing DNA.
 XX Example 2; SEQ ID NO 23; 46pp; English.
 XX The present invention relates to a variant of bovine pancreatic
 CC desoxyribonuclease I (pancreatic DNase I), by way of amino acid
 CC substitution, where at least one different amino acid substitutes for an
 CC amino acid residue chosen from Cys173, Cys101, Cys104, Lys117, Arg185,
 CC Arg187, Ile3, Phe82, and Phe128. Bovine pancreatic DNase I is useful for
 CC hydrolyzing DNA and subsequently reducing the specific desoxyribonuclease
 CC activity of the variant of the enzyme to approximately zero units per mg
 CC of protein. The present sequence is a mutagenic primer used to alter the
 CC wild-type bovine pancreatic DNase I coding sequence.

PS Example 2; SEQ ID NO 23; 46pp; English.

XX The present invention relates to a variant of bovine pancreatic
 CC desoxyribonuclease I (pancreatic DNase I), by way of amino acid
 CC substitution, where at least one different amino acid substitutes for an
 CC amino acid residue chosen from Cys173, Cys101, Cys104, Lys117, Arg185,
 CC Arg187, Ile3, Phe82, and Phe128. Bovine pancreatic DNase I is useful for
 CC hydrolyzing DNA and subsequently reducing the specific desoxyribonuclease
 CC activity of the variant of the enzyme to approximately zero units per mg
 CC of protein. The present sequence is a mutagenic primer used to alter the
 CC wild-type bovine pancreatic DNase I coding sequence.

XX Sequence 37 BP; 12 A; 4 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 57.6%; Score 14.4; DB 12; Length 37;
 Best Local Similarity 75.0%; Pred. No. 9.2e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 2 TGGGCTTCACCTTCAGAGGAGAAA 25
 Db 32 TGGCTTCACCTTCAGAGGAGAAA 9

```

RESULT 18
ID ABA02365 standard; DNA; 41 BP.
XX
XX ABA02365;
AC ABA02365;
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Human nucleotide reductase 9 probe, SEQ ID NO:9.
DE
XX
XX Human; nucleotide reductase 9; recombinant production; malignant tumour;
KW cancer; blood disease; HIV infection; human immunodeficiency virus;
KW immune disorder; inflammatory condition; purine; pyrimidine;
KW metabolism disorder; embryonic disorder; growth disorder; Gene therapy;
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.
XX
XX Homo sapiens.
OS
XX WO200181385-A1.
FN
XX
XX 01-NOV-2001.
PD
XX
XX 23-APR-2001; 2001WO-CN000591.
PF
XX
XX 27-APR-2000; 2000CN-00115483.
PR
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-026142/03.
DR
XX
XX Human reductase nucleotide 9 and encoded polynucleotide, used in
PT diagnosis and treatment of malignant tumors, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.
XX
XX Example 7; Page 15; 35pp; Chinese.
XX
XX The invention relates to human nucleotide reductase 9 (AAM52683), nucleic
CC acids encoding it (ABA02365), and a method for the recombinant production
CC of nucleotide reductase 9. The protein has a molecular weight of 9 kD.
CC The present invention additionally discloses an antagonist of nucleotide
CC reductase 9 for therapeutic use, and an antibody which specifically binds
CC to nucleotide reductase 9. Nucleotide reductase 9, and nucleotides which
CC encode it may be used for treating a variety of diseases, such as
CC malignant tumours, blood diseases, HIV (human immunodeficiency virus)
CC infection, immune disorders, inflammatory conditions, disorders of purine
CC and pyrimidine metabolism, and embryonic and growth disorders. The
CC protein may also be used to screen for modulators of its activity or for
CC peptide fingerprinting identification. The polynucleotide can be used as
CC a primer for nucleic acid amplification reactions or as a probe for
CC hybridisation reactions, or in producing gene chips or microarrays.
CC Sequences ABA02364-ABA02365 represent human nucleotide reductase 9 probes
CC used in an exemplification of the invention
XX
XX Sequence 41 BP; 10 A; 6 C; 9 G; 16 T; 0 U; 0 Other;
SQ
Query Match 57.6%; Score 14.4; DB 6; Length 41;
Best Local Similarity 75.0%; Pred. No. 9.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 TGGGCTTCACCTCAGAGGAGAAA 25
DB 15 TGGGTTCCACTTCAGTTGAACAA 38
RESULT 19
ID AC131972/c
XX
XX AC131972 standard; DNA; 25 BP.
XX
XX AC131972;
AC
13-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 31963.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX US2003104410-A1.
FN
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
PF
XX
XX 16-MAR-2001; 2001US-0276759P.
PR
XX
XX (AFFY-) AFFYMETRIX INC.
PA
XX
XX Mittmann MP;
PI
XX
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 31963; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX Sequence 25 BP; 3 A; 9 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 56.8%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GGGCTTCACCTCAGAGGAG 21
DB 22 GGGCTACACTACCGGAG 4
RESULT 20
ID ADP14058/c
XX
XX ADP14058 standard; DNA; 25 BP.
XX
XX ADP14058;
AC
26-AUG-2004 (first entry)
DT
```

```
XX Renal cell carcinoma differentially expressed gene probe #463.
DE ss; diagnosis; non-blood disease; solid tumor; gene expression;
XX peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
KW Homo sapiens.
XX WO2004048933-A2.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 794; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX SQ Sequence 25 BP; 4 A; 5 C; 6 G; 10 T; 0 U; 0 Other;
Query Match 56.8%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 GGCTTCACTTCAGAGGAGA 22
DB 19 GGCTTCACTTCAGAGGAGA 1
RESULT 21
ADP14057/c ADP14057 standard; DNA; 25 BP.
XX AC ADP14057;
XX 26-AUG-2004 (first entry)
DT XX
```

```
DE Renal cell carcinoma differentially expressed gene probe #462.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX WO2004048933-A2.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 793; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX SQ Sequence 25 BP; 3 A; 6 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 56.8%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 GGCTTCACTTCAGAGGAGA 22
DB 21 GGCTTCACTTCAGAGGAGA 3
RESULT 22
AAT31079
ID AAT31079 standard; DNA; 33 BP.
XX AC AAT31079;
XX 08-JAN-1997 (first entry)
DT XX
DE Probe for fungal saccharopine dydrogenase gene.
```

XX Probe; primer; fungal pathogen; detection; screening; AIDS;
 KW acquired immune deficiency syndrome; Candida albicans;
 KW Cryptococcus neoformans; Yarrowia lipolytica; Aspergillus fumigatus;
 KW Histoplasma capsulatum; postoperative patients; immunocompromised;
 KW immunosuppressed; ss.
 XX Synthetic.
 OS
 XX WO9619588-A2.
 PN
 XX 27-JUN-1996.
 XX
 XX 20-DEC-1995; 95WO-US016684.
 PF
 XX 21-DEC-1994; 94US-00360606.
 PR
 XX (UYMI-) UNIV MIAMI.
 PA (ELIL) LILLY & CO ELI.
 PA
 XX Bhattacharjee JK, Garrad RC, Skatrud PL, Peery RB;
 PI
 XX WPI; 1996-309602/31.
 DR
 XX Detecting fungal infection by detection of saccharopine dehydrogenase
 PT gene - uses probe, primer or antibody specific to conserved Candida
 PT albicans sequences as detection agents.
 PT
 XX Claim 3; Page 54; 84pp; English.
 PS
 XX Nucleic acid sequences derived from polypeptide fragments of Candida
 CC albicans saccharopine dehydrogenase and which are conserved in fungi can
 CC be used as probes and primers in methods for detecting fungal pathogens.
 CC They may be used for the detection of C. albicans, Yarrowia lipolytica,
 CC and Cryptococcus neoformans. They may also be used for the detection of
 CC Aspergillus fumigatus and Histoplasma capsulatum, especially in patients
 CC suffering from AIDS, those under treatment with immunosuppressive drugs,
 CC postoperative patients and other immunocompromised patients. The nucleic
 CC acid sequences are described in AAT31079-T31093. The peptide epitopes
 CC from which they are derived are described in AAW00483-W00495
 CC
 XX Sequence 33 BP; 15 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 56.8%; Score 14.2; DB 2; Length 33;
 Best Local Similarity 84.2%; Pred. No. 1.1e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAA 24
 ||||| ||||| ||||| |||||
 Db 1 CTTCACTTCAGAGGAGAA 19

RESULT 23
 ADF50502/c
 ID ADF50502 standard; DNA; 39 BP.
 AC ADF50502;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE PCR primer used to amplify human GPR43 DNA (SeqID 182).
 XX
 KW human; PCR; primer; ss; transformation; endocrine cell line;
 KW expression cloning system; bioactive peptide; GPCR ligand.
 XX
 OS Homo sapiens.
 PN WO2003087366-A1.
 XX
 XX 23-OCT-2003.
 PD
 XX 16-APR-2003; 2003WO-JP004840.
 PF
 XX

PR 16-APR-2002; 2002JP-00113030.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;
 PI Nishi T, Obinata M;
 PI
 XX WPI; 2003-833737/77.
 DR
 XX Endocrine cell lines originated from mammalian hypothalamus and
 PT pancreatic islet, applicable in expression cloning systems of bioactive
 PT peptide precursor genes, and in screening G protein-coupled receptor
 PT ligands.
 PT
 XX Example 25; SEQ ID NO 182; 316pp; Japanese.
 PS
 XX This invention relates to a novel method for obtaining a DNA that encodes
 CC a peptide acting as agonist, antagonist or inverse agonist on a target
 CC receptor. Specifically, it comprises transformation of endocrine cell
 CC lines originating from mammalian hypothalamus and pancreatic islets,
 CC culturing the transformants and contacting with cells expressing the
 CC target receptor. The identification of those cells with a response
 CC reaction can be used for selecting a transformant cell line with the
 CC appropriate target activity that is expressing the novel transformed DNA.
 CC Accordingly, the present invention describes novel cell lines that are
 CC applicable in expression cloning systems of bioactive peptide precursor
 CC genes, and in screening GPCR ligands for use as drugs including agonists,
 CC antagonists and inverse agonists i.e. activators and inhibitors. Such
 CC cell lines can provide a highly sensitive and convenient GPCR ligand
 CC assay system. This oligonucleotide sequence is a PCR primer used to
 CC amplify human GPCR DNA of the invention.
 CC
 XX Sequence 39 BP; 7 A; 11 C; 12 G; 9 T; 0 U; 0 Other;
 SQ

Query Match 56.8%; Score 14.2; DB 10; Length 39;
 Best Local Similarity 84.2%; Pred. No. 1.1e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTCAGAGGAG 21
 ||||| ||||| ||||| |||||
 Db 33 GGACTTCACCTCAGAGTAG 15

RESULT 24
 ABZ24931/c
 ID ABZ24931 standard; DNA; 41 BP.
 XX
 AC ABZ24931;
 XX
 DT 25-MAR-2003 (first entry)
 XX
 DE Cell division cycle regulatory protein 137.17 probe #1.
 XX
 KW Cell division cycle regulatory protein 137.17; tumour; cytostatic;
 KW diabetes; cell division; probe; ss.
 XX
 OS Unidentified.
 XX
 XX CN1359915-A.
 PN
 XX 24-JUL-2002.
 PD
 XX 20-DEC-2000; 2000CN-00135176.
 XX
 XX 20-DEC-2000; 2000CN-00135176.
 PR
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA
 XX Mao Y, Xie Y;
 PI
 XX WPI; 2002-733604/80.
 DR
 XX Polypeptide-cell division cycle regulatory protein 137.17 and
 PT

PT polynucleotide encoding it.

PS Example 7; Page 21 (Disclosure); 38pp; Chinese.

XX

CC The present invention relates to cell division cycle regulatory protein

CC 137.17 (see ABP59091). The protein can be used for treating diseases such

CC as diabetes and tumours. The present sequence is a probe, which was used

CC in an example from the invention

XX

SQ Sequence 41 BP; 13 A; 8 C; 8 G; 12 T; 0 U; 0 Other;

Query Match 56.8%; Score 14.2; DB 6; Length 41;

Best Local Similarity 84.2%; Pred. No. 1.2e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAA 24

Db 38 CTTCACTTCGGATGACAA 20

RESULT 25

AAAX78849

ID AAAX78849 standard; DNA; 47 BP.

XX

AC AAAX78849;

XX

DT 07-SEP-1999 (first entry)

XX

DE Paraquat binding antibody PQXB1/2 variable heavy chain PCR primer VH3.

XX

XX Paraquat; antibody; light chain; herbicide; resistant; crop plant;

KW weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I;

KW free radical; lipid peroxidation; electron transport; photosystem II;

KW vacuole; cell surface; cytotoxic; sensitive; heavy chain; PQXB1/2;

KW variable region; PCR primer; ss.

XX

OS Synthetic.

XX

FN WO9932630-A1.

XX

PD 01-JUL-1999.

XX

PF 15-DEC-1998; 98WO-GB003760.

XX

PR 19-DEC-1997; 97GB-00026955.

XX

PA (ZENE) ZENECA LTD.

XX

PI Holt DC, Jones PG;

XX

DR WPI; 1999-405173/34.

XX

PT Herbicide binding proteins and related polynucleotides.

XX

PS Disclosure; Page 42; 60pp; English.

XX

CC This invention describes a novel herbicide binding protein which can

CC confer herbicide resistance activity. Crop plants, such as soybean,

CC cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower,

CC potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas,

CC barley, oat, turf grass, forage grass, sugar cane, pea, field bean, rice,

CC pine, poplar, apple, grape, citrus or nut plants, transformed with a

CC herbicide binding protein gene are resistant to the herbicide. Hence,

CC weeds can be selectively controlled in a field of the transformed crops.

CC The plants are substantially resistant or tolerant to herbicides, such as

CC paraquat or diquat, that inhibit photosynthesis by accepting electrons

CC from photosystem I thus generating free radicals which cause lipid

CC peroxidation or by blocking electron transport in photosystem II. The

CC herbicide binding proteins advantageously sequester the herbicide, e.g.

CC at the cell surface or in the vacuoles of a treated plant. Sequestration

CC at the cell surface prevents the entry of the herbicide into the cell so

CC that the herbicide cannot reach its intracellular target and exert any

CC significant cytotoxic effect. The herbicide binding protein inhibits the

CC

CC mobility of the herbicide from the application site to the whole plant

CC preventing the herbicide reaching particularly sensitive organs.

CC Additionally, tolerant plants can be produced against herbicides that

CC have more than one target site

XX

SQ Sequence 47 BP; 16 A; 11 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 56.8%; Score 14.2; DB 2; Length 47;

Best Local Similarity 84.2%; Pred. No. 1.2e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GGCTTCACTTCAGAGGAGA 22

Db 20 GACTTACCTTCAGAGGAGA 38

RESULT 26

ADB73490

ID ADB73490 standard; DNA; 48 BP.

XX

AC ADB73490;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human breakpoint region AF-4 #4.

XX

XX Human; ds; MLL; cancer; AF-4; CDK-6; SEPTIN6; ALL;

KW acute lymphoblastic leukaemia; AML; acute myeloid leukaemia;

KW chromosomal break point; chromosome 11q23; ATF; BCR; B cell receptor.

XX

OS Homo sapiens.

XX

FN US2003096255-A1.

XX

PD 22-MAY-2003.

XX

PF 09-APR-2002; 2002US-00118783.

XX

PR 19-FEB-1997; 97US-0038624P.

PR 25-AUG-1997; 97US-0056938P.

PR 17-NOV-1997; 97US-0065911P.

PR 19-FEB-1998; 98US-00026033.

XX

PA (FELI/) FELIX C A.

PA (JONE/) JONES D H.

PA (RAPP/) RAPPAPORT E.

XX

PI Felix CA, Jones DH, Rappaport E;

XX

DR WPI; 2003-606415/57.

XX

PT Amplifying an unknown region that flanks a known region of a cancer-

PT associated DNA sequence by subjecting the panhandle structure to

PT extension and to PCR in the presence of a first primer homologous to the

PT second portion.

XX

PS Example 8; Fig 18; 80pp; English.

XX

CC The invention relates to amplifying an unknown region that flanks a known

CC region of a cancer-associated DNA sequence comprising providing a

CC template polynucleotide, ligating a loop-forming oligonucleotide to the

CC 3'-end of the sense strand, annealing the loop-forming oligonucleotide

CC with the first portion to generate a panhandle structure, subjecting the

CC panhandle structure to extension, and subjecting the panhandle structure

CC to PCR in the presence of a first primer homologous to the second

CC portion, where the unknown region is amplified. In the method of

CC amplifying an unknown region that flanks a known region of a cancer-

CC associated DNA sequence, the template polynucleotide comprises a sense

CC strand, comprising the known and unknown regions. The unknown region is

CC nearer the 3'-end of the sense strand than is the known region. The known

CC region is comprises a first or second portion. The first portion is

CC nearer the unknown region than is the second portion. The loop-forming

CC oligonucleotide is complementary to the first portion. The third region

complementary to the second portion is generated at the free end of the loop-forming oligonucleotide. The cancer-associated DNA sequence comprises Aflr1 (not defined) or BCR (B cell receptor). The method is useful for amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence. Also disclosed as new is the use of the method in the analysis of the breakpoint in gene of the human MLL gene, where the chromosomal breaks results in gene fusions with AP-4, CDK-6 and SPTAN6 and are associated with ALL and AML (acute lymphoblastic leukaemia and acute myeloid leukaemia). MLL is located on chromosome 11q23. The present sequence is an MLL breakpoint junction region.

SQ Sequence 48 BP; 18 A; 11 C; 8 G; 11 T; 0 U; 0 Other;

Query Match 56.8%; Score 14.2; DB 10; Length 48;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
6 CTTCACTTCAGAGGAGAAA 24
|||
Db
20 CTGCACCTTCAGAGGCCAAA 38

RESULT 27
ABZ02803
ID ABZ02803 standard; DNA; 50 BP.

AC ABZ02803;

DT 09-JAN-2003 (first entry)

Human leukocyte gene expression profiling probe SEQ ID NO 2794.

T7; leukocyte; gene expression profiling; allograft rejection;
KW KW
KW KW
KW KW
KW KW
SS.

OS Homo sapiens.

PN WO200257414-A2.

25-JUL-2002.

22-OCT-2001: 2001WO-US047856.

PR 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.

PA (BIOC-) BIOCARDIA INC.

AA Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quettermous T, Johnson F;
PI

DR WPI; 2002-636525/68.

New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.

PS Claim 1: Page 416; Opp; English.

The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of a143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX	
SQ	Sequence 50 BP; 15 A; 12 C; 9 G; 14 T; 0 U; 0 Other;
Query Match	56.8%; Score 14.2; DB 6; Length 50;
Best Local Similarity	84.2%; Pred. No. 1.2e+04;

Qy 7 TTCACTTCAGAGGAGAAA 25
| | | | | | | | | |
Db 24 TCCACTTCACAGGATAAA 42

RESULT 28
AAF06504
ID AAF06504 standard; RNA: 29 BP.

AA
AC AAF06504;

DT 16-FEB-2001 (first entry)

DE Hammerhead ribozyme #3301.

KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.

OS Homo sapiens.

PN WO200061729-A2.

PD 19-OCT-2000.

11-APR-2000; 2000WO-US009721.

PR 12-APR-1999; 99US-0129390P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Zwick M, Pavco P, Mcswiggen J;

DR WPI; 2000-647423/62.

Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor protein,
 interferon alpha and erythropoietin.

PS Claim 59: Page 132; 164pp: English.

The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha

Sequence 29 BP: 9 A; 5 C; 7 G; 0 T; 7 U; 1 Other:

Query Match 56.0%; Score 14; DB 3; Length 29;
Best Local Similarity 60.9%; Pred. No. 1.4e+04;
Matches 14: Conservative 3; Mismatches 6; Indels

Qy 3 GGGCTTCACTTCAGAGGAGAAA 25
|||::|||:
Db 1 GGACUUCACUUGAGNCGAAAA 23

RESULT 29
ABA99901/c
ID ABA99901 standard; DNA; 30 BP.
XX
AC ABA99901;
XX

CC comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC multimer at the cleavage site to produce (I) having well defined ends.
CC The method is used for the large-scale synthesis of DNA and RNA oligomers
CC for use, e.g. as probes and diagnostic agents and/or therapeutic agents

XX SQ Sequence 49 BP; 9 A; 14 C; 8 G; 18 T; 0 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 49;
Best Local Similarity 77.3%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAAA 24
Db 43 GGGCTTTCTGAAGAGGCGGAAA 22

RESULT 32

AAV12941
ID AAV12941 standard; RNA; 49 BP.

AC AAV12941;

XX 15-MAY-1998 (first entry)

DE Oligonucleotide SEQ ID NO:50 from US5174320 Example 25.

XX Synthesis; selection; amplification; circular oligonucleotide;
XX rolling circle synthesis; diagnosis; therapeutic agent; ss.

XX Synthetic.

XX OS Homo sapiens.

XX US5714320-A.

XX 03-FEB-1998.

XX 23-FEB-1995; 95US-00393439.

XX 15-APR-1993; 93US-00047860.

XX (UVRP) UNIV ROCHESTER.

XX Kool ET;

XX WPI; 1998-144278/13.

XX Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
XX template to produce oligonucleotide multimer for cleavage.

XX Example 25; Col 63; 38pp; English.

XX The present sequence represents an oligonucleotide used in an example of
XX the present invention. The present invention describes a method for
XX synthesising a selected oligonucleotide (I) having well defined ends. The
XX method comprises: (a) annealing a primer to a single-stranded (ss)
XX circular template to yield a primed circular template, where the template
XX comprises: (i) at least one nucleotide sequence complementary to (I); and
XX (ii) at least one nucleotide effective to produce a cleavage site in the
XX oligonucleotide multimer; (b) combining the primed circular template with
XX at least two types of nucleotide triphosphates and a polymerase enzyme
XX without the addition of auxiliary proteins to yield a ss oligonucleotide
XX multimer complementary to the circular oligonucleotide template,
XX comprising multiple copies of (I); and (c) cleaving the oligonucleotide
XX multimer at the cleavage site to produce (I) having well defined ends.
XX The method is used for the large-scale synthesis of DNA and RNA oligomers
XX for use, e.g. as probes and diagnostic agents and/or therapeutic agents

XX SQ Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAAA 24
Db 11 GGGCUUUUCUGAAGAGGCGGAAA 32

RESULT 33

AAV12938

ID AAV12938 standard; RNA; 49 BP.

AC AAV12938;

XX 15-MAY-1998 (first entry)

DE Oligonucleotide SEQ ID NO:47 from US5174320 Example 25.

XX Synthesis; selection; amplification; circular oligonucleotide;
XX rolling circle synthesis; diagnosis; therapeutic agent; ss.

XX Synthetic.

XX OS Homo sapiens.

XX US5714320-A.

XX 03-FEB-1998.

XX 23-FEB-1995; 95US-00393439.

XX 15-APR-1993; 93US-00047860.

XX (UVRP) UNIV ROCHESTER.

XX Kool ET;

XX WPI; 1998-144278/13.

XX Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
XX template to produce oligonucleotide multimer for cleavage.

XX Example 25; Col 61; 38pp; English.

XX The present sequence represents an oligonucleotide used in an example of
XX the present invention. The present invention describes a method for
XX synthesising a selected oligonucleotide (I) having well defined ends. The
XX method comprises: (a) annealing a primer to a single-stranded (ss)
XX circular template to yield a primed circular template, where the template
XX comprises: (i) at least one nucleotide sequence complementary to (I); and
XX (ii) at least one nucleotide effective to produce a cleavage site in the
XX oligonucleotide multimer; (b) combining the primed circular template with
XX at least two types of nucleotide triphosphates and a polymerase enzyme
XX without the addition of auxiliary proteins to yield a ss oligonucleotide
XX multimer complementary to the circular oligonucleotide template,
XX comprising multiple copies of (I); and (c) cleaving the oligonucleotide
XX multimer at the cleavage site to produce (I) having well defined ends.
XX The method is used for the large-scale synthesis of DNA and RNA oligomers
XX for use, e.g. as probes and diagnostic agents and/or therapeutic agents

XX SQ Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAAA 24
Db 3 GGGCUUUUCUGAAGAGGCGGAAA 24

RESULT 34

AAV12939

ID AAV12939 standard; RNA; 49 BP.

AC AAV12939;


```
Db      43 GGGCTTTTCTGAAGAGCGGAAA 22
RESULT 36
AAV59252
ID      AAV59252 standard; RNA; 49 BP.
XX
AC      AAV59252;
XX
DT      21-OCT-2004 (revised)
DT      14-DEC-1998 (first entry)
XX
DE      multimeric RNA transcript sequence ID No.47.
XX
KW      ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.
XX
OS      Synthetic.
XX
FH      Key
FH      misc_binding
FT      Location/Qualifiers
FT      6..10
FT      /tag= a
FT      /bound_moiety= "Bound to positions 42 to 46"
FT      misc_binding
FT      18..20
FT      /tag= b
FT      /bound_moiety= "Bound to positions 25 to 27"
FT      misc_binding
FT      25..27
FT      /tag= c
FT      /bound_moiety= "Bound to positions 18 to 20"
FT      misc_binding
FT      31..34
FT      /tag= d
FT      /bound_moiety= "Bound to positions 37 to 40"
FT      misc_binding
FT      37..40
FT      /tag= e
FT      /bound_moiety= "Bound to positions 31 to 34"
FT      misc_feature
FT      41..42
FT      /tag= f
FT      /note= "Cleavage site"
FT      misc_binding
FT      42..46
FT      /tag= g
FT      /bound_moiety= "Bound to positions 6 to 10"
XX
XX      WO9838300-A1.
XX
XX      03-SEP-1998.
XX
XX      26-FEB-1998; 98WO-US003784.
XX
XX      26-FEB-1997; 97US-00805631.
XX      (UYRP ) UNIV ROCHESTER.
XX      Kool ET;
XX
XX      WPI; 1998-481202/41.
XX
XX      Synthesis of oligo:nucleotide(s) - using a single-stranded circular
XX      oligo:nucleotide template ribonucleotide triphosphate(s) and a
XX      polymerase to form multimer(s) which can be cleaved.
XX
XX      Example 25; Page 67; 100pp; English.
XX
XX      The oligomer sequence ID No.47 was used in an example of the invention
XX      for synthesising an RNA oligonucleotide, comprising combining a single-
XX      stranded circular oligonucleotide template comprising at least one copy
XX      of a nucleotide sequence complementary to the sequence of the desired RNA
XX      oligonucleotide with at least 2 types of ribonucleotide triphosphate and
XX      a polymerase enzyme to yield a single-stranded RNA oligonucleotide
XX      multimer complementary to the circular oligonucleotide template, where
XX      the RNA oligonucleotide multimer comprises multiple copies of the desired
XX      RNA oligonucleotide. The methods can be used for producing RNA
XX      oligonucleotides having a specific sequence and well defined ends. The
XX      RNA oligonucleotides produced can be used as probes, standards and
XX      diagnostic or therapeutic agents. They can be used for modifying the
XX
XX      structure or function of a target molecule. They can also be used to
XX      cleave disease-associated RNA, DNA or protein
XX
XX      Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
XX      Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
XX
XX      Query Match 56.0%; Score 14; DB 2; Length 49;
XX      Best Local Similarity 63.6%; Pred.No.1.5e+04;
XX      Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
OY      3 GGGCTTCACTTCAGAGGAGAAA 24
      ||||:|:|||||
Db      3 GGGCUUUCUGAAGAGCGGAAA 24
RESULT 37
AAV59253
ID      AAV59253 standard; RNA; 49 BP.
XX
AC      AAV59253;
XX
DT      14-DEC-1998 (first entry)
XX
DE      Monomeric ribozyme sequence ID No.48.
XX
KW      ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.
XX
OS      Synthetic.
XX
FH      Key
FH      misc_binding
FT      Location/Qualifiers
FT      11..18
FT      /tag= a
FT      /bound_moiety= "K28 junction in chronic myeloid leukemia"
FT      /note= "Forms double stranded region with bases 8 to 15
FT      of AAV59254"
FT      misc_structure
FT      19..38
FT      /tag= b
FT      /function= "Catalytic_domain"
FT      stem_loop
FT      26..35
FT      /tag= c
FT      misc_binding
FT      39..44
FT      /tag= d
FT      /bound_moiety= "K28 junction in chronic myeloid leukemia"
FT      /note= "Forms double stranded region with bases 1 to 6 of
FT      AAV59254"
XX
XX      WO9838300-A1.
XX
XX      03-SEP-1998.
XX
XX      26-FEB-1998; 98WO-US003784.
XX
XX      26-FEB-1997; 97US-00805631.
XX      (UYRP ) UNIV ROCHESTER.
XX      Kool ET;
XX
XX      WPI; 1998-481202/41.
XX
XX      Synthesis of oligo:nucleotide(s) - using a single-stranded circular
XX      oligonucleotide template ribonucleotide triphosphate(s) and a
XX      polymerase to form multimer(s) which can be cleaved.
XX
XX      Example 25; Page 67; 100pp; English.
XX
XX      The oligomer sequence ID No.48 was used in an example of the invention
XX      for synthesising an RNA oligonucleotide, comprising combining a single-
XX      stranded circular oligonucleotide template comprising at least one copy
XX      of a nucleotide sequence complementary to the sequence of the desired RNA
XX      oligonucleotide with at least 2 types of ribonucleotide triphosphate and
XX      a polymerase enzyme to yield a single-stranded RNA oligonucleotide
```

CC multimer complementary to the circular oligonucleotide template, where
CC the RNA oligonucleotide multimer comprises multiple copies of the desired
CC RNA oligonucleotide. The methods can be used for producing RNA
CC oligonucleotides having a specific sequence and well defined ends. The
CC RNA oligonucleotides produced can be used as probes, standards and
CC diagnostic or therapeutic agents. They can be used for modifying the
CC structure or function of a target molecule. They can also be used to
CC cleave disease-associated RNA, DNA or protein
XX
XX Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||: |: ||||| ||||
Db 11 GGGCUUUUCUGAAGAGCGGAA 32

RESULT 38

AAX30039
ID AAX30039 standard; RNA; 49 BP.

AC AAX30039;

DT 16-JUN-1999 (first entry)

XX RNA oligonucleotide SEQ ID NO:50.

DE Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.

XX Synthetic.

OS WO9909216-A2.

XX 25-FEB-1999.

XX 13-AUG-1998; 98WO-US016776.

XX 13-AUG-1997; 97US-00910632.

XX (UYRP) UNIV ROCHESTER.

XX Kool ET;

XX WPI; 1999-181062/15.

XX New detectably labelled oligonucleotide multimer, comprising multiple
XX contiguous copies of a repeated oligonucleotide - useful for detecting
XX target molecules in diagnosis and medicinal applications.

XX Example 25; Page 70; 103pp; English.

XX The present invention describes a detectably labelled oligonucleotide
XX multimer, comprising multiple contiguous copies of a repeated
XX oligonucleotides. The detectably labelled oligonucleotide multimer is
XX useful for detecting a target molecule. Oligonucleotide multimers may be
XX produced in sufficient quantity to be useful for diagnostic and medical
XX applications. The multimers are useful for affinity labelling of
XX proteins, and for signal amplification in highly sensitive affinity
XX capture and sequence identification applications. The method provides a
XX faster, cheaper and simpler way for large-scale production of DNA and RNA
XX oligomers and multimers. The incorporation of labels enables the
XX oligonucleotide multimers to be useful in diagnostics and medicine. The
XX present sequence represents an oligonucleotide used in an example from
XX the present invention

XX Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||: |: ||||| ||||
Db 11 GGGCUUUUCUGAAGAGCGGAA 32

RESULT 39

ADC65914
ID ADC65914 standard; RNA; 49 BP.

AC ADC65914;

XX 18-DEC-2003 (first entry)

XX RNA oligonucleotide #4.

DE RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
XX electroporation; calcium phosphate treatment; lipid-mediated delivery;
XX cation-mediated delivery; bacterial infection; viral infection;
XX drug resistant infection; double stranded DNA oligomer; ss.

OS Synthetic.

XX US2003087241-A1.

XX 08-MAY-2003.

XX 30-NOV-2001; 2001US-00997931.

XX 15-APR-1993; 93US-00047860.

XX 23-FEB-1995; 95US-00393439.

XX 26-FEB-1997; 97US-00805631.

XX 11-MAY-2000; 2000US-00569344.

XX (UYRP) UNIV ROCHESTER.

XX Kool ET;

XX WPI; 2003-755141/71.

XX Synthesizing RNA oligonucleotide involves combining single-stranded
XX circular oligonucleotide, ribonucleotide triphosphate and polymerase
XX enzyme to yield desired RNA complementary to circular oligonucleotide
XX template.

XX Example 25; SEQ ID NO 47; 78pp; English.

XX The invention relates to a method for synthesising an RNA
XX oligonucleotide, comprising combining a single-stranded circular
XX oligonucleotide template with at least two types of ribonucleotide
XX triphosphate and a polymerase enzyme to yield a single-stranded RNA
XX oligonucleotide multimer complementary to the circular oligonucleotide
XX template, where the RNA oligonucleotide multimer comprises multiple
XX copies of the desired RNA oligonucleotide. The method is useful for
XX synthesising an RNA oligonucleotide with well-defined ends. The circular
XX oligonucleotide is introduced into the cell using direct injection,
XX electroporation, calcium phosphate treatment, lipid-mediated delivery, or
XX cation-mediated delivery. The method is useful for treating bacterial
XX and/or viral infections in mammals, particularly drug resistant
XX infections, and for producing double stranded DNA oligomers. The method
XX is performed in the absence of an oligonucleotide primer, or without the
XX addition of auxiliary proteins. This sequence represents an
XX oligonucleotide used in the method of the invention.

XX Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;

Query Match 56.0%; Score 14; DB 10; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||: |: ||||| ||||
Db 3 GGGCUUUUCUGAAGAGCGGAA 24

RESULT 40
ADC65915
ID ADC65915 standard; RNA; 49 BP.
XX
AC ADC65915;
XX
DT 18-DEC-2003 (first entry)
XX
DE RNA oligonucleotide #5.
XX
KW RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW cation-mediated delivery; bacterial infection; viral infection;
KW drug resistant infection; double stranded DNA oligomer; ss.
XX
OS Synthetic.
XX
FN US2003087241-A1.
XX
PD 08-MAY-2003.
XX
PF 30-NOV-2001; 2001US-00997931.
XX
PR 15-APR-1993; 93US-00047860.
PR 23-FEB-1995; 95US-00393439.
PR 26-FEB-1997; 97US-00805631.
PR 11-MAY-2000; 2000US-00569344.
XX
PA (UVRP) UNIV ROCHESTER.
XX
PI Kool ET;
XX
DR WPI; 2003-755141/71.
XX
PT Synthesizing RNA oligonucleotide involves combining single-stranded
PT circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT enzyme to yield desired RNA complementary to circular oligonucleotide
PT template.
XX
PS Example 25; SEQ ID NO 48; 78pp; English.
XX
CC The invention relates to a method for synthesising an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template with at least two types of ribonucleotide
CC triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC oligonucleotide multimer complementary to the circular oligonucleotide
CC template, where the RNA oligonucleotide multimer comprises multiple
CC copies of the desired RNA oligonucleotide. The method is useful for
CC synthesising an RNA oligonucleotide with well-defined ends. The circular
CC oligonucleotide is introduced into the cell using direct injection,
CC electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC cation-mediated delivery. The method is useful for treating bacterial
CC and/or viral infections in mammals, particularly drug resistant
CC infections, and for producing double stranded DNA oligomers. The method
CC is performed in the absence of an oligonucleotide primer, or without the
CC addition of auxiliary proteins. This sequence represents an
CC oligonucleotide used in the method of the invention.
XX
SQ Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
Query Match 56.0%; Score 14; DB 10; Length 49;
Best Local Similarity 63.6%; Pred. NO. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 GGGCTTCACTTCAGAGGAGAA 24
||||:|:|||||
DB 11 GGGCUUUCUGAGAGGCGAA 32

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Query Match      61.6%; Score 15.4; DB 8; Length 50;
Best Local Similarity 76.0%; Pred. No. 2.7e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```

RESULT 2
BH853060/c          BH853060          40 bp      DNA      linear      GSS 13-JUN-2002
LOCUS               SALUK_075945.23.15.x Arabidopsis thaliana TDNA insertion lines
DEFINITION          Arabidopsis thaliana genomic clone SALUK_075945.23.15.x, genomic
                    survey sequence.
ACCESSION            BH853060
VERSION              BH853060.1      GI:21423931
KEYWORDS              GSS.
SOURCE               Arabidopsis thaliana (thale cress)
ORGANISM             Arabidopsis thaliana
                    Arabidopsis thaliana
                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE            1 (bases 1 to 40)
AUTHORS              Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                    Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
                    Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE               A Sequence-Indexed Library of Insertion Mutations in the
                    Arabidopsis Genome
JOURNAL              Unpublished (2001)
COMMENT              Contact: Joseph R. Ecker
                    Salk Institute Genomic Analysis Laboratory (SIGNAL)
                    The Salk Institute for Biological Studies
                    10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                    Tel: 858 453 4100 x1752
                    Fax: 858 558 6379
                    Email: ecker@salk.edu
                    This is single pass sequence recovered from the left border of
                    TDNA. This sequence lies within an annotated exon of Atig30890.
                    Class: TDNA tagged.
FEATURES             location/Qualifiers
                    1..40
                    /organism="Arabidopsis thaliana"
                    /mol_type="genomic DNA"
                    /ecotype="Col-0"
                    /db_xref="taxon:3702"
                    /clone="SALK_075945.23.15.x"
                    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                    /note="PCR was performed on Arabidopsis thaliana lines
                    each of which contains one or more TDNA insertion
                    elements. The resultant fragment for each line was
                    directly sequenced to determine the genomic sequence at
                    the site of insertion. Details of the protocols used can
                    be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match          58.4%; Score 14.6; DB 8; Length 40;
Best Local Similarity 81.0%; Pred.No. 6.1e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GCTTCACCTTCAGAGGAGAAAA 25
| ||||| ||||| ||||| |||||
Db 23 GTTTCATTTTCAGAGGAGCCAA 3

RESULT 3
CL656736/c          CL656736          49 bp      DNA      linear      GSS 09-JUL-2004
LOCUS               PRI0127b_G02 - PRI0127b.B21 (49) Mixed stage fosmid library of P.
DEFINITION          pacificus var. California Pristionchus pacificus genomic, genomic
                    survey sequence.
ACCESSION            CL656736
VERSION              CL656736.1      GI:50137472
KEYWORDS              GSS.
SOURCE               Pristionchus pacificus
                    Pristionchus pacificus
                    Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                    Neodiplogasteridae; Pristionchus.
REFERENCE            1 (bases 1 to 49)
AUTHORS              Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE               AppADB: an AcedB database for the nematode satellite organism

```

```

Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..49
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="vector: pBpifos-5 Fosmid vector"
ORIGIN
Query Match          57.6%; Score 14.4; DB 9; Length 49;
Best Local Similarity 75.0%; Pred.No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGGCGTTTCACCTTCAGAGGAGAAAA 25
| ||||| ||||| ||||| |||||
Db 30 TGGCGTGTCTCTTTGGAGGAGATAA 7

RESULT 4
AA074188
LOCUS               zF82G02.r1 Soares pineal gland N3HPG Homo sapiens cDNA clone
DEFINITION          IMAGE:383474.5, similar to SW:NB7M_BOVIN Q02367 NADH-UBIQUINONE
                    OXIDOREDUCTASE B17 SUBUNIT ;, mRNA sequence.
ACCESSION            AA074188
VERSION              AA074188.1      GI:1614251
KEYWORDS              EST.
SOURCE               Homo sapiens (human)
ORGANISM             Homo sapiens
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE            1 (bases 1 to 43)
AUTHORS              Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
                    Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
                    Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                    Trevasaki,E., Waterston,R., Williamson,A., Wohldmann,P. and
                    Wilson,R.
                    The WashU-Merck EST Project
                    Unpublished (1995)
                    Contact: Wilson RK
                    Washington University School of Medicine
                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                    Tel: 314 286 1800
                    Fax: 314 286 1810
                    Email: est@watson.wustl.edu
                    This clone is available royalty-free through LLNL; contact the
                    IMAGE Consortium (info@image.llnl.gov) for further information.
                    Possible reversed clone: similarity on wrong strand
                    Seq primer: -28M13 rev2 from Amersham
                    High quality sequence stop: 1.
                    Location/Qualifiers
                    1..43
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="GDB:1291731"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:383474"
                    /lab_host="DH10B (ampicillin resistant)"

```



```

SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS
1 (bases 1 to 46)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL
Unpublished (2001)
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
At2g27970.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
source
1..46
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_114176.40.35.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 55.2%; Score 13.8; DB 8; Length 46;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TTCCTTCAGGAGAA 23
Db 44 TTCTCTCAGTGGAGAA 28
RESULT 8
BF322803/c 49 bp mRNA linear EST 21-NOV-2000
LOCUS
DEFINITION
maa33h03.x1 NCI_CGAP_L110 Mus musculus cDNA clone IMAGE:3812980 3',
mRNA sequence.
ACCESSION
BF322803
VERSION
BF322803.1 GI:11272264
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
REFERENCE
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Other ESTs: maa33h03.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
MGI:1455092
Seq primer: -40UP from Gibco.
FEATURES
Location/Qualifiers
source
1..49
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3812980"
/sex="female"
/dev_stage="10 weeks"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_L110"
/note="Organ: liver; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 55.2%; Score 13.8; DB 2; Length 49;
Best Local Similarity 72.0%; Pred. No. 1.5e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACTTCAGAGGAGAAA 25
Db 25 CTGTGCCTTACTTCACAAAAA 1
RESULT 9
AA479970
LOCUS
DEFINITION
zvi18b11.81 Soares NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753981 3',
similar to SW:CA1H_HUMAN P39060 COLLAGEN ALPHA 1(XVIII) CHAIN ;,
mRNA sequence.
ACCESSION
AA479970
VERSION
AA479970.1 GI:2208121
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 31)
REFERENCE
AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
source
1..31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5976854"
/db_xref="taxon:9606"
/clone="IMAGE:753981"
/tissue types="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab host="DH10B"
/clone_lib="Soares_NhHMPu_S1"

```

/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NBHPU, and fetal heart NBHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Query Match 54.4%; Score 13.6; DB 1; Length 31;
Best Local Similarity 80.0%; Pred. No. 1.7e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAAAA 25
DB 8 CTTGCGTGCAAGGAGAAAA 27

RESULT 10
BH809976/c

LOCUS BH809976 38 bp DNA linear GSS 02-MAY-2002
DEFINITION SALK 036880 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_036880, genomic survey sequence.

ACCESSION BH809976
VERSION BH809976.1 GI:20387793
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednisi,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

COMMENT Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..38
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_036880"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 54.4%; Score 13.6; DB 8; Length 38;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAAAA 25

Db

34 CTTAACTTAAGACACAAAA 15

RESULT 11

BH840479

LOCUS

DEFINITION

from 3' end of P element, genomic survey sequence.

ACCESSION BH840479

VERSION BH840479.1 GI:21264795

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 29)

Levis,R., Hoskins,R., Liao,G., Mozden,N., Taang,G., He,Y.,

Karpen,G., Bellen,H., Rubin,G. and Spradling,A.

The Berkeley Drosophila Genome Project Gene Disruption Project

Unpublished (2001)

Contact: Gerald Rubin

Berkeley Drosophila Genome Project

University of California, Berkeley

LSA Building, Berkeley, CA 94720-3200, USA

Fax: 5106439947

Email: gerry@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P

element

The P element insertion position is base 1 in the 29 bases. This

insertion position refers to the first base of the 8 base target

recognition sequence.

Class: transposon-tagged.

Location/Qualifiers

1..29

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone_lib="Drosophila melanogaster P(SUPOR-P) P element

insertion lines"

/note="Inverse PCR was performed on Drosophila

melanogaster strains each of which contains one or more

P(SUPOR-P) P-element transposon insertion. The resultant

fragment for each strain was directly sequenced to

determine the genomic sequence at the site of insertion.

Details of the protocols used can be found at

<http://www.fruitfly.org/about/methods/inverse.pcr.html>."

ORIGIN

Query Match 53.6%; Score 13.4; DB 8; Length 29;

Best Local Similarity 73.9%; Pred. No. 2.1e+05;

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTTCAGAGGAGAAAA 25

DB 6 GCGCATCGTTTCAGCCGAGAAAA 28

RESULT 12

AU105696

LOCUS AU105696

DEFINITION

AU105696 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

COL05574, mRNA sequence.

ACCESSION AU105696

VERSION AU105696.1 GI:13555217

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AU105696 50 bp mRNA linear EST 28-JAN-2004
AU105696 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COL05574, mRNA sequence.

```

REFERENCE
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
JOURNAL      EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE      21270072
PUBMED
COMMENT      Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yusuzuki@ms.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).
FEATURES
source      Location/Qualifiers
              1..50
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="COL05574"
              /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      53.6%; Score 13.4; DB 1; Length 50;
Best Local Similarity 93.3%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      8 TCACCTTCAGAGGAGA 22
        |||||
Db      31 TCACCTCCGAGGAGA 45
RESULT 13
W88034/c
LOCUS      W88034
DEFINITION      mf68d04.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
              clone IMAGE:419431 5' similar to SW:AGRI_RAT P25304 AGRIN
              PRECURSOR. [1] ;, mRNA sequence.
ACCESSION      W88034
VERSION        W88034.1 GI:1402164
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE
AUTHORS        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
              Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
              Schellenberg,K., Steptoe,M., Tan,P., Underwood,K., Moore,B.,
              Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
              Waterston,R.
              The WashU-HMMI Mouse EST Project
              Unpublished (1996)
              Contact: Marra M/Mouse EST Project
              WashU-HMMI Mouse EST Project
              Washington University School of MedicineP
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: mouseest@watson.wustl.edu
              This clone is available royalty-free through LBNL ; contact the
              IMAGE Consortium (info@image.lbnl.gov) for further information.
              MGI:253983
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
FEATURES
source      Location/Qualifiers
              1..40
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:419431"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NBME13.5 14.5"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGGAATTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p773 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo. "
Query Match      52.0%; Score 13; DB 7; Length 40;
Best Local Similarity 76.2%; Pred. No. 3.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy      1 CTGGGCTTCACCTTCAGAGGAG 21
        |||||
Db      36 CTGGCATCCACTTCACAGCAG 16
RESULT 14
CL214736
LOCUS      CL214736
DEFINITION      CL214736
ACCESSION      M073D06
VERSION        M073D06.2 GI:49489678
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE
AUTHORS        Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,
              Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
              A large-scale, gene-driven mutagenesis approach for the functional
              analysis of the mouse genome
              Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
              22810117
              12904583
              On Jun 30, 2004 this sequence version replaced gi:40731637.
              Contact: GGTC
              German Genetrap Consortium (GGTC)
              Email: info@genetrap.de
              Rosabeteago gene trap. Sequence tag generated by 5'RACE. Additional
              sequence information can be found at:
              'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
              clone_id=M073D06'. ES cell line harboring insertion mutation of
              target gene is available at:
              'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
              1' Inhouse Sequence Identifier: 09460
              Class: Gene Trap.
              Location/Qualifiers
              1..47
              /organism="Mus musculus"
              /mol_type="mRNA"
              /strain="129 Sv"
              /db_xref="taxon:10090"
              /clone="M073D06"
              /sex="Male"

```

/cell type="Embryonic stem cell"
 /cell_line="ES cells 129S2 (formerly 129/SvPas)"
 /clone_lib="GGTC Gene Trap Library GV04C04"
 /note="Vector: ROSAbetageo"

ORIGIN

Query Match 52.0%; Score 13; DB 9; Length 47;
 Best Local Similarity 76.2%; Pred. No. 3.5e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTCAGAGAG 21
 ||| ||| ||| ||| ||| ||| |||
 Db 9 CTGAGCTGTACTGCAGAGGG 29

RESULT 15

BZ289408/c

LOCUS BZ289408 48 bp DNA linear GSS 24-OCT-2002
 DEFINITION SALK_022805.55.00.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_022805.55.00.x, genomic
 survey sequence.

ACCESSION

BZ289408

VERSION

BZ289408.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

REFERENCE

1 (bases 1 to 48)

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadfinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

Arabidopsis Genome

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of

TDNA.

FEATURES

Class: TDNA tagged.

Location/Qualifiers

1..48

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_022805.55.00.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match

Best Local Similarity

Matches 16; Conservative

0; Mismatches 5; Indels

0; Gaps 0;

QY 5 GCTTCACCTCAGAGAGAAA 25

||| ||| ||| ||| ||| ||| |||

Db 47 GCTTCTCTAGAGAGAAA 27

LOCUS

AUI07432

DEFINITION

AUI07432 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

ACCESSION

AUI07432

VERSION

AUI07432.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 50)

AUTHORS

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

JOURNAL

Diverse transcriptional initiation revealed by fine, large-scale

MEDLINE

mapping of mRNA start sites

PUBMED

EMBO Rep. 2 (5), 388-393 (2001)

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

Sugano,S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

FEATURES

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="LNG11157"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match

Best Local Similarity

Matches 16; Conservative

0; Mismatches 5; Indels

0; Gaps 0;

QY 3 GGGCTTCACCTCAGAGAGAA 23

||||| ||| ||| ||| ||| ||| |||

Db 35 GGGCTTCCTCGTCGGAGAA 15

||||| ||| ||| ||| ||| ||| |||

RESULT 17

AUI07433/c

LOCUS

AUI07433

DEFINITION

AUI07433 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

ACCESSION

AUI07433

VERSION

AUI07433.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 50)

AUTHORS

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG14512"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 52.0%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 23
|||||
Db 46 GGGCTTCCTCGTGGGAGAA 26

RESULT 18

AU107434/c

LOCUS

DEFINITION AU107434 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

LNG15774, mRNA sequence.

ACCESSION AU107434

VERSION AU107434.1 GI:13556955

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

FEATURES

source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG15774"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 52.0%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 23
|||||
Db 46 GGGCTTCCTCGTGGGAGAA 26

RESULT 19

CN488991/c

LOCUS

DEFINITION Mdfw2018i03.y1 Mdfw Malus x domestica cDNA clone Mdfw2018i03 5',

mRNA sequence.

ACCESSION CN488991

VERSION CN488991.1 GI:46602340

KEYWORDS EST.

SOURCE Malus x domestica (cultivated apple)

ORGANISM Malus x domestica

REFERENCE 1

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Schuyler S. Korban

Apple Functional Genomics grant - NSF 0321702

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

Library materials provided by: Schuyler S. Korban Library

constructed by: A. Hernandez / K. Gasic Library sequenced by:

Washington University Genome Sequencing Center

WashU EST name: aaf69e02.y1

High quality sequence stop: 50.

Location/Qualifiers

1..50

/organism="Malus x domestica"

/mol_type="mRNA"

/db_xref="taxon:3750"

/clone="Mdfw2018i03"

/lab_host="DH10B ampicillin resistant"

/clone_lib="Mdfw"

/note="Vector: DH10B ampicillin resistant; Site 1: NotI;

Site 2: EcoRII; Total RNA was extracted separately from

each stage (bud, balloon, open and after pollination),

using the 'pine tree' method. Poly(A)+mRNA was isolated

twice from total RNA from each stage using the Oligotex

Direct mRNA kit (Qiagen). mRNA was reverse transcribed

into double stranded cDNA using a modified oligo18(dT)

primer with an identifying tag sequence (see table below).

cDNAs from different stages were pooled in equal amounts

before adaptor ligation. Tag identification when

sequencing from 5' end: Stage 1 (bud) insert 18(A)TCGGA;

Stage 2 (balloon) insert 18(A)TCGGA; Stage 3 (open) insert

18(A)TCGCT; Stage 4 (after pollination) insert 18(A)TCGGT.

Tag identification when sequencing from 3' end: Stage 1

(bud) TCCGAT8(T) insert; Stage 2 (balloon) TCCGAT8(T)

insert; Stage 3 (open) ACCGAT8(T) insert; Stage 4 (after

pollination) ACCGAT8(T) insert. Double stranded cDNAs were

size selected (more than 450 bp), adapted with EcoRI

adapters at both ends and then digested with NotI. The

cDNAs were then directionally cloned into EcoRI-NotI

digested pBS II SK(+) phagemid vector(Stratagene).

Identification of adaptors and tags in 5'-end sequenced

clones: <Vector>...TAAGCTT<End Vector><Start

EcoRI adaptor>GATATCGAATTCATTCATTCGTTGGG <End

EcoRI adaptor><Start Insert>...AAAAAAAAAAAAAAAAA-End

Insert><Start tag>TCGCGAC<End tag><Start

NotI site>Vector>GCGGCCCGCCCGCGG... The total number of

white colony forming units (cfu) in the primary library

before amplification was 1.1x10⁶ cfu (colony forming

units). The background of empty clones was less than 1%.

Inserts ranged from 0.5kb to 3 kb, as determined by PCR.

Purified plasmid DNA from the primary library was

converted to single-stranded circles and used as a

template for PCR amplification using the T7 and T3 priming

sites flanking the cloned cDNA inserts. The purified PCR

products, representing the entire cloned cDNA population,

were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the normalized library. The total number of clones with insert was 9x10⁶ cfu. Background of empty clones was less than 1%

ORIGIN

Query Match 52.0%; Score 13; DB 7; Length 50;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GCTTCACCTTCAGAGGAGAAAA 25
||||| - - - - - |||||
Db 36 GCTTCCTCCAGATGTGATAA 16
||||| - - - - - |||||

RESULT 20

B1388654/c

LOCUS

DEFINITION B1388654 35 bp mRNA linear EST 14-DEC-2001
EST-CD34NN-022 cDNA Library from human CD34+ stem/progenitor cells
Homo sapiens cDNA 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B1388654.1 GI:17737237

EST.

B1388654

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Qy

Db

RESULT 22

BZ660542

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Qy

Db

RESULT 22

BZ660542

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Qy

Db

RESULT 22

BZ660542

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Qy

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic
survey sequence.

```

TITLE      A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL    Arabidopsis Genome
COMMENT    Unpublished (2001)
           Contact: Joseph R. Ecker
           Salk Institute Genomic Analysis Laboratory (SIGnAL)
           The Salk Institute for Biological Studies
           10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
           Tel: 858 453 4100 x1752
           Fax: 858 558 6379
           Email: ecker@alk.edu
           This is single pass sequence recovered from the left border of
           TDNA. This sequence lies within 300 bases of the 5' end of
           Atlg16100 and 300 bases of the 5' end of Atlg16110.
           Class: TDNA tagged.

FEATURES   Location/Qualifiers
           1..41
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            /mol_type="genomic DNA"
            /ecotype="Col-0"
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            /clone="SALK_023993.41.95.x"
            /clone_lib="Arabidopsis thaliana TDNA insertion lines"
            /note="PCR was performed on Arabidopsis thaliana lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can
            be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      51.2%; Score 12.8; DB 8; Length 41;
Best Local Similarity 70.8%; Pred. No. 4.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      2 TGGCGTTCACATTCAGAGGAGAAAA 25
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      15 TGGAGTTCACATTTGATGATAAAA 38

RESULT 23
LOCUS   AU247370
DEFINITION AU247370 FL Lolium multiflorum cDNA clone FL031A04-5, mRNA
sequence.
ACCESSION AU247370
VERSION   AU247370.1 GI:46504639
KEYWORDS EST.
SOURCE    Lolium multiflorum (Italian ryegrass)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Poae; Lolium.
REFERENCE 1 (bases 1 to 44)
AUTHORS   Ikeda S.
TITLE      Lolium multiflorum EST Project
JOURNAL    Unpublished (2004)
COMMENT    Contact: Seishi Ikeda
           Japan Grassland Farming Forage Seed Association(JFSA)
           Forage Crop Research Institute(FCRI)
           Higashiakada 388-5, Nishinasuno, Tochigi 329-2742, Japan
           Tel: 81-287-37-6755
           Fax: 81-287-37-6757
           Email: sikedae7@ifsass.or.jp
           contact:Tadashi Takamizo (takamizo@affrc.go.jp)
           National Institute of Livestock and Grassland Science, Nishinasuno
           Resistance gene analog.
           Location/Qualifiers
           1..44
            /organism="Lolium multiflorum"
            /mol_type="mRNA"
            /db_xref="taxon:4521"
            /clone="FL031A04-5"
            /tissue_type="Inflorescence"

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ORIGIN
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Best Local Similarity 87.5%; Pred. No. 4.2e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      10 ACTTCAGAGGAGAAAA 25
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      25 ACTTCGAGGAGAAAAA 40

RESULT 24
LOCUS   BZ353192
DEFINITION BZ353192 47 bp DNA linear GSS 14-NOV-2002
           SALK_119906.25.15.x Arabidopsis thaliana TDNA insertion lines
           Arabidopsis thaliana genomic clone SALK_119906.25.15.x, genomic
           survey sequence.
ACCESSION BZ353192
VERSION   BZ353192.1 GI:24944054
KEYWORDS GSS.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 47)
AUTHORS   Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R.,
           Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
           Shinn,P., Zimmerman,J. and Ecker,J.R.
           A Sequence-Indexed Library of Insertion Mutations in the
           Arabidopsis Genome
           Unpublished (2001)
           Contact: Joseph R. Ecker
           Salk Institute Genomic Analysis Laboratory (SIGnAL)
           The Salk Institute for Biological Studies
           10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
           Tel: 858 453 4100 x1752
           Fax: 858 558 6379
           Email: ecker@salk.edu
           This is single pass sequence recovered from the left border of
           TDNA.
           Class: TDNA tagged.
           Location/Qualifiers
           1..47
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /ecotype="Col-0"
            /db_xref="taxon:3702"
            /clone="SALK_119906.25.15.x"
            /clone_lib="Arabidopsis thaliana TDNA insertion lines"
            /note="PCR was performed on Arabidopsis thaliana lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can
            be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      51.2%; Score 12.8; DB 8; Length 47;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 TTCACCTTCAGAGGAGA 22
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      29 TTAACCTTCAGAGGAGA 44

RESULT 25
LOCUS   AZ818575
DEFINITION AZ818575 48 bp DNA linear GSS 20-FEB-2001
           2M0089M10R Mouse 10Kb plasmid UUGCIM library Mus musculus genomic
           clone UUGC2M0089M10 R, genomic survey sequence.

```

```

ACCESSION      AZ818575
VERSION        AZ818575.1  GI:12988483
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE
AUTHORS        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 48)
                Duth,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: dmunegenetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0088 row: M column: 10
                Seq primer: CACACAGGAAACAGCTATGACC
                Class: plasmid ends
                High quality sequence stop: 48.
                Location/Qualifiers
                1..48
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0088M10"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."

ORIGIN
Query Match      51.2%; Score 12.8; DB 8; Length 48;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGCTTCACCTTCAG 16
    ||||| |||||
Db 43 CTGGGATTGACTTCAG 28

RESULT 26
CN488991
LOCUS
DEFINITION      CN488991 50 bp mRNA linear EST 24-MAY-2004
                Mdfw2018i03.y1 Mdfw Malus x domestica cDNA clone Mdfw2018i03 5',
                mRNA sequence.

```

```

ACCESSION      CN488991
VERSION        CN488991.1  GI:46602340
KEYWORDS
SOURCE         Malus x domestica (cultivated apple)
ORGANISM       Malus x domestica

REFERENCE
AUTHORS        Korbhan,S., Vodkin,L., Liu,L., Gasic,K., Gonzales,O., Hernandez,A.,
                Alwinckle,H., Malnoy,M., Carroll,N., Goldsbrough,P., Orvis,K.,
                Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T.,
                Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Ronko,I.,
                Tsagareishvili,R., Kennedy,S., Waterston,R. and Wilson,R.
                Apple Functional Genomics grant - NSF 0321702
                Unpublished (2004)
                Contact: Schuyler S. Korbhan
                Apple Functional Genomics grant - NSF 0321702
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                Library materials provided by: Schuyler S. Korbhan Library
                constructed by: A. Hernandez / K. Gasic Library sequenced by:
                Washington University Genome Sequencing Center
                WashU EST name: aaf69e02.y1
                High quality sequence stop: 50.
                Location/Qualifiers
                1..50
                /organism="Malus x domestica"
                /mol_type="mRNA"
                /db_xref="taxon:3750"
                /clone="Mdfw2018i03"
                /lab_host="DH10B ampicillin resistant"
                /clone_lib="Mdfw"
                /note="Vector: DH10B ampicillin resistant; Site 1: NotI;
                Site 2: EcoRII; Total RNA was extracted separately from
                each stage (bud, balloon, open and after pollination),
                using the 'pine tree' method. Poly(A)+mRNA was isolated
                twice from total RNA from each stage using the Oligotex
                Direct mRNA kit (Qiagen). mRNA was reverse transcribed
                into double stranded cDNA using a modified oligo18(dT)
                primer with an identifying tag sequence (see table below).
                cDNAs from different stages were pooled in equal amounts
                before adaptor ligation. Tag identification when
                sequencing from 5' end: Stage 1 (bud) insert 18(A)TCGGA;
                Stage 2 (balloon) insert 18(A)TCGGA; Stage 3 (open) insert
                18(A)TCGGT; Stage 4 (after pollination) insert 18(A)TCGGT.
                Tag identification when sequencing from 3' end: Stage 1
                (bud) TCCGAl8(T) insert; Stage 2 (balloon) TCCGAl8(T)
                insert; Stage 3 (open) ACGGAl8(T) insert; Stage 4 (after
                pollination) ACGGAl8(T) insert. Double stranded cDNAs were
                size selected (more than 450 bp), adaptor with EcoRI
                adapters at both ends and then digested with NotI. The
                cDNAs were then directionally cloned into EcoRI-NotI
                digested pBS II SK(+) phagemid vector (Stratagene).
                Identification of adaptors and tags in 5'-end sequenced
                clones: <Vector>...TAAGCTT<End Vector><Start
                EcoRI adaptor>GATATCGAATTCATTTGTGTGGG <End
                EcoRI adaptor><Start Insert>...AAAAAAAAAAAAAAAA-End
                Insert> <Start tag>TCGCA<End Tag><Start
                NotI site>Vector>GCGGCCGCCACCGG... The total number of
                white colony forming units (cfu) in the primary library
                before amplification was 1.1x10^6 cfu (colony forming
                units). The background of empty clones was less than 1%.
                Inserts ranged from 0.5kb to 3 kb, as determined by PCR.
                Purified plasmid DNA from the primary library was
                converted to single-stranded circles and used as a
                template for PCR amplification using the T7 and T3 priming
                sites flanking the cloned cDNA inserts. The purified PCR
                products, representing the entire cloned cDNA population,
                were used as a driver for normalization. Hybridization

```

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FEATURES
source

```

between the single-stranded library and the PCR products was carried out for 44 hours at 30C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the normalized library. The total number of clones with insert was 9x10⁶ cfu. Background of empty clones was less than 1%

ORIGIN

Query Match 51.2%; Score 12.8; DB 7; Length 50;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCTTCAGAGGAGAA 23

Db 19 TCACATCTGAGGAGAA 34

RESULT 27
CR449386/c
LOCUS
DEFINITION CR449386 50 bp mRNA linear EST 19-JUN-2004
CR449386 XGC-tailbud Xenopus tropicalis cDNA clone TTbA045116 5',
mRNA sequence.
ACCESSION CR449386
VERSION CR449386.1 GI:48974973
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE
1 (bases 1 to 50)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (2004)
Unpublished (2004)
CONTACT: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk

Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TTbA045116.plkSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
Seq primer: SP6.
Location/Qualifiers
1..50
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TTbA045116"
/dev_stages="tailbud (stage 28-30)"
/lab_host="Escherichia coli DH10B."
/clone_lib="XGC-tailbud"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5' of poly A+ RNA from tailbud.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

FEATURES

source

ORIGIN

Query Match 51.2%; Score 12.8; DB 7; Length 50;
Best Local Similarity 70.8%; Pred. No. 4.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAGAGGAGAAA 25

Db 39 TCGGCGGACATCAGAGCAGAACA 16

RESULT 28
AZ792764
LOCUS
DEFINITION 2M0045N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045N21 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

AZ792764
AZ792764.1 GI:12937031
GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von

Niederhausen,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: N column: 21

Seq primer: CGTTGTAAACGACGCGCCACT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0045N21"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number ligated

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 50.4%; Score 12.6; DB 8; Length 24;
Best Local Similarity 78.9%; Pred. No. 4.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGAGG 19

Db 3 CTGGGTATCACTTGGGAGG 21

RESULT 29

CG723173

LOCUS

DEFINITION

CG723173

1119075A10.1EL.x1 1119 - RescueMu Grid AA Zea mays genomic, genomic

survey sequence.

```

ACCESSION   CG7231173
VERSION     CG7231173.1  GI:37758756
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 33)
AUTHORS     Walbot,V.
TITLE       Maize genomic sequences found using engineered RescueMu transposon
JOURNAL     Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Very probable ligation site of ends cut by single endonuclease.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1119075 row: A column: 10
            Class: transposon-tagged
FEATURES    .
            source
            1..33
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="mixed background W23/A188/B73/K55"
            /db_xref="taxon:4577"
            /tissue_type="leaf"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="1119 - RescueMu Grid AA"
            /note="Organ: leaf; Vector: RescueMu (engineered from
            pBluescript backbone); Site_1: BamHI; Site_2: BglII;
            RescueMu is a 4.9 kb, modified maize Mu transposon
            designed to allow plasmid rescue from total genomic DNA.
            Mu elements insert preferentially into transcription
            units. For more information on RescueMu, go to the web
            site 'www.zmdb.iastate.edu' and follow the links for
            'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
            was extracted from leaf strips, double digested using
            BamHI and BglII, and ligated to form circular plasmids.
            DH10B cells were transformed and then screened on LB
            plates with ampicillin."
ORIGIN
Query Match      50.4%; Score 12.6; DB 9; Length 33;
Best Local Similarity 78.9%; Pred. No. 4.9e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  5  GCTTCACCTTCAGAGGAA 23
Db   6  GATCCATTTCAGAGAGAA 24

RESULT 30
BX569109/c
LOCUS      BX569109 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse97e10_glc. mRNA sequence.
ACCESSION  BX569109
VERSION    BX569109.1  GI:33437048
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
            1 (bases 1 to 34)
REFERENCE   1 (bases 1 to 34)
AUTHORS     Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE       Adult midgut expressed sequence tags from the tsetse fly Glossina

```

```

morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
            source
            1..34
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /sub_species="morsitans"
            /db_xref="taxon:37546"
            /clone="Tse97e10_glc"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"
ORIGIN
Query Match      50.4%; Score 12.6; DB 5; Length 34;
Best Local Similarity 78.9%; Pred. No. 5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  7  TTCACCTTCAGAGAGAAAA 25
Db   28 TTCACCTTAGAAGAGAAAA 10

RESULT 31
AI597737/c
LOCUS      AI597737 37 bp mRNA linear EST 21-APR-1999
DEFINITION tu91b01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2258377 3'
            similar to TR:Q08805 Q08805 SALIVARY PROLINE-RICH PROTEIN L ; mRNA
            sequence.
ACCESSION  AI597737
VERSION    AI597737.1  GI:4606785
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 37)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES    Location/Qualifiers

```


GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES source

```
Location/Qualifiers
1..39
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-598D09-021211"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
```

ORIGIN

```
Query Match      50.4%; Score 12.6; DB 9; Length 39;
Best Local Similarity 78.9%; Pred. No. 5.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 7 TTCACCTTCAGAGGAGAAAA 25
    |||||
DB 28 TTCTTTTAGCTGAAAA 10
```

RESULT 34

```
AZ776620
LOCUS      AZ776620          40 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION 2M0010223F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0010823 F, genomic survey sequence.
```

```
ACCESSION  AZ776620
VERSION     AZ776620.1  GI:12904354
```

```
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
```

ORGANISM

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
```

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dundgenetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0010 row: E column: 23

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 40.

Location/Qualifiers

```
1..40
```

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0010E23"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```
Query Match      50.4%; Score 12.6; DB 8; Length 40;
Best Local Similarity 78.9%; Pred. No. 5.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 7 TTCACCTTCAGAGGAGAAAA 25
    |||||
DB 3  TTCTTTCAGAGGAGAAAA 21
```

RESULT 35

```
CG784583/c
```

```
LOCUS      CG784583          44 bp      mRNA      linear      GSS 16-JUN-2004
DEFINITION RRR727 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA,
mRNA sequence.
```

```
ACCESSION  CG784583
```

```
VERSION     CG784583.2  GI:40647596
```

```
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
```

ORGANISM

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 44)
BayGenomics.
http://baygenomics.ucsf.edu/
```

Unpublished (2001)

On Mar 1, 2004 this sequence version replaced gi:38157143.

Contact: BayGenomics

Bay Area Functional Genomics Consortium (BayGenomics)

Email: info@baygenomics.ucsf.edu

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=RRR727

Class: Gene Trap.

Location/Qualifiers

```
1..44
```

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129 ola"

/db_xref="taxon:10090"

/sex="Male"

/cell_type="Embryonic stem cell"

/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"

/note="Vector: pGT0Lxf"

ORIGIN

```
Query Match      50.4%; Score 12.6; DB 9; Length 44;
Best Local Similarity 78.9%; Pred. No. 5.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```



```

Qy      6  CTTCACTTCAGAGGAGAA 24
Db      40 CTTCCCATCTCGAGGAGAA 22

RESULT 36
LOCUS   AI446300
DEFINITION t3jig05.x1 NCI CGAP_Panl Homo sapiens cDNA clone IMAGE:2143160 3'
similar to gb:MS9371 TYROSINE-PROTEIN KINASE RECEPTOR ECK PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION AI446300
VERSION   AI446300.1 GI:4294243
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
FEATURES
source
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2143160"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Panl"
/notes="Organ: Pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Query Match 50.4%; Score 12.6; DB 1; Length 46;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6  CTTCACTTCAGAGGAGAA 24
Db      15 CTTTATTCAGAGCAGAA 33

RESULT 37
LOCUS   BH629703
DEFINITION 1007075E03.2EL_x1 1007 - RescueMu Grid H Zea mays genomic, genomic
survey sequence.
ACCESSION BH629703
VERSION   BH629703.1 GI:18442954
KEYWORDS GSS.
SOURCE   Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 46)
AUTHORS Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007075 column: 36
Class: transposon-tagged.
Location/Qualifiers
1..46
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.lastate.edu' and follow the links for
'RescueMu.' Grid H was grown at Berkeley in 2001. DNA
was extracted from leaf punches, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match 50.4%; Score 12.6; DB 8; Length 46;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  TGGGCTTCACATTCAGAGGA 20
Db      7  TGGGCTTCGATTCGTGGA 25

RESULT 38
LOCUS   BH911440
DEFINITION SALK_068707.30.80.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_068707.30.80.x, genomic
survey sequence.
ACCESSION BH911440.1 GI:22724373
VERSION   BH911440
KEYWORDS GSS.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 47)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

```


Email: ecker@ealk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .47
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SAUK_068707.30.80.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.ealk.edu/tdna_protocols.html"

ORIGIN

Query Match 50.4%; Score 12.6; DB 8; Length 47;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TTCACTTCAGAGGAGAAA 25
Db 19 TTCTTTTACAGAGAAA 37

RESULT 39
AUI05888/c
LOCUS
DEFINITION AUI05888 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS03170, mRNA sequence.
ACCESSION AUI05888
VERSION AUI05888.1 GI:13555409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 50)
Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese.J.,
Hata.H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K.,
Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and
Sugano.S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES

source

1. .50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS03170"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 50.4%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAG 21

Db

43 GGGTGTCTCTTCAGAGCAG 25

RESULT 40

A2992198/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0276E17"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy

1 CTGGGCTTCACTTC

14

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy

1 CTGGGCTTCACTTC

14

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy

1 CTGGGCTTCACTTC

14

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy

1 CTGGGCTTCACTTC

14

Db | |||||
 16 CAGGCTTCACTTC 3

Search completed: November 18, 2005, 21:12:46
Job time : 1198.82 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 48.5741 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-5

Perfect score: 25

Sequence: 1 CTGGGCTTCACTTCAGAGGAGAAAA 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	1	US-07-989-160-5
2	16.8	67.2	25	4	US-09-396-196G-113292
3	14.6	58.4	25	4	US-09-396-196G-90079
4	14.4	57.6	30	2	US-08-353-372A-28
5	14.4	57.6	30	3	US-08-057-430A-19
6	14.2	56.8	33	2	US-08-360-606B-14
7	14	56.0	49	3	US-08-910-632-46
8	14	56.0	49	3	US-08-910-632-47
9	14	56.0	49	3	US-08-910-632-48
10	14	56.0	49	3	US-08-910-632-50
11	14	56.0	49	3	US-08-805-631A-46
12	14	56.0	49	3	US-08-805-631A-47
13	14	56.0	49	3	US-08-805-631A-48
14	14	56.0	49	3	US-08-805-631A-50
15	14	56.0	49	3	US-09-569-344-46
16	14	56.0	49	3	US-09-569-344-47
17	14	56.0	49	3	US-09-569-344-48
18	14	56.0	49	3	US-09-569-344-50
19	13.8	55.2	25	4	US-09-396-196G-113293
20	13.8	55.2	25	4	US-08-388-029A-60
21	13.6	54.4	25	2	US-08-659-251-19
22	13.6	54.4	25	3	US-09-256-490-19
23	13.6	54.4	25	4	US-09-396-196G-50968
24	13.6	54.4	25	4	US-09-396-196G-50969
25	13.6	54.4	25	4	US-09-396-196G-52946
26	13.6	54.4	25	4	US-09-396-196G-117350
27	13.6	54.4	25	5	PCT-US96-11445-19

c	28	13.6	54.4	36	3	US-09-230-288-5	Sequence 5, Appli
	29	13.4	53.6	22	3	US-08-943-731-239	Sequence 239, App
c	30	13.4	53.6	25	4	US-09-396-196G-13674	Sequence 13674, A
c	31	13.4	53.6	25	4	US-09-396-196G-56218	Sequence 56218, A
	32	13.4	53.6	25	4	US-09-396-196G-64443	Sequence 64443, A
	33	13.4	53.6	25	4	US-09-396-196G-64567	Sequence 64567, A
c	34	13.4	53.6	34	1	US-08-160-670A-19	Sequence 19, Appl
	35	13.4	53.6	42	3	US-08-660-645A-36	Sequence 36, Appl
c	36	13.4	53.6	42	3	US-09-298-718-36	Sequence 36, Appl
c	37	13.4	53.6	42	3	US-09-546-969-36	Sequence 36, Appl
c	38	13.4	53.6	42	3	US-08-980-832-15	Sequence 15, Appl
c	39	13.4	53.6	42	4	US-09-547-267-36	Sequence 36, Appl
c	40	13.4	53.6	42	4	US-09-920-923B-15	Sequence 15, Appl
c	41	13.4	53.6	47	3	US-09-336-643A-66	Sequence 66, Appl
	42	13.2	52.8	20	3	US-09-331-260-5	Sequence 5, Appli
	43	13.2	52.8	20	3	US-09-142-138-3	Sequence 3, Appli
	44	13.2	52.8	20	3	US-09-582-660-3	Sequence 3, Appli
	45	13.2	52.8	20	4	US-09-142-141A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-07-989-160-5
; Sequence 5, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-07-989-160-5

Query Match 100.0%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACTTCAGAGGAGAAAA 25
|||||

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Db      1 CTGGGCTTCACTTCAGAGAGAAA 25

RESULT 2
US-09-396-196G-113292
; Sequence 113292, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-113292

Query Match      67.2%; Score 16.8; DB 4; Length 25;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CTGGGCTTCACTTCAGAGGA 20
        |||||
Db      4 CTGGGCTTCACTTCGGAGGA 23

RESULT 3
US-09-396-196G-90079
; Sequence 90079, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-90079

Query Match      58.4%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 TGGGCTTCACTTCAGAGAGA 22
        |||||
Db      1 TGGGCTACATCGCGATGAGA 21

RESULT 4
US-08-353-372A-28
; Sequence 28, Application US/08353372A
; Patent No. 5840479
; GENERAL INFORMATION:
; APPLICANT: Little, Melvyn
```

```
; APPLICANT: Breitling, Frank B
; APPLICANT: Seehaus, Thomas
; APPLICANT: Dubel, Stefan
; APPLICANT: Klewinghaus, Iris
; TITLE OF INVENTION: Preparation and Use of Gene Banks of
; TITLE OF INVENTION: Synthetic Human Antibodies ("Synthetic Human-Antibody
; TITLE OF INVENTION: Libraries")
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,372A
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/654,207
; FILING DATE: 30-JAN-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: DE P 40 02 897.6
; FILING DATE: 01-FEB-1990
; APPLICATION NUMBER: DE P 40 03 880.7
; FILING DATE: 09-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552.1032-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-353-372A-28

Query Match      57.6%; Score 14.4; DB 2; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 CTGGGCTTCACTTCAGAGAGAAA 24
        |||||
Db      7 CTTGATTCATTAAAGAGAGAAA 30

RESULT 5
US-08-057-430A-19
; Sequence 19, Application US/08057430A
; Patent No. 6319690
; GENERAL INFORMATION:
; APPLICANT: Little, Melvyn
; APPLICANT: Breitling, Frank B.
; APPLICANT: Seehaus, Thomas
; APPLICANT: Dubel, Stefan
```

```
/ APPLICANT: Kiewinghaus, Iris
/ TITLE OF INVENTION: PREPARATION AND USE OF GENE BANKS OF
/ HUMAN ANTIBODIES ("HUMAN-ANTIBODY LIBRARIES")
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
/ ADDRESSES: DUNNER, LLP
/ STREET: 1300 I Street, NW
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/057,430A
/ FILING DATE: 06-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/648,522
/ FILING DATE: 30-JAN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE P 40 02 898.4
/ FILING DATE: 01-FEB-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE P 40 03 881.5
/ FILING DATE: 09-FEB-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Forman, David S.
/ REGISTRATION NUMBER: 33,694
/ REFERENCE/DOCKET NUMBER: 05552.1033-01000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-057-430A-19

Query Match 57.6%; Score 14.4; DB 3; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTCAGAGGAGAAA 24
Db 7 CTGGAATTCATTAAAGAGGAGAAA 30

RESULT 6
US-08-360-606B-14
; Sequence 14, Application US/08360606B
; Patent No. 5919617
; GENERAL INFORMATION:
; APPLICANT: Jnanendra K. Bhattacharjee
; APPLICANT: Richard C. Garrad
; APPLICANT: Paul L. Skatrud
; APPLICANT: Robert P. Peery
; TITLE OF INVENTION: Methods and Reagents for
; TITLE OF INVENTION: Detecting Fungal Pathogens in a
; TITLE OF INVENTION: Biological Sample
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive Suite 3200
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
```

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/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MS Word 7.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/360,606B
/ FILING DATE: December 21, 1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Berghoff, Paul H.
/ REGISTRATION NUMBER: 30,243
/ REFERENCE/DOCKET NUMBER: 94,319
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312)913-0001
/ TELEFAX: (312)913-0002
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Saccharomyces cerevisiae
US-08-360-606B-14

Query Match 56.8%; Score 14.2; DB 2; Length 33;
Best Local Similarity 84.2%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTTCACCTTCAGAGGAGAAA 24
Db 1 CTTCATTTAAGAGGAGAAA 19

RESULT 7
US-08-910-632-46/c
; Sequence 46, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220,00010130
; CURRENT APPLICATION NUMBER: US/08/910,632B
; CURRENT FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805,631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393,439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047,860
; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 46
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: coding DNA circle
US-08-910-632-46

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 77.3%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTTCAGAGGAGAAA 24
Db 43 GGGCTTTTCTGAGAGGCGAAA 22

RESULT 8
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US-08-910-632-47
; Sequence 47, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220.00010130
; CURRENT APPLICATION NUMBER: US/08/910,632B
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805,631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393,439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047,860
; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: multimeric RNA transcript
US-08-910-632-47
Query Match          56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
|||||:|:|||||
Db 3 GGGCUUUCUGAGAGGCGAA 24

RESULT 9
US-08-910-632-48
; Sequence 48, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220.00010130
; CURRENT APPLICATION NUMBER: US/08/910,632B
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805,631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393,439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047,860
; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: monomeric ribozyme
US-08-910-632-48
Query Match          56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
|||||:|:|||||
Db 11 GGGCUUUCUGAGAGGCGAA 32

RESULT 10
US-08-910-632-50
; Sequence 50, Application US/08910632B
; Patent No. 6077668
```

```
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220.00010130
; CURRENT APPLICATION NUMBER: US/08/910,632B
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805,631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393,439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047,860
; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: monomeric ribozyme
US-08-910-632-50
Query Match          56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
|||||:|:|||||
Db 11 GGGCUUUCUGAGAGGCGAA 32

RESULT 11
US-08-805-631A-46/c
; Sequence 46, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; TITLE OF INVENTION: DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GERHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,631A
; FILING DATE: 26-FEB-97
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
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STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-805-631A-46

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 77.3%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 43 GGGCTTTCGAGAGGCGAA 22

RESULT 12
US-08-805-631A-47
; Sequence 47, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; TITLE OF INVENTION: DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,631A
; FILING DATE: 26-FEB-97
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION NUMBER: 41,287
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-805-631A-47

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 3 GGGCUUUCUGAAGAGCGAA 24

RESULT 13
US-08-805-631A-48
; Sequence 48, Application US/08805631A

Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; TITLE OF INVENTION: DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,631A
; FILING DATE: 26-FEB-97
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION NUMBER: 41,287
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-805-631A-48

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 11 GGGCUUUCUGAAGAGCGAA 32

RESULT 14
US-08-805-631A-50
; Sequence 50, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; TITLE OF INVENTION: DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 11 GGGCUUUCUGAAGAGCGAA 32

RESULT 14
US-08-805-631A-50
; Sequence 50, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; TITLE OF INVENTION: DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 11 GGGCUUUCUGAAGAGCGAA 32

RESULT 14
US-08-805-631A-50
; Sequence 50, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; TITLE OF INVENTION: DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 3 GGGCUUUCUGAAGAGCGAA 24

RESULT 13
US-08-805-631A-48
; Sequence 48, Application US/08805631A

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 3 GGGCUUUCUGAAGAGCGAA 24

RESULT 13
US-08-805-631A-48
; Sequence 48, Application US/08805631A

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 3 GGGCUUUCUGAAGAGCGAA 24

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/805.631A
;; FILING DATE: 26-FEB-97
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/393,439
;; FILING DATE: 23-FEB-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/047,860
;; FILING DATE: 15-APR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SANDBERG, VICTORIA A.
;; REGISTRATION NUMBER: 41,287
;; REFERENCE/DOCKET NUMBER: 220.00010140
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-305-1226
;; TELEFAX: 612-305-1228
;; INFORMATION FOR SEQ ID NO: 50:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 49 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: RNA (genomic)
;; US-08-805-631A-50

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTCAGAGGAGAA 24
|||||:|:|||||
Db 11 GGGCTTTCGAGAGGCGAA 32

RESULT 15
US-09-569-344-46/c
; Sequence 46, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6368802th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,344
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/805,631
; FILING DATE: 26-FEB-97
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 612-305-1226
;; TELEFAX: 612-305-1228
;; INFORMATION FOR SEQ ID NO: 46:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 49 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: circular
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-569-344-46

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 77.3%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTCAGAGGAGAA 24
|||||:|:|||||
Db 43 GGGCTTTCGAGAGGCGAA 22

RESULT 16
US-09-569-344-47
; Sequence 47, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6368802th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,344
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/805,631
; FILING DATE: 26-FEB-97
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-569-344-47

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTTCAGAGGAGAA 24
||||:|:|||||
Db 3 GGGCUUUCUGAAGAGCGGAA 24

RESULT 17

US-09-569-344-48
; Sequence 48, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
DNA

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-569-344-48

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTTCAGAGGAGAA 24
||||:|:|||||
Db 11 GGGCUUUCUGAAGAGCGGAA 32

RESULT 18

US-09-569-344-50
; Sequence 50, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
DNA
NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-569-344-50

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTTCAGAGGAGAA 24
||||:|:|||||
Db 11 GGGCUUUCUGAAGAGCGGAA 32

RESULT 19

US-09-396-196G-113293
; Sequence 113293, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:

APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 113293

LENGTH: 25
TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-113293

Query Match 55.2%; Score 13.8; DB 4; Length 25;

```
Best Local Similarity 88.2%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGCTTCACTTCAGAGGA 20
Db 1 GGCTTCACTTCGAGGA 17

RESULT 20
US-08-388-029A-60
; Sequence 60, Application US/08388029A
; Patent No. 6110665
; GENERAL INFORMATION:
; APPLICANT: FENGER, CLARA K.
; APPLICANT: GRANSTROM, DAVID R.
; APPLICANT: GAJADHAR, ALVIN A.
; TITLE OF INVENTION: SARCOCYSTIS NEURONA DIAGNOSTIC PRIMER
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 CANAL CENTER PLAZA, SUITE 300
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,029A
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PRICE, ROBERT L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 434-046
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; TELEX: AMERPAT
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-388-029A-60

Query Match 55.2%; Score 13.8; DB 3; Length 50;
Best Local Similarity 78.9%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TTCACTTCAGAGGAAAA 25
Db 3 TTAACNNAGAGGTGAAAA 21

RESULT 21
US-08-659-251-19
; Sequence 19, Application US/08659251
; Patent No. 5883081
; GENERAL INFORMATION:
; APPLICANT: Kraus, Guenter
; APPLICANT: Wong-Staal, Flossie
; APPLICANT: Talbott, Randy
; APPLICANT: Poeschla, Eric
; TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses
; NUMBER OF SEQUENCES: 50
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,251
; FILING DATE: No. 5883081 yet assigned
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,441
; FILING DATE: 26-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 02307E-056410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..25
; OTHER INFORMATION: /note= "GR72 (outside, left) primer for
; OTHER INFORMATION: HIV-2KR env"
; US-08-659-251-19

Query Match 54.4%; Score 13.6; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGCTTCACTTCAGAGGAA 23
Db 5 GGACTAACTCGAGAGGAA 24

RESULT 22
US-09-256-490-19
; Sequence 19, Application US/09256490
; Patent No. 6235881
; GENERAL INFORMATION:
; APPLICANT: Kraus, Guenter
; APPLICANT: Wong-Staal, Flossie
; APPLICANT: Talbott, Randy
; APPLICANT: Poeschla, Eric
; TITLE OF INVENTION: Isolation of No. 6235881el HIV-2 Proviruses
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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RESULT 24
US-09-396-196G-50969
; Sequence 50969, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION;

```

; Patent No. 6821724
;
; GENERAL INFORMATION:
;
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
;
; TITLE OF INVENTION: Methods of Genetic Analysis
;
; FILE REFERENCE: 3101.1
;
; CURRENT APPLICATION NUMBER: US/09/396,196G
;
; CURRENT FILING DATE: 1999-09-15
;
; PRIOR APPLICATION NUMBER: 60/100,678
;

```

```

; PRIOR FILING DATE: 1998-09-17
;
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 117350
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-117350

```

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels

Qy 2 TGGGCTTCACTTCAGAGGAG 21
||| | ||||| |||||
Db 25 TGGGATACACTTCTGTGGAG 6

RESULT 27

```

PCT-US96-11445-19
; Sequence 19, Application PC/TUS9611445
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruses
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11445

```

```

/ CLASSIFICATION:
/
/ ATTORNEY/AGENT INFORMATION:
/
/   NAME: Berliner, Robert
/
/   REGISTRATION NUMBER: 20,121
/
/   REFERENCE/DOCKET NUMBER: 5555-399C1
/
/ TELECOMMUNICATION INFORMATION:
/
/   TELEPHONE: (213) 977-1001
/
/   TELEFAX: (213) 977-1003
/
/ INFORMATION FOR SEQ ID NO: 19:
/
/ SEQUENCE CHARACTERISTICS:
/
/   LENGTH: 25 base pairs
/
/   TYPE: nucleic acid
/
/   STRANDEDNESS: single
/
/   TOPOLOGY: linear
/
/   MOLECULE TYPE: DNA
/
/   FEATURE:
/

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; NAME/KEY: -
; LOCATION: 1.25
; OTHER INFORMATION: /note= "GR72 (outside, left) primer for
; OTHER INFORMATION: HIV-2KR env"
PCT-US96-11445-19

```

Query Match 54.4%; Score 13.6; DB 5; Length 25;
Best Local Similarity 80.0%; Pred. NO. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels

Qy

4 GGCTTCACTTCAGAGGAGAA 23
||| ||| ||| ||| ||| |||

Db

5 GGACTAAGTGCAGAGGAGAA 24

RESULT 28

US-09-230-288-5/c

```

1 Sequence 5, Application US/09230288
2 Patent No. 6329160
3 GENERAL INFORMATION:
4 APPLICANT: SCHNEIDER, Rene
5 VANCOV, Tony
6 JURY, Karen
7 TITLE OF INVENTION: BIOSENSORS
8 NUMBER OF SEQUENCES: 18
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
11 STREET: 624 Ninth Street, N.W., Suite 300
12 CITY: Washington
13 STATE: D.C.
14 COUNTRY: USA
15 ZIP: 20001
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patentrin Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 FILING DATE: 07-Sep-1999
23 CLASSIFICATION: <Unknown>
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: PCT/AU97/00473
26 FILING DATE: 25-JUL-1997
27 APPLICATION NUMBER: AU POL280
28 FILING DATE: 29-JUL-1996
29 ATTORNEY/AGENT INFORMATION:
30 NAME: NEWMARK, Sheridan
31 REGISTRATION NUMBER: 20,520
32 REFERENCE/DOCKET NUMBER: SCHNEIDER-2
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 202-628-5197
35 TELEFAX: 202-737-3528
36 INFORMATION FOR SEQ ID NO: 5:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 36 base pairs
39 TYPE: nucleic acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 MOLECULE TYPE: cDNA
43 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
44 US-09-230-288-5

```

```

Query Match          54.4%; Score 13.6; DB 3; Length 36;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

Qy 1 CTGGCTTCACTTCAGAGGA 20
Db 34 CGGCGTTTCACTTCTGAGGA 15

RESULT 29

```

US-08-343-731-239
? Sequence 239, Application US/08943731
? Patent No. 6265157
? GENERAL INFORMATION:
? APPLICANT: PROCKOP, DARWIN J.
? APPLICANT: SPOTILA, LORETTA D.
? APPLICANT: DELTAS, CONSTANTINOS D.
? APPLICANT: SEREDA, LARISA
? APPLICANT: LARSON, ANDREA W.
? APPLICANT: PACK, MICHAEL
? APPLICANT: COLIGE, ALAIN
? APPLICANT: EARLY, JAMES
? APPLICANT: KORKKO, JARMO
? APPLICANT: ALA-KOKKO, LEENA, et al.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
? TYPE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE
? NUMBER OF SEQUENCES: 666

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
;; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
;; STREET: .FLR.
;; CITY: PHILADELPHIA
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103-7086
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/943,731
;; FILING DATE: 03-OCT-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/212,322
;; FILING DATE: 14-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/803,628
;; FILING DATE: 03-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DOYLE LEARY Ph.D., KATHRYN
;; REGISTRATION NUMBER: 36,317
;; REFERENCE/DOCKET NUMBER: 9598-27
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-965-1284
;; TELEFAX: 215-567-2991
;; TELEX: 831-494
;; INFORMATION FOR SEQ ID NO: 239:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-943-731-239

Query Match 53.6%; Score 13.4; DB 3; Length 22;
Best Local Similarity 93.3%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCA 15
Db 7 CTGGGCTTCACGTCA 21

RESULT 30
US-09-396-196G-13674/c
; Sequence 13674, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13674
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-13674

Query Match 53.6%; Score 13.4; DB 4; Length 25;

Best Local Similarity 73.9%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2 TGGGCTTCACCTCAGAGGAGAA 24
Db 25 TGGCATTGCTGTGATGGGAAA 3

RESULT 31
US-09-396-196G-56218/c
; Sequence 56218, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56218
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-56218

Query Match 53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACCTCAGAGGAGAA 23
Db 23 CTGGTATTGCTCCAGGGGAGAA 1

RESULT 32
US-09-396-196G-64443
; Sequence 64443, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64443
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-64443

Query Match 53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GGGCTTCACCTCAGAGGAGAA 25
Db 2 GAGCATCTTCTGTGAGAGAA 24

RESULT 33

Query Match 53.6%; Score 13.4; DB 1; Length 34;
Best Local Similarity 69.6%; Pred. NO. 3.8e+03;
Matches 16; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

RESULT 36
US-09-298-718-36/c
; Sequence 36, Application US/09298718
; Patent No. 6124113
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tessier, Michel
; APPLICANT: van Loon, Adolphus
; TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION

NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,718
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-298-718-36

Query Match 53.6%; Score 13.4; DB 3; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACCTTCAGAGGAGAA 23
Db 32 CTGGCCGTCGCTTGAAGAGGA 10

RESULT 37
US-09-546-969-36/c
Sequence 36, Application US/09546969
Patent No. 6207409
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,969
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-546-969-36

Query Match 53.6%; Score 13.4; DB 3; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACCTTCAGAGGAGAA 23
Db 32 CTGGCCGTCGCTTGAAGAGGA 10

RESULT 38
US-08-980-832-15/c
Sequence 15, Application US/08980832B
Patent No. 6291204
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentative Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 42
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer MUT6
US-08-980-832-15

Query Match 53.6%; Score 13.4; DB 3; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACCTTCAGAGGAGAA 23
Db 32 CTGGCCGTCGCTTGAAGAGGA 10

RESULT 39
US-09-547-267-36/c
Sequence 36, Application US/09547267
Patent No. 6613543
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-547-267-36

Query Match 53.6%; Score 13.4; DB 4; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGCGTTCACCTTCAGAGGAGAA 23
|||||
Db 32 CTGGCGTTCGCTTGAAGGAGGA 10

RESULT 40
US-09-920-923B-15/c
Sequence 15, Application US/09920923B
Patent No. 6677134
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)
CURRENT APPLICATION NUMBER: US/09/920,923B
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent In version 3.1
SEQ ID NO 15
LENGTH: 42
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Primer MUT6
US-09-920-923B-15

Query Match 53.6%; Score 13.4; DB 4; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGCGTTCACCTTCAGAGGAGAA 23

Db 32 CTGGCGTTCGCTTGAAGGAGGA 10
|||||

Search completed: November 18, 2005, 11:22:00
Job time : 49.5741 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 336.027 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-5

Perfect score: 25

Sequence: 1 CTGGGCTTCACTTCAGAGGAGAA 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	8	US-08-469-172-5
2	25	100.0	25	20	US-10-788-779-5
3	17.2	68.8	25	22	US-10-719-900-593102
4	17	68.0	25	22	US-10-719-900-978129
5	16.8	67.2	25	22	US-10-719-900-424739

6	16.8	67.2	25	22	US-10-809-189-113292
7	16.8	67.2	25	26	US-11-036-317-100259
8	16.8	67.2	25	26	US-11-036-317-633439
9	16.8	67.2	25	26	US-11-036-317-764997
10	16.6	66.4	25	22	US-10-719-900-970185
11	16.6	66.4	25	22	US-10-719-900-970186
12	16.4	65.6	25	24	US-10-719-956-261669
13	16.2	64.8	25	24	US-10-719-900-482864
14	16.2	64.8	25	24	US-10-719-956-243899
15	16.2	64.8	25	24	US-10-719-956-419311
16	16	64.0	25	22	US-10-956-157-311797
17	16	64.0	25	26	US-11-036-317-209513
18	16	64.0	25	26	US-11-036-317-366428
19	16	64.0	25	26	US-11-036-317-823362
20	16	64.0	25	26	US-11-036-317-823363
21	15.8	63.2	25	22	US-10-719-900-383306
22	15.8	63.2	25	22	US-10-719-900-430473
23	15.8	63.2	25	22	US-10-719-900-866704
24	15.8	63.2	25	26	US-11-036-317-788701
25	15.6	62.4	25	22	US-10-719-900-248480
26	15.6	62.4	25	22	US-10-719-900-387762
27	15.6	62.4	25	22	US-10-719-900-593103
28	15.6	62.4	25	22	US-10-956-157-279510
29	15.6	62.4	25	22	US-10-956-157-315928
30	15.6	62.4	25	26	US-11-036-317-270365
31	15.6	62.4	25	26	US-11-036-317-366190
32	15.6	62.4	25	26	US-11-036-317-423606
33	15.4	61.6	25	22	US-10-719-900-978130
34	15.4	61.6	25	24	US-10-719-956-62957
35	15.4	61.6	25	24	US-10-719-956-439125
36	15.4	61.6	25	26	US-11-036-317-430286
37	15.4	61.6	25	26	US-11-036-317-828846
38	15.4	61.6	25	26	US-11-060-756-182301
39	15.2	60.8	25	22	US-10-719-900-424738
40	15.2	60.8	25	22	US-10-719-900-823343
41	15.2	60.8	25	24	US-10-719-956-626249
42	15.2	60.8	25	26	US-11-036-317-9865
43	15.2	60.8	25	26	US-11-036-317-629374
44	15.2	60.8	25	26	US-11-036-317-633436
45	15.2	60.8	25	26	US-11-036-317-764996

ALIGNMENTS

RESULT 1
US-08-469-172-5
; Sequence 5, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

Sequence 113292,
Sequence 100259,
Sequence 633439,
Sequence 764997,
Sequence 970185,
Sequence 970186,
Sequence 261669,
Sequence 482864,
Sequence 243899,
Sequence 419311,
Sequence 311797,
Sequence 209513,
Sequence 366428,
Sequence 823362,
Sequence 823363,
Sequence 383306,
Sequence 430473,
Sequence 866704,
Sequence 788701,
Sequence 248480,
Sequence 387762,
Sequence 593103,
Sequence 279510,
Sequence 62957, A
Sequence 439125,
Sequence 430286,
Sequence 828846,
Sequence 182301,
Sequence 424738,
Sequence 823343,
Sequence 626249,
Sequence 9865, Ap
Sequence 629374,
Sequence 633436,
Sequence 764996,

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-469-172-5

Query Match 100.0%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACTTCAGAGGAGAAAA 25
| | | | | | | | | | | | | | | | | | | | |
Db 1 CTGGGCTTCACTTCAGAGGAGAAAA 25

RESULT 2
US-10-788-779-5
; Sequence 5, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;
; MOLECULE TYPE: cDNA
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-788-779-5

Query Match 100.0%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACTTCAGAGGAGAAAA 25
| | | | | | | | | | | | | | | | | | | | |
Db 1 CTGGGCTTCACTTCAGAGGAGAAAA 25

RESULT 3
US-10-719-900-593102
; Sequence 593102, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 593102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-593102

Query Match 68.8%; Score 17.2; DB 22; Length 25;
Best Local Similarity 86.4%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACTTCAGAGGAGA 22
| | | | | | | | | | | | | | | |
Db 4 CTAGGCTTCACTACAGAGGACA 25

RESULT 4
US-10-719-900-978129/c
; Sequence 978129, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 978129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-978129

Query Match 68.0%; Score 17; DB 22; Length 25;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACTTCAGAGGAGAAAA 25
| | | | | | | | | | | | | | | | |
Db 25 CTGGGCTTTATATCGGAGGTGAAAA 1

RESULT 5
```

US-10-719-900-424739/c
; Sequence 424739, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 424739
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-424739

Query Match 67.2%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCTTCACCTTCAGAGAGAAA 24
||||| ||||| ||||| |||||
DB 25 GCTTCACCTGGAGAGAGAAA 6

RESULT 6

US-10-809-189-113292
; Sequence 113292, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mitmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-113292

Query Match 67.2%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTTCAGAGA 20
||||| ||||| ||||| |||||
DB 4 CTGGGCTTCACCTCCGAGGA 23

RESULT 7

US-11-036-317-100259/c
; Sequence 100259, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: 2005-01-13
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 100259
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-100259

; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 100259
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-100259

Query Match 67.2%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCTTCACCTTCAGAGAGAAA 24
||||| ||||| ||||| |||||
DB 25 GCTTCACCTGGAGAGAGAAA 6

RESULT 8

US-11-036-317-633439/c
; Sequence 633439, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 633439
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-633439

Query Match 67.2%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCTTCACCTTCAGAGAGAAA 24
||||| ||||| ||||| |||||
DB 25 GCTTCACCTGGAGAGAGAAA 6

RESULT 9

US-11-036-317-764997/c
; Sequence 764997, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 764997
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-764997

Query Match 67.2%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      6  CTTCACTTCAGAGGAGAAA 25
      |||||
Db     24  CCTCACTTCGGAGGAGAAA 5
      |||||

RESULT 10
US-10-719-900-970185/c
; Sequence 970185, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 970185
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-970185

Query Match      66.4%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  TGGGCTTCACATTCAGAGGAGAAA 24
      |||||
Db     23  TGGGCTTCACATTCGCGCTGAGAAA 1
      |||||

RESULT 11
US-10-719-900-970186/c
; Sequence 970186, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 970186
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-970186

Query Match      66.4%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  TGGGCTTCACATTCAGAGGAGAAA 24
      |||||
Db     23  TGGGCTTCACCTCGGCTGAGAAA 1
      |||||

RESULT 12
US-10-719-956-261669/c
; Sequence 261669, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
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; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 261669
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-261669

Query Match      65.6%; Score 16.4; DB 24; Length 25;
Best Local Similarity 94.4%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8  TCACCTTCAGAGGAGAAA 25
      |||||
Db     25  TCACCTTAAGAGGAGAAA 8
      |||||

RESULT 13
US-10-719-900-482864/c
; Sequence 482864, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 482864
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-482864

Query Match      64.8%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2  TGGGCTTCACATTCAGAGGAGAGA 22
      |||||
Db     25  TGGGCTTCACATCAGAGAGA 5
      |||||

RESULT 14
US-10-719-956-243899/c
; Sequence 243899, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 243899
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-243899

Query Match      64.8%; Score 16.2; DB 24; Length 25;
Best Local Similarity 85.7%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 CTGGGCTTCACCTTCAGAGAG 21
|||||
DB 22 CTGGGCTTCACCTTCAGAGGTG 2

RESULT 15

US-10-719-956-419911/c
; Sequence 419911, Application US/10719956
; Publication No. US20040146910A1

GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002-11-20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 419911

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-419911

Query Match 64.8%; Score 16.2; DB 24; Length 25;

Best Local Similarity 85.7%; Pred. No. 9.9e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGGCTTCACCTTCAGAGAGA 22

|||||

DB 25 TGGTCTTCACCTTCAAAGGACA 5

RESULT 16

US-10-956-157-311797/c

; Sequence 311797, Application US/10956157

; Publication No. US20050118625A1

GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 311797

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-311797

Query Match 64.0%; Score 16; DB 22; Length 25;

Best Local Similarity 79.2%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGGGCTTCACCTTCAGAGAGAAA 25

|||||

DB 24 TGGGTTTATCTACAGAGACAAA 1

RESULT 17

US-11-036-317-209513/c

; Sequence 209513, Application US/11036317

; Publication No. US20050214823A1

GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 209513

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-209513

Query Match 64.0%; Score 16; DB 26; Length 25;

Best Local Similarity 79.2%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTTCAGAGAGAAA 24

|||||

DB 25 CAGGGCTAGCCTTCAGAGGAGAGA 2

RESULT 18

US-11-036-317-366428/c

; Sequence 366428, Application US/11036317

; Publication No. US20050214823A1

GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 366428

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-366428

Query Match 64.0%; Score 16; DB 26; Length 25;

Best Local Similarity 79.2%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTTCAGAGAGAAA 24

|||||

DB 24 CAGGGCTAGCCTTCAGAGGAGAGA 1

RESULT 19

US-11-036-317-823362

; Sequence 823362, Application US/11036317

; Publication No. US20050214823A1

GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 823362

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-823362

Query Match 64.0%; Score 16; DB 26; Length 25;

Best Local Similarity 79.2%; Pred. No. 1.2e+03;

```

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGAGAAAA 25
   ||| ||| ||| ||| ||| ||| |||
Db 1 TGGTCTTCACCTCAGGATGAGAAAA 24

RESULT 20
US-11-036-317-823363
; Sequence 823363, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 823363
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-823363

Query Match 64.0%; Score 16; DB 26; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGAGAAAA 25
   ||| ||| ||| ||| ||| ||| |||
Db 1 TGGTCTTCACCTGATGAGAAAA 24

RESULT 21
US-10-719-900-383306/c
; Sequence 383306, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 383306
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-383306

Query Match 63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGG 19
   ||| ||| ||| ||| ||| ||| |||
Db 23 CTGGCTTCACCTCAGTGG 5

RESULT 22
US-10-719-900-430473
; Sequence 430473, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

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; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 430473
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-430473

Query Match 63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGCTTCACCTCAGAGGAGA 22
   ||| ||| ||| ||| ||| ||| |||
Db 4 GGCTTAACCTCAGAGGAGA 22

RESULT 23
US-10-719-900-866704/c
; Sequence 866704, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 866704
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-866704

Query Match 63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGG 19
   ||| ||| ||| ||| ||| ||| |||
Db 22 CTGGCTTCACCTCAGTGG 4

RESULT 24
US-11-036-317-788701
; Sequence 788701, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 788701
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-788701

Query Match 63.2%; Score 15.8; DB 26; Length 25;

```

Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGCTTCACCTTCAGAGGAGA 22
Db 4 GGATTCACCTTCAGAGGAGA 22

RESULT 25

US-10-719-900-248480/c
; Sequence 248480, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248480
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-248480

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGAGGAGA 22
Db 23 CTCGCTTCACCTTCAGAGGAGA 2

RESULT 26

US-10-719-900-387762
; Sequence 387762, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 387762
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-387762

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGAGGAGA 22
Db 1 CTGGGCTACACGTCGGATGAGA 22

RESULT 27

US-10-719-900-593103
; Sequence 593103, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 593103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-593103

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGAGGAGA 22
Db 4 CTAGGCTTCCTCAGAGGAGA 25

RESULT 28

US-10-956-157-279510
; Sequence 279510, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 279510
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-279510

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAGAGGAGAA 23
Db 3 TGGACATCCCTTCAGAGGAGAA 24

RESULT 29

US-10-956-157-315928/c
; Sequence 315928, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 315928
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-315928

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;

```
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGAGAA 23
Db 22 TAGTCTTCATTCAGGGAGAA 1

RESULT 30
US-11-036-317-270365/c
; Sequence 270365, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 270365
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-270365

Query Match 62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGAGAA 22
Db 23 CAGGCGTAGCCTTCAGAGAGAA 2

RESULT 31
US-11-036-317-366190/c
; Sequence 366190, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366190
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-366190

Query Match 62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGAGAA 22
Db 22 CAGGCGTAGCCTTCAGAGAGAA 1

RESULT 32
US-11-036-317-423606
; Sequence 423606, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
```

```
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 423606
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-423606

Query Match 62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGAGAA 22
Db 2 CTGGGCTACACGTCGGATGAGA 23

RESULT 33
US-10-719-900-978130/c
; Sequence 978130, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 978130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-978130

Query Match 61.6%; Score 15.4; DB 22; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGAGAAA 25
Db 25 CTGGGCTTTATAACGGAGGTGAAAA 1

RESULT 34
US-10-719-956-62957
; Sequence 62957, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 62957
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-62957
```


Query Match 61.6%; Score 15.4; DB 24; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGCTTCACCTTCAGAGA 20
| | | | | | | | | |
Db 7 GGCTTCACCTGCAGAGA 23

RESULT 35

US-10-719-956-439125/c
; Sequence 439125, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 439125
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-439125

Query Match 61.6%; Score 15.4; DB 24; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACTTCAGAGAGAGAAA 25
| | | | | | | | | |
Db 21 CACTTCATGAGAGAAA 5

RESULT 36

US-11-036-317-430286/c
; Sequence 430286, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 430286
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-430286

Query Match 61.6%; Score 15.4; DB 26; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAGAG 18
| | | | | | | | | |
Db 20 TGGGCTTCACCTGCAGAG 4

RESULT 37

US-11-036-317-828846/c
; Sequence 828846, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:

; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 828846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-828846

Query Match 61.6%; Score 15.4; DB 26; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGA 17
| | | | | | | | | |
Db 19 CTGGGCTTGACTTCAGA 3

RESULT 38

US-11-060-756-182301
; Sequence 182301, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 182301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-182301

Query Match 61.6%; Score 15.4; DB 26; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGAGAGAAA 25
| | | | | | | | | |
Db 1 CTGGGCTCCAGCTCTGAGAGGACA 25

RESULT 39

US-10-719-900-424738/c
; Sequence 424738, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 424738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-424738

Query Match 60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GCTTCACCTTCAGAGGAGAAA 24
||||| |||||
Db 25 GCTTCACCTGGAGTGGAGAAA 6

RESULT 40
US-10-719-900-823343
; Sequence 823343, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 823343
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-823343

Query Match 60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CTTTCACCTTCAGAGGAGAAA 25
||||| |||||
Db 6 CTTTCACATCAGAGAAGCAAA 25

Search completed: November 18, 2005, 15:41:06
Job time : 337.027 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 832.357 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-6

Perfect score: 30

Sequence: 1 GCGGTACCCAGCAGCCCGCCTTGAGAA 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	6	I12899 Sequence 6
2	18.2	60.7	26	6	AR256113 Sequence
3	18.2	60.7	26	6	AR410127 Sequence
4	16.6	55.3	48	6	A42996 Sequence 11
5	16.6	55.3	48	6	A72867 Sequence 11
6	16.6	55.3	48	6	AR023759 Sequence 11
7	16.6	55.3	48	6	I91791 Sequence 11
8	16.4	54.7	30	6	I85833 Sequence 11
9	16.2	54.0	28	6	AR256115 Sequence
10	16.2	54.0	28	6	AR256117 Sequence
11	16.2	54.0	28	6	AR410129 Sequence
12	16.2	54.0	28	6	AR410131 Sequence
13	16.2	54.0	33	6	A06417 Sequence
14	16.2	54.0	33	6	A10235 Sequence
15	16.2	54.0	33	6	A157316 Sequence
16	15.8	52.7	50	6	CQ008354 Sequence
17	15.6	52.0	32	6	A37857 Sequence
18	15.6	52.0	32	6	AR069895 Sequence
19	15.6	52.0	32	6	AR099292 Sequence

C 20	15.6	52.0	32	6	AR124176	AR124176 Sequence
C 21	15.6	52.0	32	6	AR442783	AR442783 Sequence
C 22	15.6	52.0	43	6	AR036016	AR036016 Sequence
C 23	15.6	52.0	43	6	AR161840	AR161840 Sequence
C 24	15.6	52.0	43	6	I85694	I85694 Sequence 43
C 25	15.4	51.3	27	6	BD000197	BD000197 Viral vec
C 26	15.4	51.3	40	6	AR035911	AR035911 Sequence
C 27	15.4	51.3	40	6	AR035913	AR035913 Sequence
C 28	15.4	51.3	40	6	I20147	I20147 Sequence 10
C 29	15.4	51.3	40	6	I20149	I20149 Sequence 10
C 30	15.4	51.3	40	6	AR340325	AR340325 Sequence
C 31	15.4	51.3	40	6	AR340327	AR340327 Sequence
C 32	15.4	51.3	42	9	HS010898	AJ010898 Homo sapi
C 33	15.4	51.3	43	6	A59897	A59897 Sequence 15
C 34	15.4	51.3	50	6	CQ006450	CQ006450 Sequence
C 35	15.2	50.7	40	6	A58595	A58595 Sequence 1
C 36	15.2	50.7	44	6	A58596	A58596 Sequence 2
C 37	15.2	50.7	44	6	A58603	A58603 Sequence 9
C 38	14.8	49.3	28	6	BD016942	BD016942 Plant pro
C 39	14.8	49.3	30	6	AX069192	AX069192 Sequence
C 40	14.8	49.3	32	6	E59198	E59198 Method for
C 41	14.8	49.3	32	6	E64379	E64379 Process of
C 42	14.8	49.3	33	6	AX781258	AX781258 Sequence
C 43	14.6	48.7	30	6	AX697914	AX697914 Sequence
C 44	14.6	48.7	44	6	I90211	I90211 Sequence 37
C 45	14.6	48.7	48	6	I90209	I90209 Sequence 35

ALIGNMENTS

RESULT 1
LOCUS I12899 30 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 6 from patent US 5429923.
ACCESSION I12899
VERSION I12899.1 GI:910876
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 6 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..30
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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGGTACCCAGCAGCCCGCCTTGAGAA 30
Db 1 GCGGTACCCAGCAGCCCGCCTTGAGAA 30

RESULT 2
LOCUS AR256113 26 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 9 from patent US 6482923.
ACCESSION AR256113
VERSION AR256113.1 GI:27305503
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Shi,Y. and Ruben,S.M.

RESULT 7
LOCUS I91791 48 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 11 from patent US 5726032.
ACCESSION I91791
VERSION I91791.1 GI:3936261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Bovenberg,R.Ary.Jans., Koekman,B.Pieter., Hoekema,A., Van Der Laan,J.Metske., Verweij,J. and De Vroom,E.
TITLE Process for the efficient production of 7-ADCA via 2-(carboxyethylthio)acetyl-7-ADCA and 3-(carboxymethylthio)propionyl-7-ADCA
JOURNAL Patent: US 5726032-A 11 10-MAR-1998;
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ORIGIN
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Best Local Similarity 82.6%; Pred. No. 5e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 ACCCCAGCAGCCGGCCTTGAG 28
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Db 18 ACCGCCGCGCCGGCTTGAG 40
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RESULT 8
I95833/c
LOCUS I85833 30 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 1 from patent US 5698763.
ACCESSION I85833
VERSION I85833.1 GI:3205551
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Weissmann,C., Bueler,H., Aguett,M., Fischer,M. and Sailer,A.
TITLE Transgenic animals lacking prion proteins
JOURNAL Patent: US 5698763-A 1 16-DEC-1997;
FEATURES Location/Qualifiers
source 1..30
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Best Local Similarity 76.9%; Pred. No. 6.2e+04;
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Qy 5 TACCCAGCAGCCGGCCTTGAAGAA 30
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Db 29 TACAGCAGGACAGGACTTGAAGAA 4
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RESULT 9
AR256115
LOCUS AR256115 28 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 11 from patent US 6482923.
ACCESSION AR256115
VERSION AR256115.1 GI:27305505
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Shi,Y. and Ruben,S.M.

Interleukin 17-like receptor protein
Patent: US 6482923-A 11 19-NOV-2002;
Location/Qualifiers
1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCGCT 23
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Db 6 GGTACCCAGCCTCCCGGCTT 26
|||||

RESULT 10
AR256117
LOCUS AR256117 28 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 13 from patent US 6482923.
ACCESSION AR256117
VERSION AR256117.1 GI:27305507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Shi,Y. and Ruben,S.M.
TITLE Interleukin 17-like receptor protein
JOURNAL Patent: US 6482923-A 13 19-NOV-2002;
FEATURES Location/Qualifiers
source 1..28
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/mol_type="genomic DNA"

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Query Match 54.0%; Score 16.2; DB 6; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCGCT 23
|||||
Db 6 GGTACCCAGCCTCCCGGCTT 26
|||||

RESULT 11
AR410129
LOCUS AR410129 28 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 11 from patent US 6635443.
ACCESSION AR410129
VERSION AR410129.1 GI:40161306
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Shi,Y. and Ruben,S.M.
TITLE Polynucleotides encoding a novel interleukin receptor termed interleukin-17 receptor-like protein
JOURNAL Patent: US 6635443-A 11 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCGCT 23
|||||
Db 6 GGTACCCAGCCTCCCGGCTT 26
|||||

Db 6 GGTACCCAGCCTCCCGGCTT 26

RESULT 12
LOCUS AR410131 28 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 13 from patent US 6635443.
ACCESSION AR410131
VERSION AR410131.1 GI:40161308
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Shi, Y. and Ruben, S. M.
TITLE Polynucleotides encoding a novel interleukin receptor termed interleukin-17 receptor-like protein
JOURNAL Patent: US 6635443-A 13 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..28
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ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCTT 23
|||||
Db 6 GGTACCCAGCCTCCCGGCTT 26
|||||

RESULT 13
LOCUS A06417/c 33 bp DNA linear PAT 22-JUN-1993
DEFINITION Oligonucleotide primer.
ACCESSION A06417
VERSION A06417.1 GI:412865
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 33)
AUTHORS
TITLE NOVEL GLUCOSE ISOMERASE ENZYMES AND THEIR USE
JOURNAL Patent: WO 9000601-A 7 25-JAN-1990;
FEATURES Location/Qualifiers
source 1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 33;
Best Local Similarity 72.4%; Pred. No. 7.4e+04;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGGCTTGAAGAA 30
|||||
Db 32 CGCGACTCCATCATCTCGACCTTCAGAA 4
|||||

RESULT 14
LOCUS A10235/c 33 bp DNA linear PAT 25-JAN-1994
DEFINITION oligonucleotide primer.
ACCESSION A10235
VERSION A10235.1 GI:490665
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Shimkets, R. A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 33)
AUTHORS Luiten, R. G. M., Quax, W. J., Schuurhuizen, P. W. and Mrabet, N.
TITLE Novel glucose isomerase enzymes and their use
JOURNAL Patent: EP 0351029-A 8 17-JAN-1990;
GIST-BROCADES N.V.; PLANT GENETIC SYSTEMS, N.V.
FEATURES Location/Qualifiers
source 1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 33;
Best Local Similarity 72.4%; Pred. No. 7.4e+04;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGGCTTGAAGAA 30
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Db 32 CGCGACTCCATCATCTCGACCTTCAGAA 4
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RESULT 15
LOCUS AX157316/c 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 644 from Patent WO0140521.
ACCESSION AX157316
VERSION AX157316.1 GI:14538647
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R. A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 644 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg20705188"
misc_feature 26
/note="2 of 2 allelic variants (643 is other entry)"

ORIGIN
Query Match 53.3%; Score 16; DB 6; Length 50;
Best Local Similarity 79.2%; Pred. No. 8.7e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCTTGA 26
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Db 38 GGCCCCCAACAGCCAGGCTTGA 15
|||||

RESULT 16
LOCUS CQ008354/c 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 6994 from Patent WO0147944.
ACCESSION CQ008354
VERSION CQ008354.1 GI:41015052
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R. A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof
Patent: WO 0147944-A 6994 05-JUL-2001;
Curagen Corporation (US)
JOURNAL
FEATURES
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Location/Qualifiers
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Accession number CG41501665"
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Best Local Similarity 89.5%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 CCCAGCAGCCGCGCCTTG 25
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Db 21 CCCAGCAGCGCGCCTTG 3
RESULT 17
A37857/c
LOCUS
DEFINITION Sequence 27 from Patent WO9408014.
ACCESSION A37857
VERSION A37857.1 GI:2294537
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D. and Zagorec,M.
TITLE POLYPEPTIDES INVOLVED IN STREPTOGRAMIN BIOSYNTHESIS, NUCLEOTIDE
SEQUENCES CODING FOR SAID POLYPEPTIDES AND USE THEREOF
JOURNAL Patent: WO 9408014-A 27 14-APR-1994;
COMMENT RHONE-POULENC RORER SA (FR)
Other publication AU 4823393 940426
Other publication CA 2145523 940414
Other publication ZA 9307102 940422
Other publication FI 951403 950324
Other publication FR 2696189 940401
Other publication JP 8501696T 960227.
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/db_xref="taxon:32644"
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Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CGGTACCCAGCAGCCGCGCCTTG 25
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Db 32 CGGTACCASAGSGSGGCTTS 9
RESULT 18
AR069895/c
LOCUS
DEFINITION Sequence 43 from patent US 5891695.
ACCESSION AR069895
VERSION AR069895.1 GI:7220783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D., Zagorec,M., Debusche,L. and De Crecy-Lagard,V.
TITLE Polypeptides involved in the biosynthesis of streptogramins, use
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 5891695-A 43 06-APR-1999;
FEATURES
Location/Qualifiers
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Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
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Db 32 CGGTACCASAGSGSGGCTTS 9
RESULT 19
AR099292/c
LOCUS
DEFINITION Sequence 45 from patent US 6077699.
ACCESSION AR099292
VERSION AR099292.1 GI:12809058
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D., Zagorec,M., Debusche,L. and De Crecy-Lagard,V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 6077699-A 45 20-JUN-2000;
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Location/Qualifiers
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ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 32;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CGGTACCCAGCAGCCGCGCCTTG 25
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Db 32 CGGTACCASAGSGSGGCTTS 9
RESULT 20
AR124176/c
LOCUS
DEFINITION Sequence 43 from patent US 6171846.
ACCESSION AR124176
VERSION AR124176.1 GI:14109537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D., Zagorec,M., Debusche,L. and De Crecy-Lagard,V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 6171846-A 43 09-JAN-2001;
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Location/Qualifiers
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Query Match 52.0%; Score 15.6; DB 6; Length 32;

Thibaut,D., Zagorec,M., Debusche,L. and De Crecy-Lagard,V.
Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 5891695-A 43 06-APR-1999;
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Query Match 52.0%; Score 15.6; DB 6; Length 32;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CGGTACCCAGCAGCCGCGCCTTG 25
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Db 32 CGGTACCASAGSGSGGCTTS 9
RESULT 19
AR099292/c
LOCUS
DEFINITION Sequence 45 from patent US 6077699.
ACCESSION AR099292
VERSION AR099292.1 GI:12809058
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D., Zagorec,M., Debusche,L. and De Crecy-Lagard,V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 6077699-A 45 20-JUN-2000;
FEATURES
source
Location/Qualifiers
1..32
/organism="unassigned DNA"
ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 32;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CGGTACCCAGCAGCCGCGCCTTG 25
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Db 32 CGGTACCASAGSGSGGCTTS 9
RESULT 20
AR124176/c
LOCUS
DEFINITION Sequence 43 from patent US 6171846.
ACCESSION AR124176
VERSION AR124176.1 GI:14109537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D., Zagorec,M., Debusche,L. and De Crecy-Lagard,V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 6171846-A 43 09-JAN-2001;
FEATURES
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Location/Qualifiers
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ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 32;

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Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGCGCTTG 25
Db 32 CGGTACCASAGSGSGGCTTS 9

RESULT 21
AR442783/c
LOCUS AR442783 32 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 43 from patent US 6670157.
ACCESSION AR442783
VERSION AR442783.1 GI:42670187
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 32;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGCGCTTG 25
Db 32 CGGTACCASAGSGSGGCTTS 9

RESULT 22
AR036016/c
LOCUS AR036016 43 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 43 from patent US 5871974.
ACCESSION AR036016
VERSION AR036016.1 GI:5952684
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/mol_type="unassigned DNA"

ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 43;
Best Local Similarity 70.0%; Pred. No. 1.3e+05;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAAA 13

RESULT 23
AR161840/c
LOCUS AR161840 43 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 42 from patent US 6258530.
ACCESSION AR161840
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VERSION ARL161840.1 GI:16228821
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/mol_type="unassigned DNA"

ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 43;
Best Local Similarity 70.0%; Pred. No. 1.3e+05;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAAA 13

RESULT 24
I85694/c
LOCUS I85694 43 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 43 from patent US 5698426.
ACCESSION I85694
VERSION I85694.1 GI:3205412
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 43;
Best Local Similarity 70.0%; Pred. No. 1.3e+05;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAAA 13

RESULT 25
BD000197
LOCUS BD000197 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Viral vector.
ACCESSION BD000197
VERSION BD000197.1 GI:18623276
KEYWORDS JP 2000279178-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 (bases 1 to 27)
TITLE Hamada,H.
JOURNAL Patent: JP 2000279178-A 10 10-OCT-2000;
COMMENT JAPANESE FOUNDATION FOR CANCER RESEARCH
OS Artificial Sequence
PN JP 2000279178-A/10
PD 10-OCT-2000
PR 24-FEB-1999 JP 1999093263
```


PI HIROFUMI HAMADA
PC C12N15/09,A61K31/00,A61K38/00,A61K39/235,A61K48/00,
PC C07K14/075,
PC C07K14/52,C07K14/68,C07K14/72,C12N7/00,C12N9/12,C12N9/80, PC
G01N33/574,
PC C12N15/00,A61K37/02
CC
FH Key Location/Qualifiers
FT source 1..27
FT /organism='Artificial Sequence'.
PT Location/Qualifiers
1..27

FEATURES
source
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 51.3%; Score 15.4; DB 6; Length 27;
Best Local Similarity 76.0%; Pred. No. 1.6e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGTACCCAGCAGCCGCGCTTG 25
|||||
DB 3 GCGTACCACAGCATCGTGACCTG 27

RESULT 26
AR035911/c
LOCUS AR035911 40 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 104 from patent US 5871962.
ACCESSION AR035911
VERSION AR035911.1 GI:5952579
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Bukh,J., Miller,R.H. and Purcell,R.H.
TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene
of 51 isolates of hepatitis C virus and the use of reagents derived
from these sequences in diagnostic methods
JOURNAL Patent: US 5871962-A 104 16-FEB-1999;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 51.3%; Score 15.4; DB 6; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGTACCCAGCAGCCGCGCTTGAA 27
|||||
DB 40 GGCACATCAATAGCAGCGCCTTGAA 16

RESULT 27
AR035913/c
LOCUS AR035913 40 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 106 from patent US 5871962.
ACCESSION AR035913
VERSION AR035913.1 GI:5952581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Bukh,J., Miller,R.H. and Purcell,R.H.
TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene
of 51 isolates of hepatitis C virus and the use of reagents derived
from these sequences in diagnostic methods
JOURNAL Patent: US 5871962-A 106 16-FEB-1999;

FEATURES
source
Location/Qualifiers
1..40
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/mol_type="unassigned DNA"

ORIGIN

Query Match 51.3%; Score 15.4; DB 6; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGTACCCAGCAGCCGCGCTTGAA 27
|||||
DB 27 GGCACATCAATAGCAGCGCCTTGAA 3

RESULT 28

LOCUS I20147/c 40 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 104 from patent US 5514539.
ACCESSION I20147
VERSION I20147.1 GI:1600502
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Bukh,J., Miller,R.H. and Purcell,R.H.
TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene
of 51 isolates of hepatitis C virus and the use of reagents derived
from these sequences in diagnostic methods and vaccines
JOURNAL Patent: US 5514539-A 104 07-MAY-1996;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 51.3%; Score 15.4; DB 6; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGTACCCAGCAGCCGCGCTTGAA 27
|||||
DB 40 GGCACATCAATAGCAGCGCCTTGAA 16

RESULT 29

LOCUS I20149/c 40 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 106 from patent US 5514539.
ACCESSION I20149
VERSION I20149.1 GI:1600504
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Bukh,J., Miller,R.H. and Purcell,R.H.
TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene
of 51 isolates of hepatitis C virus and the use of reagents derived
from these sequences in diagnostic methods and vaccines
JOURNAL Patent: US 5514539-A 106 07-MAY-1996;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 51.3%; Score 15.4; DB 6; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGTACCCAGCAGCCGCGCTTGAA 27

[illegible]

```

Db      4 GTACTCCAGCAGCTGGCCAGGAAG 28
||||| ||||| ||||| ||| |||||
RESULT 34
CQ006450
LOCUS      50 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION Sequence 5090 from Patent WO0147944.
ACCESSION CQ006450
VERSION    CQ006450.1 GI:41013082
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Shinketsu, R.A. and Leach, M.
TITLE       Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL     Patent: WO 0147944-A 5090 05-JUL-2001;
            Curagen Corporation (US)
FEATURES   source
            1..50
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
misc_feature
            25..26
            /note="Nucleotide deleted between bases 25 and 26
            Accession number c943958634"
ORIGIN
Query Match      51.3%; Score 15.4; DB 6; Length 50;
Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 GCGGTACCCACAGCAGCCGCGCTTG 25
||||| ||||| ||||| ||||| |||||
Db      22 GAGGCACAGCAGCAGCGCGGCGCTG 46

RESULT 35
A58595/c
LOCUS      40 bp      DNA      linear      PAT 06-MAR-1998
DEFINITION Sequence 1 from Patent EP0754700.
ACCESSION A58595
VERSION    A58595.1 GI:3714175
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS     Davison, A.R., Duckworth, G.S., Rao, V., Brown, T. and McClean, J.P.
TITLE       Labelling and detection of nucleic acids
JOURNAL     Patent: EP 0754700-A 1 22-JAN-1997;
            CRUACHEM LTD (GB)
FEATURES   source
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Query Match      50.7%; Score 15.2; DB 6; Length 40;
Best Local Similarity 85.0%; Pred. No. 1.9e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 ACCCCAGCAGCCGCGCCTTG 25
||||| ||||| ||||| ||||| |||||
Db      32 ACTCCAGCAGCCGCGCCTTG 13

RESULT 36
A58596/c
LOCUS      44 bp      DNA      linear      PAT 06-MAR-1998
DEFINITION Sequence 2 from Patent EP0754700.
ACCESSION A58596
VERSION    A58596.1 GI:3714176
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS     Davison, A.R., Duckworth, G.S., Rao, V., Brown, T. and McClean, J.P.
TITLE       Labelling and detection of nucleic acids
JOURNAL     Patent: EP 0754700-A 2 22-JAN-1997;
            CRUACHEM LTD (GB)
FEATURES   source
            1..44
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      50.7%; Score 15.2; DB 6; Length 44;
Best Local Similarity 85.0%; Pred. No. 1.8e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 ACCCCAGCAGCCGCGCCTTG 25
||||| ||||| ||||| ||||| |||||
Db      36 ACTCCAGCAGCCGCGCCTCG 17

RESULT 37
A58603/c
LOCUS      44 bp      DNA      linear      PAT 06-MAR-1998
DEFINITION Sequence 9 from Patent EP0754700.
ACCESSION A58603
VERSION    A58603.1 GI:3714183
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS     Davison, A.R., Duckworth, G.S., Rao, V., Brown, T. and McClean, J.P.
TITLE       Labelling and detection of nucleic acids
JOURNAL     Patent: EP 0754700-A 9 22-JAN-1997;
            CRUACHEM LTD (GB)
FEATURES   source
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            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      50.7%; Score 15.2; DB 6; Length 44;
Best Local Similarity 85.0%; Pred. No. 1.8e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 ACCCCAGCAGCCGCGCCTTG 25
||||| ||||| ||||| ||||| |||||
Db      36 ACTCCAGCAGCCGCGCCTCG 17

RESULT 38
BD016942
LOCUS      28 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Plant promoter.
ACCESSION BD016942
VERSION    BD016942.1 GI:22558118
KEYWORDS   JP 2001258558-A/4.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Yoshida, M., Yanai, Y. and Takahashi, S.
TITLE       Plant promoter

```

JOURNAL Patent: JP 2001258558-A 4 25-SEP-2001;
MITSUI CHEM INC
COMMENT OS Artificial Sequence
PN JP 2001258558-A/4
PD 25-SEP-2001
PF 17-MAR-2000 JP 2000075781
PI MASANORI YOSHIDA, YUKIHIRO YANAI, SHIGERU TAKAHASHI PC
C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC Description of
Artificial Sequence: oligo nucleotide primer FH Key
Location/Qualifiers
Location/Qualifiers
1. .28
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
Query Match 49.3%; Score 14.8; DB 6; Length 28;
Best Local Similarity 73.1%; Pred. No. 2.7e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ORIGIN
Oy 2 CGGTACCCAGCAGCCGGCCTTGAA 27
|||||
Db 1 CGGGATCCTAATAGCAGCGCTTGAA 26
|||||

RESULT 39
AX069192
LOCUS AX069192 30 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 3 from Patent WO0102594.
ACCESSION AX069192
VERSION AX069192.1 GI:12579073
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Greaves, D.R., Thomsen, L., Catchpole, I.R. and Ford, M.J.
TITLE Dna constructs based on the elf4a gene promoter
JOURNAL Patent: WO 0102594-A 3 11-JAN-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
source
Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 49.3%; Score 14.8; DB 6; Length 30;
Best Local Similarity 73.1%; Pred. No. 2.7e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 3 GGTACCCAGCAGCCGGCCTTGAG 28
|||||
Db 5 GGTACCATGGCTGCCAGCGCTCGAG 30
|||||

RESULT 40
E59198
LOCUS E59198 32 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for searching antibacterial or herbicidally active compound.
ACCESSION E59198
VERSION E59198.1 GI:18622469
KEYWORDS JP 2000300257-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 32)
AUTHORS Miyake, K., Hashimoto, S., Motoyama, H., Ozaki, A., Set, H., Kuzuyama, T.
and Takahashi, S.
TITLE Method for searching antibacterial or herbicidally active compound
JOURNAL Patent: JP 2000300257-A 18 31-OCT-2000;

JOURNAL Patent: JP 2001258558-A 4 25-SEP-2001;
MITSUI CHEM INC
COMMENT OS Artificial Sequence
PN JP 2000300257-A/18
PD 31-OCT-2000
PF 12-APR-1999 JP 1999104590
PR
PI KOICHIRO MIYAKE, SHINICHI HASHIMOTO, HIROAKI MOTOYAMA, AKIO
OZAKI, HARUO SETO,
PI TOMOHIISA KUZUYAMA, SHUNJI TAKAHASHI
PC C12N15/09, A01N57/12, C12N1/21, C12N9/00, C12P23/00, C12Q1/18// PC
(C12N1/21, C12R1:18), (C12P23/00, C12R1:19), (C12P23/00, C12R1:18), PC
C12N15/00
CC Key Location/Qualifiers
FH source 1. .32
FT /organism="Artificial Sequence".

FEATURES
source
Location/Qualifiers
1. .32
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 49.3%; Score 14.8; DB 6; Length 32;
Best Local Similarity 73.1%; Pred. No. 2.7e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 GCGGTACCCAGCAGCCGGCCTTGA 26
|||||
Db 1 GGGGATCCTGCCAGCCAGCGCTTGA 26
|||||

Search completed: November 18, 2005, 17:42:57
Job time : 834.457 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 206.578 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-6

Perfect score: 30

Sequence: 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
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- 7: geneseqn2002bs:*
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- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	2	AAQ91126
2	30	100.0	30	9	ACA63116
3	30	100.0	30	13	ADR05302
4	18.2	60.7	26	3	AZ35752 Human IL1
5	18.2	60.7	26	3	AZ52041 3'primer
6	18.2	60.7	26	3	AA75767
7	18.2	60.7	26	13	ADT93849
8	17.2	57.3	24	12	ACF36917
9	17.2	57.3	37	12	ACF36933
10	16.6	55.3	48	2	AQ84993
11	16.6	55.3	48	2	AQ82717
12	16.2	54.0	25	9	ACT28074
13	16.2	54.0	25	9	ACT1032
14	16.2	54.0	28	3	AZ35754
15	16.2	54.0	28	3	AZ35756
16	16.2	54.0	28	3	AZ52043
17	16.2	54.0	28	3	AA75769
18	16.2	54.0	28	3	AA75771
19	16.2	54.0	28	13	ADT93853
20	16.2	54.0	28	13	ADT93851

21	16.2	54.0	38	10	ADF72771
22	16.2	54.0	38	12	ADH34521
23	16	53.3	29	6	ABK49653
24	16	53.3	50	4	AAI73703
25	15.8	52.7	19	9	ACD82439
26	15.8	52.7	19	9	ACD82353
27	15.8	52.7	39	10	ACF79913
28	15.8	52.7	41	6	ABN86094
29	15.8	52.7	50	4	AAI33786
30	15.6	52.0	43	2	AAI16927
31	15.6	52.0	43	3	AAZ91566
32	15.4	51.3	20	9	ACD82542
33	15.4	51.3	27	3	AA93835
34	15.4	51.3	40	2	AAQ83899
35	15.4	51.3	40	2	AAQ83897
36	15.4	51.3	40	2	AAI16692
37	15.4	51.3	40	2	AAI16690
38	15.4	51.3	40	10	ADF08491
39	15.4	51.3	50	4	AAI31882
40	15.2	50.7	25	11	ADL96717
41	15.2	50.7	33	10	ADJ72409
42	15.2	50.7	40	2	AAI58818
43	15.2	50.7	44	2	AAI58825
44	15.2	50.7	44	2	AAI58819
45	15	50.0	25	9	ACK29080

ALIGNMENTS

RESULT 1
AAQ91126
ID AAQ91126 standard; cDNA; 30 BP.
XX

AC AAQ91126;
XX

DT 19-FEB-1996 (first entry)
XX

DE Beta-cardiac myosin heavy chain PCR primer D.
XX

XX Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
KW diagnosis; primer; mutation; detection; ss.
XX

OS Synthetic.
XX

FN US429923-A.
XX

PD 04-JUL-1995.
XX

PF 11-DEC-1992; 92US-00989160.
XX

PR 11-DEC-1992; 92US-00989160.
XX

PA (HARD) HARVARD COLLEGE.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.

PI Seidman J, Seidman C, Watkins H, Rosenzweig A;
XX

DR WPI; 1995-245715/32.
XX

XX Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
PT useful for testing asymptomatic individual(s).
XX

XX Example 1; Col 10; 22pp; English.
XX

XX AAQ91121-091130 are nested PCR primers used for the amplification and
CC identification of beta-cardiac myosin heavy-chain RNA. They are used in a
CC new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
CC the method involves detecting the presence or absence of specific HC-
CC associated mutations in the beta-cardiac myosin heavy-chain obtained from
CC a blood sample. The method may be used to diagnose familial or sporadic
CC HC and the non-invasive method is particularly important when testing

asymptomatic individuals suspected of having the disease. The method has a broad applicability and may be used to detect mutations responsible for other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-Sachs disease and phenylketonuria

SQ Sequence 30 BP; 7 A; 11 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 30; Conservative 0; Mismatches 0; Indels

Qy 1 GCGGTACCCAGCAGCCCGGCTTGAAGAA 30
|||
Db 1 GCGGTACCCAGCAGCCCGGCTTGAAGAA 30

RESULT 2

ACA63116
ID ACA63116 standard; DNA; 30 BP.

28-AUG-2003 (first entry)

DE Human beta cardiac myosin heavy chain PCR primer D. XX

Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
 sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
 Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
 phenylketonuria; cystic fibrosis.

OS Homo sapiens.

PN US2003054343-A1.

PD 20-MAR-2003.

06-JUN-1995; 95US-00469172.

PR 11-DEC-1992; 92US-00989160.

PA (SEID/) SEIDMAN C.
PA (SEID/) SEIDMAN J.
PA (WATK/) WATKINS H.
PA (ROSE/) ROSENZWEIG A.

PI Seidman C, Seidman J, Watkins H, Rosenzweig A;

DR WPI; 2003-512374/48.

PT Detecting a presence or absence of a mutation associated with
 PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
 PT hemophilia, by detecting a mutation in an amplified product of a beta
 PT cardiac myosin heavy-chain DNA.

Example 1; Page 5; 22pp; English.

The invention relates to detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy (sporadic or familial, SHC and FHC) comprises detecting a mutation associated with hypertrophic cardiomyopathy in an amplified product of a beta cardiac myosin heavy chain DNA. The mutations associated with SHC/FHC are detected in the myosin gene isolated from blood, by detecting mis-matched areas in RNA-DNA hybrid double strands (RNA from the normal gene, DNA from the suspect sample). FHC associated point mutation can be classified and used to determine life expectancy in affected individuals e.g. using a Kaplan-Meier curve for the classified type of FHC causing point mutation. Also included are an RNA probe comprising ribonucleotides arranged in a sequence which is complementary to at least a portion of beta-cardiac myosin heavy-chain DNA and a set of DNA oligonucleotide primers for amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

SQ Sequence 30 BP; 7 A; 11 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 13; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCGGTACCCCGACGACCGCGCTTCAAGAA 30
|||
Db 1 GCGGTACCCCGACGACCGCGCTTCAAGAA 30

RESULT 4

AAZ35752
ID AAZ35752 standard; DNA; 26 BP.

XX AAZ35752;

XX 01-FEB-2000 (first entry)

XX Human IL17RLP PCR 3' primer SEQ ID NO:9.

XX Human; interleukin 17 receptor like protein; IL17RLP; IL-17; diagnosis;
KW detection; immune system related disorder; haemostasis;
KW cellular activation; angiogenesis; tumour metastasis; ovulation;
KW cellular migration; neurogenesis; infection; T-cell proliferation;
KW autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation;
KW sepsis; tumour; cancer; interstitial lung disease; arthritis; lymphoma;
KW immunosuppression; immunity; inflammatory bowel disease;
KW myelo suppression; PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9914240-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-US019121.

XX 17-SEP-1997; 97US-0059133P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Shi Y, Ruben SM;

XX WPI; 2000-061918/05.

PT New human interleukin-17 receptor like protein, e.g. to treat disorders
XX relating to cellular activation.

XX Example 2; Page 95; 133pp; English.

XX The present invention describes human interleukin 17 receptor like
CC protein (IL17RLP), isolated from a cDNA library of human adult pulmonary
CC tissue. The present sequence represents a PCR primer for human IL17RLP.
CC IL17RLP and its agonists can be used to treat disorders relating to
CC cellular activation, haemostasis, angiogenesis, tumour metastasis,
CC cellular migration and ovulation, and neurogenesis. They can also be used
CC to enhance host defences against resistant chronic and acute infections,
CC e.g. mycobacterial infections via the attraction and activation of
CC microbial leukocytes. IL17RLP may also be used to increase T-cell
CC proliferation by the stimulation of IL-2 biosynthesis for the treatment
CC of T-cell mediated autoimmune diseases and lymphocytic leukaemias, to
CC regulate haematopoiesis by regulating the activation and differentiation
CC of various haematopoietic progenitor cells, e.g. to release mature
CC leukocytes from the bone marrow following chemotherapy, i.e. in stem cell
CC mobilisation or to treat sepsis. The products can also be used for the
CC diagnosis or treatment of immune system related disorders e.g. tumours,
CC cancers, interstitial lung disease, and any dysregulation of immune cell
CC function including autoimmunity, arthritis, leukaemias, lymphomas,
CC immunosuppression, immunity, humoral immunity, inflammatory bowel
CC disease, or myelo suppression

SQ Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 60.7%; Score 18.2; DB 3; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GCGGTACCCCGACGACCGCGCT 23
|||
Db 2 GCGGTACCCCGACGCTCCGCGCTT 24

RESULT 5

AAZ52041
ID AAZ52041 standard; DNA; 26 BP.

XX AAZ52041;

XX 09-AUG-2000 (first entry)

XX 3'primer for amplification of IL-17RLP leader sequence.

XX Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;
KW resistant chronic infection; acute infection; mycobacterial infection;
KW T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia;
KW T-cell mediated autoimmune disease; hematopoiesis; sepsis; hyridoma;
KW IL-6 expression; myeloma; plasmacytoma; Lemert's Lymphoma;
KW immunoprotective; cytostatic; hematopoietic; proliferative;
KW antibacterial; PCR primer; ss.

OS Homo sapiens.

XX WO200015759-A1.

XX 23-MAR-2000.

XX 15-SEP-1999; 99WO-US021048.

XX 16-SEP-1998; 98US-00154219.

XX 16-SEP-1998; 98WO-US019121.

XX 16-MAR-1999; 99WO-00268311.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Shi Y;

XX WPI; 2000-271403/23.

PT Novel polynucleotides encoding interleukin-17-like receptor protein,
 PT useful for diagnosis and treatment of immune system-related disorders,
 XX e.g. sepsis and cancers.
 PS Example 2; Page 98; 147pp; English.
 XX The patent relates to novel interleukin-17-like receptor protein (IL-
 CC 17RLP). IL-17RLP is a homologue of the IL-17 receptor and has a wide
 CC range of cytokine receptor-like activities. IL-17RLP or its agonists may
 CC be used to enhance host defenses against resistant chronic and acute
 CC infections, e.g. mycobacterial infections, via the attraction and
 CC activation of microbicidal leukocytes. It may also be used to increase T-
 CC cell proliferation by stimulating IL-2 biosynthesis, for the treatment of
 CC T-cell mediated autoimmune diseases and lymphocytic leukaemias. IL-17RLP
 CC may also be used to regulate hematopoiesis and to treat sepsis.
 CC Extracellular IL-17RLP domains may be used as antagonists of IL-17RLP. IL
 CC -17RLP agonists and antagonists can also be used to modulate IL-6
 CC expression, useful in treatment of cancers such as myelomas.
 CC plasmacytomas and hybridomas and Lennert's lymphoma. The present sequence
 CC is the 3' PCR primer used for the amplification of IL-17RLP leader
 CC sequence. This is used in the cloning and expression of IL-17RLP protein
 CC in a baculovirus expression system
 XX
 SQ Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 60.7%; Score 18.2; DB 3; Length 26;
 Best Local Similarity 87.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GCGGTACCCAGCAGCCGGCT 23
 Db 2 GCGGTACCCAGCAGCCGGCTT 24

RESULT 6

AA75767
 ID AA75767 standard; DNA; 26 BP.
 XX
 AC AA75767;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE PCR primer for a human interleukin 17 receptor-like cDNA fragment.
 XX
 KW Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;
 KW cellular activation; haemostasis; angiogenesis; tumour metastasis;
 KW cellular migration; ovulation; neurogenesis; arthritis;
 KW autoimmune disorder; systemic lupus erythromatosus; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200055204-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 06-MAR-2000; 2000WO-US005759.
 XX
 PR 16-MAR-1999; 99US-00268311.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Shi Y, Ruben SM;
 XX
 DR WPI; 2000-647065/62.
 XX
 PT Novel gene encoding a polypeptide of the interleukin-17 receptor family,
 PT and an antagonist and agonist of the polypeptide, useful for treating,
 PT diagnosing, detecting and/or preventing immune system related disorders.
 XX
 PS Example 2; Page 179; 247pp; English.
 XX
 CC PCR primers AA75766-67 were used to amplify a fragment of cDNA encoding
 CC a human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP

CC polypeptide is useful for screening for agonists and antagonists. These
 CC antagonists and agonists are useful for treating, diagnosing, detecting
 CC and or preventing disorders related to cellular activation, haemostasis,
 CC angiogenesis, tumour metastasis, cellular migration, ovulation or
 CC neurogenesis, such as osteoporosis, arthritis and autoimmune disorders
 CC e.g. systemic lupus erythromatosus
 XX
 SQ Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 60.7%; Score 18.2; DB 3; Length 26;
 Best Local Similarity 87.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GCGGTACCCAGCAGCCGGCT 23
 Db 2 GCGGTACCCAGCAGCCGGCTT 24

RESULT 7

ADT93849
 ID ADT93849 standard; DNA; 26 BP.
 XX
 AC ADT93849;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human interleukin 17 receptor-like protein cDNA expression 3' primer.
 XX
 KW ss; antiinflammatory; cytostatic; gastrointestinal; immunosuppressive;
 KW interleukin 17-receptor-like protein; IL17RLP; cellular activation;
 KW hemostasis; angiogenesis; tumour metastasis; cellular migration;
 KW ovulation; neurogenesis; immune-related disorder; Crohn's disease; tumor;
 KW inflammatory bowel disease; autoimmune disease; lymphocytic leukemia;
 KW graft versus host disease; chromosomal identification; primer; PCR.
 XX
 OS Homo sapiens.
 XX
 FN AU2004200961-A1.
 XX
 PD 01-APR-2004.
 XX
 PF 09-MAR-2004; 2004AU-00200961.
 XX
 PR 09-MAR-2004; 2004AU-00200961.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Shi Y, Ruben SM;
 XX
 DR WPI; 2004-662639/65.
 XX
 PT Novel isolated interleukin 17-receptor-like protein useful for treating
 PT immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel
 PT disease, autoimmune diseases, lymphocytic leukemias, or graft versus host
 PT disease.
 XX
 PS Example 2; SEQ ID NO 9; 145pp; English.
 XX
 CC The invention relates to an isolated interleukin 17-receptor-like protein
 CC (IL17RLP) (I) comprising an amino acid sequence that is 95% or more
 CC identical to a sequence e.g., sequence having amino acids from positions
 CC 19-407 of a fully defined sequence (S1) of 426 amino acids as given in
 CC the specification, sequence having amino acids from positions 18-407 of
 CC (S1) that comprises N-terminal methionine or sequence having amino acids
 CC from positions 1-407 of (S1). (I) is useful for treating disorders
 CC related to cellular activation, hemostasis, angiogenesis, tumor
 CC metastasis, cellular migration, ovulation or neurogenesis. (I) is useful
 CC for treating immune-related disorders e.g., Crohn's disease, tumor,
 CC inflammatory bowel disease, autoimmune diseases, lymphocytic leukemias,
 CC or graft versus host disease. (II) is useful for chromosomal
 CC identification. (I) exhibits enhanced activity, solubility and stability,
 CC and is produced in large quantities. This sequence corresponds to a PCR
 CC primer to amplify the extracellular region DNA from the human IL17RLP


```
CC cDNA sequence (AD793841) for expression in a baculovirus expression
CC system.
XX
SQ Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match      60.7%; Score 18.2; DB 13; Length 26;
  Best Local Similarity 87.0%; Pred. No. 1.1e+03;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGGTACCCAGCAGCCCGGCTT 23
   |||||
Db 2 GCGGTACCCAGCAGCCCGGCTT 24

RESULT 8
ACF36917
ID ACF36917 standard; DNA; 24 BP.
XX
AC ACF36917;
XX
15-APR-2004 (first entry)
XX
Human alpha1,3 fucosyltransferase VII plasmid PCR primer #1.
XX
Alpha1,3 fucosyltransferase; FT; glycosyltransferase; fusion protein;
KW enzyme; PCR; primer; ss.
XX
Homo sapiens.
XX
WO2003093448-A2.
XX
13-NOV-2003.
XX
05-MAY-2003; 2003WO-US014235.
XX
03-MAY-2002; 2002US-0377730P.
XX
(NEOS-) NEOSE TECHNOLOGIES INC.
XX
Bayer RJ, Mendoza G;
XX
WPI; 2004-053043/05.
XX
New fusion protein comprising a stem region of fucosyltransferase VI and
a catalytic domain of fucosyltransferase VII, useful for enzymatically
synthesizing glycoproteins, glycolipids, and oligosaccharide moieties.
XX
Example 1; Page 72; Opp; English.
XX
The present invention relates to a fusion protein comprising a stem
region of human fucosyltransferase VI and a catalytic domain of
fucosyltransferase VII, where the fusion protein has high enzymatic
activity, and catalyses the transfer of fucose residue from a donor
substrate to an acceptor substrate. The fusion protein is useful for
enzymatically synthesizing glycoproteins, glycolipids, and
oligosaccharide moieties. The present sequence is a PCR primer used to
isolate a coding sequence in the exemplification of the invention
XX
Sequence 24 BP; 4 A; 13 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match      57.3%; Score 17.2; DB 12; Length 24;
  Best Local Similarity 86.4%; Pred. No. 2.7e+03;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGGTACCCAGCAGCCCGGCTT 22
   |||||
Db 1 GCGGTACCCAGCAGCCCGGCTT 22

RESULT 9
ACF36933
ID ACF36933 standard; DNA; 37 BP.
XX
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```
AC ACF36933;
XX
15-APR-2004 (first entry)
XX
Human alpha1,3 fucosyltransferase VII plasmid PCR primer #9.
XX
Alpha1,3 fucosyltransferase; FT; glycosyltransferase; fusion protein;
KW enzyme; PCR; primer; ss.
XX
Homo sapiens.
XX
WO2003093448-A2.
XX
13-NOV-2003.
XX
05-MAY-2003; 2003WO-US014235.
XX
03-MAY-2002; 2002US-0377730P.
XX
(NEOS-) NEOSE TECHNOLOGIES INC.
XX
Bayer RJ, Mendoza G;
XX
WPI; 2004-053043/05.
XX
New fusion protein comprising a stem region of fucosyltransferase VI and
a catalytic domain of fucosyltransferase VII, useful for enzymatically
synthesizing glycoproteins, glycolipids, and oligosaccharide moieties.
XX
Example 3; Page 81; Opp; English.
XX
The present invention relates to a fusion protein comprising a stem
region of human fucosyltransferase VI and a catalytic domain of
fucosyltransferase VII, where the fusion protein has high enzymatic
activity, and catalyses the transfer of fucose residue from a donor
substrate to an acceptor substrate. The fusion protein is useful for
enzymatically synthesizing glycoproteins, glycolipids, and
oligosaccharide moieties. The present sequence is a PCR primer used to
isolate a coding sequence in the exemplification of the invention
XX
Sequence 37 BP; 7 A; 18 C; 10 G; 2 T; 0 U; 0 Other;

  Query Match      57.3%; Score 17.2; DB 12; Length 37;
  Best Local Similarity 86.4%; Pred. No. 2.8e+03;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGGTACCCAGCAGCCCGGCTT 22
   |||||
Db 14 GCGGTACCCAGCAGCCCGGCTT 35

RESULT 10
AAQ84993
ID AAQ84993 standard; DNA; 48 BP.
XX
AAQ84993;
XX
25-MAR-2003 (revised)
DT 04-OCT-1995 (first entry)
XX
Expandase gene amplification primer #11 for expression cassette.
XX
Primer; amplify; PCR; expandase gene; cefE; Nicotiana lactamurans;
KW Streptomyces clavuligerus; expression cassette; acyltransferase; fungus;
KW Penicillin chrysogenum; hybrid promoter; Aspergillus nidulans; 7-ADCA;
KW 7-amino-desacetoxycephalosporanic acid; cephalosporin; antibiotic; ss.
XX
Synthetic.
XX
WO9504148-A1.
XX
09-FEB-1995.
XX
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PF 29-JUL-1994; 94WO-EP002543.
XX
XX
PR 30-JUL-1993; 93EP-00202259.
PR 24-DEC-1993; 93EP-00203696.
XX
XX (KONN ) GIST-BROCADES NV.
XX
XX Bovenberg RAL, Koekman BP, Hoekema A, Van Der Laan JM, Verweij J;
XX
XX WPI; 1995-082231/11.
XX
XX 7-amino-desacetoxy-cephalosporanic acid prodn. in Penicillium chrysogenum
PT - by simultaneous expression of expandase and acyl-transferase.
XX
XX Example 1; Page 14; 37pp; English.
XX
XX Primers (AAQ84983-95) were used to amplify the expandase gene (cefE) from
CC either Nicotidia lactamurans or Streptomyces clavuligerus. The resultant
CC sequences were placed in an expression cassette for simultaneous
CC expression of the cefE gene and the gene encoding an acyltransferase. The
CC expression cassette is placed in the fungus Penicillium chrysogenum.
CC Expression of the genes in the cassette is driven either by a trp-lac
CC hybrid promoter or the promoter from the Aspergillus nidulans gpdA gene.
CC The terminator is the 3'-end of the P.chrysogenum penDE gene. The primers
CC AAQ84991-3 were used to amplify a 0.5 kb region containing the
CC P.chrysogenum penDE (acyltransferase gene) terminator sequence. This
CC sequence was linked by PCR to the 3' end of the N.lactamurans cefE gene.
CC The cassette is used in the production of 7-amino-
CC desacetoxycephalosporanic acid (7-ADCA), an intermediate in the
CC production of cephalosporin antibiotics. Note: the sequences shown in
CC this patent are identical to those in patent WO 95/04149. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX SQ Sequence 48 BP; 11 A; 18 C; 11 G; 8 T; 0 U; 0 Other;
Query Match 55.3%; Score 16.6; DB 2; Length 48;
Best Local Similarity 82.6%; Pred. No. 5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 ACCCCAGCAGCCGCGCTTGAAG 28
| | | | | | | | | | | | | | | |
DB 18 ACCGCGCGCGCGCGCTTGAAG 40
| | | | | | | | | | | | | | | |

RESULT 11
AAQ82717
ID AAQ82717 standard; DNA; 48 BP.
XX
XX AAQ82717;
AC
XX 25-MAR-2003 (revised)
DT 04-OCT-1995 (first entry)
XX
XX P. chrysogenum cefE gene expression cassette construction oligo.
DE
XX N. lactamurans; S. clavuligerus; P. chrysogenum; cefE gene;
KW expression cassette; 7-amino-desacetoxy-cephalosporanic acid;
KW expandase gene; cephalosporin antibiotics; ss.
XX
XX Synthetic.
XX
XX WO9504149-A1.
FN
XX
XX 09-FEB-1995.
PD
XX
XX 29-JUL-1994; 94WO-EP002544.
PF
XX
XX 30-JUL-1993; 93EP-00202260.
PR 24-DEC-1993; 93EP-00203695.
XX
XX (KONN ) GIST-BROCADES NV.
XX
XX Bovenberg RAL, Koekman BP, Hoekema A, Van Der Laan JM, Verweij J;
PI
```

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XX
DR WPI; 1995-082232/11.
XX
XX 7-amino-desacetoxy-cephalosporanic acid prodn. in Penicillium chrysogenum
PT - transformed with expandase gene, using 3,3'-thiodi:propionic acid as
PT side chain precursor and deacylation of intermediate.
XX
XX Example 1; Page 14; 37pp; English.
XX
XX AAQ82707-Q82719 are oligonucleotides used in the construction of P.
CC chrysogenum expression cassettes for the N. lactamurans and S.
CC clavuligerus cefE (expandase) gene. The transformed P. chrysogenum can
CC now be used for 7-amino-desacetoxy-cephalosporanic acid prodn. an
CC intermediate for cephalosporin antibiotics. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX SQ Sequence 48 BP; 11 A; 18 C; 11 G; 8 T; 0 U; 0 Other;
Query Match 55.3%; Score 16.6; DB 2; Length 48;
Best Local Similarity 82.6%; Pred. No. 5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 ACCCCAGCAGCCGCGCTTGAAG 28
| | | | | | | | | | | | | | | |
DB 18 ACCGCGCGCGCGCGCTTGAAG 40
| | | | | | | | | | | | | | | |

RESULT 12
ACI28074
ID ACI28074 standard; DNA; 25 BP.
XX
XX ACI28074;
AC
XX 13-OCT-2003 (first entry)
DT
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 28065.
DE
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX US2003104410-A1.
FN
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
PF
XX
XX 16-MAR-2001; 2001US-0276759P.
PR
XX (AFFY-) AFFYMETRIX INC.
XX
XX Mittmann MP;
PI
XX WPI; 2003-567953/53.
DR
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 28065; 9pp; English.
FS
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
```

CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX
SQ Sequence 25 BP; 3 A; 9 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 6.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGTACCCCGAGCGCCGCC 22

Db 4 CGGTACCTAGGAGCCCGTC 24

RESULT 13

ACI41032

ID ACI41032 standard; DNA; 25 BP.

XX AC ACI41032;

XX AC ACI41032;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 41023.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;

KW genetic variation; biallelic marker; polymorphism; human;

KW cross-species comparison.

XX Homo sapiens.

OS US2003104410-A1.

PN 05-JUN-2003.

PD 15-MAR-2002; 2002US-00098263.

PF 16-MAR-2001; 2001US-0276759P.

PR (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

DR New array of nucleic acid probes, useful for in situ hybridization, in

XX Southern, Northern or dot-blot hybridization to identify or detect the

XX sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 41023; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic

XX acid probes including one of 2,018,500 fully defined sequences, or its

XX perfect match, perfect mismatch, antisense match or antisense mismatch.

XX Also disclosed is a method of gene expression analysis. The array is used

XX in monitoring gene expression levels by hybridisation to a DNA library,

XX in analysis of genetic variation or in hybridisation of tag-labelled

XX compounds. The nucleic acid probes are specifically designed for analysis

XX of at least one target sequence. The method of analysis comprises

XX hybridising at least one or more nucleic acids to at least two or more

XX nucleic acid probes and detecting the hybridisation. The nucleic acid

XX probes are attached to a solid support. The analysis comprises monitoring

XX gene expression levels, identifying biallelic markers or polymorphisms,

CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 3 A; 9 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 9; Length 25;

Best Local Similarity 85.7%; Pred. No. 6.8e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGTACCCCGAGCGCCGCC 22

Db 3 CGGTACCTAGGAGCCCGTC 23

RESULT 14

AAZ35754

ID AAZ35754 standard; DNA; 28 BP.

XX AC AAZ35754;

XX AC AAZ35754;

DT 01-FEB-2000 (first entry)

DE Human IL17RLP PCR 3' primer SEQ ID NO:11.

XX Human; interleukin 17 receptor like protein; IL17RLP; IL-17; diagnosis;

KW detection; immune system related disorder; haemostasis;

KW cellular activation; angiogenesis; tumour metastasis; ovulation;

KW cellular migration; neurogenesis; infection; T-cell proliferation;

KW autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation;

KW sepsis; tumour; cancer; interstitial lung disease; arthritis; lymphoma;

KW immunosuppression; immunity; inflammatory bowel disease;

KW myelo suppression; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9914240-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-US019121.

XX 17-SEP-1997; 97US-0059133P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Shi Y, Ruben SM;

XX WPI; 2000-061918/05.

XX New human interleukin-17 receptor like protein, e.g. to treat disorders

XX relating to cellular activation.

XX Example 3; Page 100; 133pp; English.

XX The present invention describes human interleukin 17 receptor like

XX protein (IL17RLP), isolated from a cDNA library of human adult pulmonary

XX tissue. The present sequence represents a PCR primer for human IL17RLP.

XX IL17RLP and its agonists can be used to treat disorders relating to

XX cellular activation, haemostasis, angiogenesis, tumour metastasis,

XX cellular migration and ovulation, and neurogenesis. They can also be used

XX to enhance host defences against resistant chronic and acute infections,

XX e.g. mycobacterial infections via the attraction and activation of

XX microbial leukocytes. IL17RLP may also be used to increase T-cell

CC proliferation by the stimulation of IL-2 biosynthesis for the treatment
 CC of T-cell mediated autoimmune diseases and lymphocytic leukaemias, to
 CC regulate haematopoiesis by regulating the activation and differentiation
 CC of various haematopoietic progenitor cells, e.g. to release mature
 CC leukocytes from the bone marrow following chemotherapy, i.e. in stem cell
 CC mobilisation or to treat sepsis. The products can also be used for the
 CC diagnosis or treatment of immune system related disorders e.g. tumours,
 CC cancers, interstitial lung disease, and any dysregulation of immune cell
 CC function including autoimmunity, arthritis, leukaemias, lymphomas,
 CC immunosuppression, immunity, humoral immunity, inflammatory bowel
 CC disease, or myelo suppression
 XX
 SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 3; Length 28;
 Best Local Similarity 85.7%; Pred. NO. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTACCCCGAGCGCCGGCCT 23
 |||||
 Db 6 GGTACCCCGAGCTCCCGCCT 26

RESULT 15
 AAZ35756

ID AAZ35756 standard; DNA; 28 BP.

AC AAZ35756;

DT 01-FEB-2000 (first entry)

DE Human IL17RLP PCR primer SEQ ID NO:13.

XX Human; interleukin 17 receptor like protein; IL17RLP; IL-17; diagnosis;
 KW detection; immune system related disorder; haemostasis;
 KW cellular activation; angiogenesis; tumour metastasis; ovulation;
 KW cellular migration; neurogenesis; infection; T-cell proliferation;
 KW autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation;
 KW sepsis; tumour; cancer; interstitial lung disease; arthritis; lymphoma;
 KW immunosuppression; immunity; inflammatory bowel disease;
 KW myelo suppression; PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9914240-A1.

PD 25-MAR-1999.

PF 16-SEP-1998; 98WO-US019121.

PR 17-SEP-1997; 97US-0059133P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Shi Y, Ruben SM;

XX WPI; 2000-061918/05.

XX New human interleukin-17 receptor like protein, e.g. to treat disorders
 PT relating to cellular activation.

XX Example 3; Page 102; 133pp; English.

XX The present invention describes human interleukin 17 receptor like
 CC protein (IL17RLP), isolated from a cDNA library of human adult pulmonary
 CC tissue. The present sequence represents a PCR primer for human IL17RLP.
 CC IL17RLP and its agonists can be used to treat disorders relating to
 CC cellular activation, haemostasis, angiogenesis, tumour metastasis,
 CC cellular migration and ovulation, and neurogenesis. They can also be used
 CC to enhance host defences against resistant chronic and acute infections,
 CC e.g. mycobacterial infections via the attraction and activation of
 CC microbial leukocytes. IL17RLP may also be used to increase T-cell

CC proliferation by the stimulation of IL-2 biosynthesis for the treatment
 CC of T-cell mediated autoimmune diseases and lymphocytic leukaemias, to
 CC regulate haematopoiesis by regulating the activation and differentiation
 CC of various haematopoietic progenitor cells, e.g. to release mature
 CC leukocytes from the bone marrow following chemotherapy, i.e. in stem cell
 CC mobilisation or to treat sepsis. The products can also be used for the
 CC diagnosis or treatment of immune system related disorders e.g. tumours,
 CC cancers, interstitial lung disease, and any dysregulation of immune cell
 CC function including autoimmunity, arthritis, leukaemias, lymphomas,
 CC immunosuppression, immunity, humoral immunity, inflammatory bowel
 CC disease, or myelo suppression
 XX
 SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 3; Length 28;
 Best Local Similarity 85.7%; Pred. NO. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTACCCCGAGCGCCGGCCT 23
 |||||
 Db 6 GGTACCCCGAGCTCCCGCCT 26

RESULT 16

AAZ52043

ID AAZ52043 standard; DNA; 28 BP.

AC AAZ52043;

DT 09-AUG-2000 (first entry)

DE 3'primer for amplification of IL-17RLP cDNA.

XX Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;
 KW resistant chronic infection; acute infection; mycobacterial infection;
 KW T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia;
 KW T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;
 KW IL-6 expression; myeloma; plasmacytoma; Lennert's lymphoma;
 KW immunoprotective; cytostatic; hematopoietic; proliferative;
 KW antibacterial; PCR primer; ss.

XX Homo sapiens.

XX WO200015759-A1.

XX 23-MAR-2000.

XX 15-SEP-1999; 99WO-US021048.

XX 16-SEP-1998; 98US-00154219.

XX 16-SEP-1998; 98WO-US019121.

XX 16-MAR-1999; 99US-00268311.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Shi Y;

XX WPI; 2000-271403/23.

XX Novel polynucleotides encoding interleukin-17-like receptor protein,
 PT useful for diagnosis and treatment of immune system-related disorders,
 PT e.g. sepsis and cancers.

XX Example 3; Page 102; 147pp; English.

XX The patent relates to novel interleukin-17-like receptor protein (IL-
 CC 17RLP). IL-17RLP is a homologue of the IL-17 receptor and has a wide
 CC range of cytokine receptor-like activities. IL-17RLP or its agonists may
 CC be used to enhance host defenses against resistant chronic and acute
 CC infections, e.g. mycobacterial infections, via the attraction and
 CC activation of microbicidal leukocytes. It may also be used to increase T-
 CC cell proliferation by stimulating IL-2 biosynthesis, for the treatment of
 CC T-cell mediated autoimmune diseases and lymphocytic leukaemias. IL-17RLP

CC may also be used to regulate hematopoiesis and to treat sepsis.
 CC Extracellular IL-17RLP domains may be used as antagonists of IL-17RLP. IL
 CC -17RLP agonists and antagonists can also be used to modulate IL-6
 CC expression, useful in treatment of cancers such as myelomas,
 CC plasmacytomas and hybridomas and Lennert's lymphoma. The present sequence
 CC is the 3'PCR primer used for the amplification of IL-17RLP cDNA. This
 CC primer comprises Asp18 and 17 of nucleotides complementary to the
 CC 3'coding region immediately before the stop codon. This is used in the
 CC construction of vectors for expression in E. coli
 XX
 SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 3; Length 28;
 Best Local Similarity 85.7%; Pred. No. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCT 23
 Db 6 GGTACCCCGAGCGCTCCCGGCTT 26

RESULT 17
 AAA75769
 ID AAA75769 standard; DNA; 28 BP.
 XX
 AC AAA75769;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE PCR primer for a human interleukin 17 receptor-like cDNA fragment.
 XX
 KW Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;
 KW cellular activation; haemostasis; angiogenesis; tumour metastasis;
 KW cellular migration; ovulation; neurogenesis; arthritis;
 KW autoimmune disorder; systemic lupus erythromatosus; PCR primer; ss.
 XX

OS Homo sapiens.

PN WO200055204-A1.

PD 21-SEP-2000.

PF 06-MAR-2000; 2000WO-US005759.

PR 16-MAR-1999; 99US-00268311.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Shi Y, Ruben SM;

DR WPI; 2000-647065/62.

XX Novel gene encoding a polypeptide of the interleukin-17 receptor family,
 PT and an antagonist and agonist of the polypeptide, useful for treating,
 PT diagnosing, detecting and/or preventing immune system related disorders.

PS Example 3a; Page 182; 247pp; English.

CC PCR primers AAA75768-69 were used to amplify a fragment of cDNA encoding
 CC a human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP
 CC polypeptide is useful for screening for agonists and antagonists. These
 CC antagonists and agonists are useful for treating, diagnosing, detecting
 CC and or preventing disorders related to cellular activation, haemostasis,
 CC angiogenesis, tumour metastasis, cellular migration, ovulation or
 CC neurogenesis, such as osteoporosis, arthritis and autoimmune disorders
 CC e.g. systemic lupus erythromatosus
 XX

SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 3; Length 28;
 Best Local Similarity 85.7%; Pred. No. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCT 23
 Db 6 GGTACCCCGAGCGCTCCCGGCTT 26

RESULT 18

AAA75771

ID AAA75771 standard; DNA; 28 BP.

XX AAA75771;

XX 22-JAN-2001 (first entry)

DE PCR primer for a human interleukin 17 receptor-like DNA fragment.

XX Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;
 KW cellular activation; haemostasis; angiogenesis; tumour metastasis;
 KW cellular migration; ovulation; neurogenesis; arthritis;
 KW autoimmune disorder; systemic lupus erythromatosus; PCR primer; ss.

XX Homo sapiens.

PN WO200055204-A1.

PD 21-SEP-2000.

PF 06-MAR-2000; 2000WO-US005759.

PR 16-MAR-1999; 99US-00268311.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Shi Y, Ruben SM;

DR WPI; 2000-647065/62.

XX Novel gene encoding a polypeptide of the interleukin-17 receptor family,
 PT and an antagonist and agonist of the polypeptide, useful for treating,
 PT diagnosing, detecting and/or preventing immune system related disorders.

PS Example 3b; Page 185; 247pp; English.

CC PCR primers AAA75770-71 were used to amplify a fragment of DNA encoding a
 CC human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP
 CC polypeptide is useful for screening for agonists and antagonists. These
 CC antagonists and agonists are useful for treating, diagnosing, detecting
 CC and or preventing disorders related to cellular activation, haemostasis,
 CC angiogenesis, tumour metastasis, cellular migration, ovulation or
 CC neurogenesis, such as osteoporosis, arthritis and autoimmune disorders
 CC e.g. systemic lupus erythromatosus
 XX

SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 3; Length 28;

Best Local Similarity 85.7%; Pred. No. 6.9e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCT 23
 Db 6 GGTACCCCGAGCGCTCCCGGCTT 26

RESULT 19

ADT93853

ID ADT93853 standard; DNA; 28 BP.

XX ADT93853;

XX 16-DEC-2004 (first entry)

XX Human interleukin 17 receptor-like protein extracellular domain primer 3.
 KW ss; antiinflammatory; cytostatic; gastrointestinal; immunosuppressive;

KW interleukin 17-receptor-like protein; IL17RLP; cellular activation;
 KW hemostasis; angiogenesis; tumor metastasis; cellular migration;
 KW ovulation; neurogenesis; immune-related disorder; Crohn's disease; tumor;
 KW inflammatory bowel disease; autoimmune disease; lymphocytic leukemia;
 KW graft versus host disease; chromosomal identification; primer; PCR.

XX Homo sapiens.
 XX AU2004200961-A1.
 XX 01-APR-2004.
 XX 09-MAR-2004; 2004AU-00200961.
 XX 09-MAR-2004; 2004AU-00200961.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Shi Y, Ruben SM;
 XX WPI; 2004-662639/65.
 XX Novel isolated interleukin 17-receptor-like protein useful for treating
 PT immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel
 PT disease, autoimmune diseases, lymphocytic leukemias, or graft versus host
 PT disease.

XX Example 3; SEQ ID NO 13; 145pp; English.

XX The invention relates to an isolated interleukin 17-receptor-like protein
 CC (IL17RLP) (I) comprising an amino acid sequence that is 95% or more
 CC identical to a sequence e.g., sequence having amino acids from positions
 CC 19-407 of a fully defined sequence (S1) of 426 amino acids as given in
 CC the specification, sequence having amino acids from positions 18-407 of
 CC (S1) that comprises N-terminal methionine or sequence having amino acids
 CC from positions 1-407 of (S1). (I) is useful for treating disorders
 CC related to cellular activation, hemostasis, angiogenesis, tumor
 CC metastasis, cellular migration, ovulation or neurogenesis. (I) is useful
 CC for treating immune-related disorders e.g., Crohn's disease, tumor,
 CC inflammatory bowel disease, autoimmune diseases, lymphocytic
 CC or graft versus host disease. (II) is useful for chromosomal
 CC identification. (I) exhibits enhanced activity, solubility and stability,
 CC and is produced in large quantities. This sequence corresponds to a PCR
 CC primer to amplify the extracellular domain from the human IL17RLP cDNA
 CC sequence (ADT93841) for expression in Chinese Hamster Ovary (CHO) cells.

XX Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 13; Length 28;
 Best Local Similarity 85.7%; Pred. No. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GGATCCCGCAGCGCCGCGCT 23
 DB 6 GGATCCCGCAGCGCTCCCGGCTT 26

RESULT 20
 ADT93851
 ID ADT93851 standard; DNA; 28 BP.
 XX
 AC ADT93851;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human interleukin 17 receptor-like protein extracellular domain primer.

ss; antiinflammatory; cytostatic; gastrointestinal; immunosuppressive;
 KW interleukin 17-receptor-like protein; IL17RLP; cellular activation;
 KW hemostasis; angiogenesis; tumor metastasis; cellular migration;
 KW ovulation; neurogenesis; immune-related disorder; Crohn's disease; tumor;
 KW inflammatory bowel disease; autoimmune disease; lymphocytic leukemia;
 KW graft versus host disease; chromosomal identification; primer; PCR.

XX Homo sapiens.
 XX AU2004200961-A1.
 XX 01-APR-2004.
 XX 09-MAR-2004; 2004AU-00200961.
 XX 09-MAR-2004; 2004AU-00200961.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Shi Y, Ruben SM;
 XX WPI; 2004-662639/65.
 XX Novel isolated interleukin 17-receptor-like protein useful for treating
 PT immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel
 PT disease, autoimmune diseases, lymphocytic leukemias, or graft versus host
 PT disease.

XX Example 3; SEQ ID NO 11; 145pp; English.

XX The invention relates to an isolated interleukin 17-receptor-like protein
 CC (IL17RLP) (I) comprising an amino acid sequence that is 95% or more
 CC identical to a sequence e.g., sequence having amino acids from positions
 CC 19-407 of a fully defined sequence (S1) of 426 amino acids as given in
 CC the specification, sequence having amino acids from positions 18-407 of
 CC (S1) that comprises N-terminal methionine or sequence having amino acids
 CC from positions 1-407 of (S1). (I) is useful for treating disorders
 CC related to cellular activation, hemostasis, angiogenesis, tumor
 CC metastasis, cellular migration, ovulation or neurogenesis. (I) is useful
 CC for treating immune-related disorders e.g., Crohn's disease, tumor,
 CC inflammatory bowel disease, autoimmune diseases, lymphocytic
 CC or graft versus host disease. (II) is useful for chromosomal
 CC identification. (I) exhibits enhanced activity, solubility and stability,
 CC and is produced in large quantities. This sequence corresponds to a PCR
 CC primer to amplify the extracellular domain from the human IL17RLP cDNA
 CC sequence (ADT93841).

XX Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 13; Length 28;
 Best Local Similarity 85.7%; Pred. No. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGATCCCGCAGCGCCGCGCT 23
 DB 6 GGATCCCGCAGCGCTCCCGGCTT 26

RESULT 21
 ADT93841
 ID ADF72771 standard; DNA; 38 BP.
 XX
 AC ADF72771;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Fusarium solani cutinase gene primer, Exon1B.

immobilizing; functional organic molecule; predetermined density;
 KW mixed monolayer surface; MMS; reducing end; peracetylated sugar;
 KW chemoselective; ss; primer; cutinase.
 XX Synthetic.
 OS Fusarium solani.
 XX WO2003018854-A2.
 XX
 PD 06-MAR-2003.
 XX

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PF 27-AUG-2002; 2002WO-US027195.
XX
XX 27-AUG-2001; 2001US-0315261P.
XX 28-AUG-2001; 2001US-0315544P.
XX 15-FEB-2002; 2002US-0356765P.
XX 15-FEB-2002; 2002US-0358412P.
XX 19-FEB-2002; 2002US-0357136P.
XX 20-FEB-2002; 2002US-0375023P.
XX 26-APR-2002; 2002US-0380259P.
XX
XX (SURF-) SURFACE LOGIX INC.
XX
XX Hodneland C, Campbell S, Duffy D, Agosto M, Wang E;
XX
XX WPI; 2003-393250/37.
XX
XX Immobilizing functional organic molecule in a predetermined density on a
XX mixed monolayer surface, by contacting the surface with the organic
XX molecule to form a covalent bond and to immobilize the organic molecule.
XX
XX Example 6; SEQ ID NO 2; 234pp; English.
XX
XX The invention relates to a novel method for immobilizing a functional
XX organic molecule in a predetermined density on a mixed monolayer surface
XX (MMS). The novel method comprises a first monolayer moiety (MM1) having a
XX covalent bond forming reactive group and a second monolayer moiety (MM2)
XX having an inert group. The method involves contacting MMS with the
XX functional organic molecule to form a covalent bond between the
XX functional organic molecule and MM1 to immobilize the functional organic
XX molecule. The novel method of the invention is useful for immobilizing a
XX functional organic molecule in a predetermined density on a mixed
XX monolayer surface, where the functional organic molecule is selected from
XX oligonucleosides, peptides, polypeptides, oligonucleotides, nucleotides,
XX enzymes, enzyme substrates, ligands, receptors, antibodies, antigens,
XX lipids, and small molecules, but preferably a carbohydrate. The
XX carbohydrate comprises a reducing end, the reducing end comprises a
XX peracetylated sugar having an n-pentenyl group. This polynucleotide
XX sequence represents a primer used in the exemplification of the
XX invention.
XX
XX Sequence 38 BP; 5 A; 14 C; 10 G; 9 T; 0 U; 0 Other;
SQ
    Query Match      54.0%; Score 16.2; DB 10; Length 38;
    Best Local Similarity 72.4%; Pred. No. 7e+03;
    Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CGGTACCCCGACGAGCCGCGCTTGAAGAA 30
   ||||| || ||||| || |||||
Db 2 CGGTACCCCAAGTTGCCCGTCTCTGTGAA 30

RESULT 22
ADH34521
ID ADH34521 standard; DNA; 38 BP.
XX
XX ADH34521;
XX
XX 11-MAR-2004 (first entry)
XX
XX PCR primer #2 for Fusarium solani cutinase gene.
XX
XX Alkanethiol; reactant ligand; substrate; protein chip;
XX polypeptide immobilisation; enzyme activity; antibody detection;
XX cutinase; PCR; primer; ss.
XX
XX Fusarium solani.
XX
XX US2003119054-A1.
XX
XX 26-JUN-2003.
XX
XX 07-AUG-2001; 2001US-00923760.

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XX 07-AUG-2001; 2001US-00923760.
XX
XX (MRKS/) MRKSICH M.
XX (HODN/) HODNELAND C.
XX
XX Mrksich M, Hodneland C;
XX
XX WPI; 2004-080248/08.
XX
XX New alkanethiols substituted with a reactant ligand useful for
XX immobilizing polypeptides on gold surfaces, e.g. for determining enzyme
XX activity or detecting antibodies.
XX
XX Example 7; SEQ ID NO 2; 57pp; English.
XX
XX The present invention relates to alkanethiols substituted with a reactant
XX ligand. Also disclosed is a substrate comprising a surface and a
XX plurality of moieties on the surface. The moieties are of formula Surf-L-
XX Q-T where T comprises a reactant ligand, and Surf designates where the
XX moiety attaches to the surface. The substrate can be incorporated into a
XX protein chip comprising a substrate bearing the reaction product of a
XX reactant ligand and a fusion polypeptide comprising a capture polypeptide
XX corresponding to the reactant ligand. The alkanethiols of the invention
XX are useful for immobilising polypeptides on gold surfaces, e.g. for
XX determining enzyme (especially kinase or protease) activity or detecting
XX antibodies. The present sequence represents a PCR primer used in the
XX examples of the present invention.
XX
XX Sequence 38 BP; 5 A; 14 C; 10 G; 9 T; 0 U; 0 Other;
SQ
    Query Match      54.0%; Score 16.2; DB 12; Length 38;
    Best Local Similarity 72.4%; Pred. No. 7e+03;
    Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CGGTACCCCGACGAGCCGCGCTTGAAGAA 30
   ||||| || ||||| || |||||
Db 2 CGGTACCCCAAGTTGCCCGTCTCTGTGAA 30

RESULT 23
ABK49653
ID ABK49653 standard; DNA; 29 BP.
XX
XX ABK49653;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human intron 1 3' acceptor site.
XX
XX RhCG; mouse; human; non-erythroid Rh type C glycoprotein; ss; intron.
XX
XX Homo sapiens.
XX
XX WO200220719-A2.
XX
XX 14-MAR-2002.
XX
XX 05-SEP-2001; 2001WO-US027503.
XX
XX 07-SEP-2000; 2000US-0230660P.
XX
XX (NYBL-) NEW YORK BLOOD CENT INC.
XX
XX Huang C, Liu Z;
XX
XX WPI; 2002-351774/38.
XX
XX Nucleic acid sequences encoding novel mammalian nonerythroid Rh type C
XX and glycoproteins which have a characteristic twelve transmembrane domain
XX structure.
XX
XX Example; Fig 6; 53pp; English.

```

XX	CC	This invention relates to the nucleic acid and protein sequences of novel
XX	CC	human and mouse non-erythroid Rh type C glycoprotein (RhCG). The RhCG
XX	CC	protein and the mouse homologue (rhcg) have a characteristic 12
XX	CC	transmembrane domain structure and are expressed in kidneys and testis.
XX	CC	The invention also comprises a method for antibody that specifically
XX	CC	binds an epitope of the glycoprotein and a method for detecting the
XX	CC	protein using this antibody. The antibodies of the invention may be used
XX	CC	in Western blots, enzyme linked immunosorbent assays (ELISA) or
XX	CC	immunohistochemical assays to identify the non- erythroid tissues,
XX	CC	particularly kidney and testis, that express the RhCG or Rhcg
XX	CC	glycoproteins. The methods are used for detecting an Rhcg or and RhCG
XX	CC	glycoprotein in a sample. The present sequence represents the intronic
XX	CC	sequence at an intron/exon splice site of the rhcg gene of the invention
XX	SQ	Sequence 29 BP; 5 A; 11 C; 10 G; 3 T; 0 U; 0 Other;
		Query Match 53.3%; Score 16; DB 6; Length 29;
		Best Local Similarity 79.2%; Pred. No. 8.3e+03;
		Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY	3	GGTACCCAGCAGCAGCCGCGCCTTGA 26
DB	6	GGCACCCCTGCAGCATGGCCTTGA 29
RESULT 24		
AAI73703/c		
ID	AAI73703	standard; DNA; 50 BP.
XX	AAI73703;	
AC		
XX	09-NOV-2001	(first entry)
DT		
XX		
DE	Human silent SNP containing nucleic acid SEQ:644.	
XX		
KW	Human; single nucleotide polymorphism; SNP; genome; gene therapy;	
KW	protein therapy; vaccine; probe; diagnostic assay; detection;	
KW	quantitation; restorative therapy; polymorphic; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200140521-A2.	
XX		
PD	07-JUN-2001.	
XX		
PF	30-NOV-2000; 2000WO-US032758.	
XX		
PR	30-NOV-1999; 99US-0168138P.	
PR	29-NOV-2000; 2000US-00726173.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Shimkets RA, Leach M;	
XX		
DR	WPI; 2001-356160/37.	
XX		
PT	Polymorphic nucleic acid sequences, useful in genetic testing and	
PT	therapy.	
XX		
PS	Claim 1; Page 251; 2653pp; English.	
XX		
CC	AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide	
CC	sequences (I), which contain single nucleotide polymorphisms (SNPs).	
CC	AAW53114 to AAM53329 represent peptides related to human polymorphic	
CC	polynucleotide sequences. The sequences can be used in gene and protein	
CC	therapy, and in vaccine production. (I) and the polypeptides encoded by	
CC	them may be used in the prevention, diagnosis and treatment of diseases	
CC	associated with inappropriate expression of polymorphic polypeptides. For	
CC	example, (I) may be used to treat disorders by rectifying mutations or	
CC	deletions in a patient's genome that affect the activity of polypeptides	
CC	by expressing inactive proteins or to supplement the patients own	
CC	production of polypeptide. Additionally, (I) and its complementary	

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTACCCCGACGCCGGCC 22
|||||
Db 19 GTACCCCTGCAGCGCGCC 1

RESULT 26

ACD82353/c
ID ACD82353 standard; DNA; 19 BP.

XX
AC ACD82353;

DT 19-SEP-2003 (first entry)

XX Nucleic acid cloning associated adaptor molecule #54.

KW Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
KW internal deletion mutagenesis analysis; cloning vehicle; ss.

XX Synthetic.

OS US2003044791-A1.

FN PD 06-MAR-2003.

XX PF 13-JUN-2001; 2001US-00880313.

XX PR 13-JUN-2001; 2001US-00880313.

XX PA (FLEM/) FLEMINGTON E K.

XX PI Flemington EK;

XX DR WPI; 2003-521745/49.

XX New adaptor molecules, useful for cloning nucleic acid molecules that
PT does not require the design and synthesis of oligonucleotides or PCR
PT primers.

XX PS Claim 12; Fig 1; 100pp; English.

XX The invention describes adaptor molecules, where each end of the adaptor
CC is compatible with a nucleic acid digested with a restriction enzyme or a
CC nucleic acid comprising an end that is compatible with a nucleic acid
CC digested with a restriction enzyme. The adaptor molecules, compositions,
CC kits and arrays are useful for cloning nucleic acid molecules that does
CC not require the design and synthesis of oligonucleotides or PCR primers.
CC The adaptors, kits and arrays are also useful for ligating two ends of a
CC single nucleic acid molecule, or ligating two or more nucleic acid
CC molecules. The kits can also be used for performing internal deletion
CC mutagenesis analysis. The adaptor molecules are ligated to a cloning
CC vehicle, making the cloning procedure more rapid and efficient, and less
CC error-prone. This sequence represents a nucleic acid cloning associated
CC adaptor molecule

SQ Sequence 19 BP; 2 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 52.7%; Score 15.8; DB 9; Length 19;

Best Local Similarity 89.5%; Pred. No. 9.6e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTACCCCGACGCCGGCC 22

Db 19 GTACCCCTGCAGCGCGCC 1

RESULT 27

ACF79913/c

ID ACF79913 standard; DNA; 39 BP.

XX AC ACF79913;

XX

DT 15-JAN-2004 (first entry)

XX Human Her-2 protein cytoplasmic kinase domain PCR primer.

KW Human; Her-2; chitin binding domain; affinity tag; protein purification;
KW PCR; primer; ss.

XX Homo sapiens.

FN WO2003074660-A2.

XX PD 12-SEP-2003.

XX PF 26-FEB-2003; 2003WO-US005851.

XX PR 28-FEB-2002; 2002US-0360354P.

XX PA (NEWE) NEW ENGLAND BIOLABS INC.

XX PI Xu M, Ferrandon SM, Taron CH, Colussi PA;

XX WPI; 2003-712883/67.

XX A (mutant) chitin binding domain capable of reversibly binding a chitin
PT substrate under a selected non-denaturing condition, useful for producing
PT and purifying a target protein molecule.

XX Example 1; Page 29; 74pp; English.

XX The present sequence is that of a primer used, with the primer given in
CC ACF79912, for the PCR amplification of cDNA encoding the human Her-2
CC protein cytoplasmic kinase domain. The PCR product was used in the
CC construction of a fusion protein comprising the Her-2 kinase domain and a
CC modified (W687F mutant) chitin binding domain (CBD) of Bacillus circulans
CC WL-12 chitinase A1. The modified CBD acted as an affinity tag for
CC purification of the Her-2 kinase domain, allowing protein elution under
CC non-denaturing conditions

SQ Sequence 39 BP; 4 A; 16 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 52.7%; Score 15.8; DB 10; Length 39;

Best Local Similarity 89.5%; Pred. No. 1e+04;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTACCCCGACGCCGGCC 21

Db 28 GGTACCCCGACGCCGGCC 10

RESULT 28

ABN86094

ID ABN86094 standard; DNA; 41 BP.

XX AC ABN86094;

XX 02-OCT-2002 (first entry)

XX Lymphocyte activator protein 33 related probe 1.

KW Lymphocyte activator protein 33; body fluid immunity disorder; tumour;
KW probe; ss.

XX Unidentified.

XX CN1340527-A.

XX PD 20-MAR-2002.

XX PF 31-AUG-2000; 2000CN-00119839.

XX PR 31-AUG-2000; 2000CN-00119839.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

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XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-436421/47.
XX
PT Lymphocyte activator protein 33 and encoding polynucleotide, useful for
XX treating body fluid disorder and tumor.
XX
PS Example 6; Page 19 (disclosure); 33pp; Chinese.
XX
CC The invention relates to a lymphocyte activator protein 33, the encoding
XX polynucleotide, and a method for preparing the polypeptide by DNA
XX recombination technique. The polypeptide is used in treating diseases
XX such as body fluid immunity disorder and tumours. The current sequence
XX represents a lymphocyte activator protein 33 related probe sequence
XX
SQ Sequence 41 BP; 11 A; 13 C; 13 G; 4 T; 0 U; 0 Other;
Query Match 52.7%; Score 15.8; DB 6; Length 41;
Best Local Similarity 74.1%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 4 GTACCCACGAGCCGCGCTTGAGAA 30
| | | | | | | | | | | | | | | | | |
Db 2 GGACCCACGAGCCGCGCTTGAGAA 28
| | | | | | | | | | | | | | | | | |
RESULT 29
AAL33786/c
ID AAL33786 standard; DNA; 50 BP.
XX
AC AAL33786;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #6994.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 95US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
PS Claim 1; Page 3387; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 50 BP; 7 A; 20 C; 18 G; 5 T; 0 U; 0 Other;
Query Match 52.7%; Score 15.8; DB 4; Length 50;
Best Local Similarity 89.5%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 CCCGAGCAGCCGCGCCCTTG 25
| | | | | | | | | | | | | | | |
Db 21 CCCGAGCAGCCGCGCCCTTG 3
| | | | | | | | | | | | | | | |
RESULT 30
AAX16927/c
ID AAX16927 standard; DNA; 43 BP.
XX
AC AAX16927;
XX
DT 11-MAY-1999 (first entry)
XX
DE Primer #17 for constructing plasmid M13IX30.
XX
KW Heteromeric; receptor; immunoglobulin; superfamily; plasmid; primer; PCR;
KW bacteriophage; fusion protein; amplification; heavy chain; light chain;
KW immune system; diagnosis; ss.
XX
OS Synthetic.
XX
PN US5871974-A.
XX
PD 16-FEB-1999.
XX
PF 02-DEC-1994; 94US-00349131.
XX
PR 28-SEP-1990; 90US-00590219.
XX
PR 27-SEP-1991; 91US-00767136.
XX
PR 13-SEP-1993; 93US-00120648.
XX
PA (IXSY-) IXSYS INC.
XX
PI Huse WD;
XX
DR WPI; 1999-166647/14.
XX
PT New surface expression libraries expressing heteromeric receptors -
XX comprising cells containing vectors containing combinations of DNA
XX sequences encoding first and second polypeptides.
XX
PS Example 1; Col 12; 58pp; English.
XX
CC The invention relates to the expression of heteromeric receptor proteins,
XX e.g. from an immunoglobulin (Ig) superfamily, in cells containing the
XX heteromeric receptor genes on a single plasmid. Especially mentioned, the
XX cell may be a bacteriophage, where the receptor protein are expressed as
XX fusion proteins with the surface protein gVIII. Primers AAX16911-X16936
XX were used in the construction of plasmid M13IX30 (AAX16937) for
XX expression of receptor heavy chain proteins. Light chain genes are cloned
XX into the plasmid M13IX11 (AAX16953). The methods can be used to generate
XX diverse populations of heteromeric receptors which mimic the natural
XX immune system and can be used for diagnostic and therapeutic purposes
XX
```

```
SQ Sequence 43 BP; 12 A; 8 C; 15 G; 8 T; 0 U; 0 Other;
Query Match 52.0%; Score 15.6; DB 2; Length 43;
Best Local Similarity 70.0%; Fred. No. 1.2e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCGTTACCCAGCAGCCGCGCTTGAAGAA 30
   ||| |||| ||| ||| ||| ||| |||
DB 42 GCGTTACCCAGCTTAATCGCCTTGCAAGAA 13

RESULT 31
AAZ91566/c
ID AAZ91566 standard; DNA; 43 BP.
XX
AC AAZ91566;
XX
DT 25-MAY-2000 (first entry)
XX
DE Lac Z mutagenesis oligonucleotide SEQ ID NO:43.
XX
KW Bacteriophage M13 vector; prokaryotic cell; heteromeric receptor;
KW antibody; immune system; filamentous bacteriophage; cloning; screening;
KW coexpression; PCR primer; mutagenesis; ss.
XX
OS Enterobacteria phage M13.
XX Synthetic.
XX
PN US6027933-A.
XX
PD 22-FEB-2000.
XX
PF 05-JUN-1995; 95US-00470297.
XX
PR 28-SEP-1990; 90US-00590219.
PR 27-SEP-1991; 91US-00767136.
PR 13-SEP-1993; 93US-00120648.
PR 01-DEC-1994; 94US-00349131.
XX
PA (IXSY-) IXSYS INC.
XX
PI Huse WD;
XX
XX WPI; 2000-194835/17.
XX
DR Kit for the preparation of vectors for the coexpression of two or more
PT DNA sequences encoding proteins that form heteromeric receptors.
XX
PS Example 1; Col 13; 58pp; English.
XX
CC The present invention describes a kit (I) for the preparation of vectors
CC for the coexpression of two or more DNA sequences encoding polypeptides
CC comprising two vectors which operatively combine through two pairs of
CC restriction sites to form a single vector. The kit is useful for the
CC preparation of vectors for the coexpression of two or more DNA sequences
CC encoding polypeptides which form heteromeric receptors. The kit simply
CC and efficiently generates a large repertoire of diverse combinations of
CC heteromeric receptors. Only proper combinations of vector portions are
CC randomly brought together for the coexpression of different DNA sequences
CC without loss of population size or diversity. AAZ91524 to AAZ91528
CC represent bacteriophage M13 vector nucleotide sequences constructed in
CC the exemplification of the present invention. AAZ91529 to AAZ91599
CC represent oligonucleotides used in the construction of vectors in the
CC exemplification of the present invention
XX
SQ Sequence 43 BP; 12 A; 8 C; 15 G; 8 T; 0 U; 0 Other;
Query Match 52.0%; Score 15.6; DB 3; Length 43;
Best Local Similarity 70.0%; Fred. No. 1.2e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCGTTACCCAGCAGCCGCGCTTGAAGAA 30
   ||| |||| ||| ||| ||| ||| |||
DB 42 GCGTTACCCAGCTTAATCGCCTTGCAAGAA 13

RESULT 32
ACD82542/c
ID ACD82542 standard; DNA; 20 BP.
XX
AC ACD82542;
XX
DT 19-SEP-2003 (first entry)
XX
DE Nucleic acid cloning associated adaptor molecule #243.
XX
KW Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
KW internal deletion mutagenesis analysis; cloning vehicle; ss.
XX
OS Synthetic.
XX
PN US2003044791-A1.
XX
PD 06-MAR-2003.
XX
PF 13-JUN-2001; 2001US-00880313.
XX
PR 13-JUN-2001; 2001US-00880313.
XX
PA (FLEM/) FLEMINGTON E K.
XX
PI Flemington EK;
XX
XX WPI; 2003-521745/49.
XX
DR New adaptor molecules, useful for cloning nucleic acid molecules that
PT does not require the design and synthesis of oligonucleotides or PCR
PT primers.
XX
PS Claim 12; Fig 5; 100pp; English.
XX
CC The invention describes adaptor molecules, where each end of the adaptor
CC is compatible with a nucleic acid digested with a restriction enzyme or a
CC nucleic acid comprising an end that is compatible with a nucleic acid
CC digested with a restriction enzyme. The adaptor molecules, compositions,
CC kits and arrays are useful for cloning nucleic acid molecules that does
CC not require the design and synthesis of oligonucleotides or PCR primers.
CC The adaptors, kits and arrays are also useful for ligating two ends of a
CC single nucleic acid molecule, or ligating two or more nucleic acid
CC molecules. The kits can also be used for performing internal deletion
CC mutagenesis analysis. The adaptor molecules are ligated to a cloning
CC vehicle, making the cloning procedure more rapid and efficient, and less
CC error-prone. This sequence represents a nucleic acid cloning associated
CC adaptor molecule
XX
SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 51.3%; Score 15.4; DB 9; Length 20;
Best Local Similarity 94.1%; Fred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTACCCCGCAGCAGCCCGG 20
   ||| |||| ||| ||| ||| ||| |||
DB 20 GTACCCCGCAGCAGCCCGG 4

RESULT 33
AAA93835
ID AAA93835 standard; DNA; 27 BP.
XX
AC AAA93835;
XX
DT 11-JAN-2001 (first entry)
XX
DE PCR primer for human MSH receptor DNA amplification.
XX
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QY      3  GGTACCCAGCAGCCGGCCTTGAA 27
Db      40  GGCACATCAATAGCAGCGCCTTGAA 16

RESULT 36
AAT16692/c
ID      AAT16692 standard; cDNA; 40 BP.
XX
AC      AAT16692;
XX
DT      02-OCT-1996 (first entry)
XX
DE      Hepatitis C virus E1 gene RT-PCR primer.
XX
KW      HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
KW      hepatitis; reverse transcriptase polymerase chain reaction; RT-PCR; ss.
XX
OS      Synthetic.
XX
PN      WO9605315-A2.
XX
PD      22-FEB-1996.
XX
PF      15-AUG-1995; 95WO-US010398.
XX
PR      15-AUG-1994; 94US-00290665.
XX
PA      (USSH ) US SEC DEPT HEALTH.
XX
PI      Bukh J, Miller RH, Purcell RH;
XX
PW      WPI; 1996-139709/14.
XX
PT      DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
PT      determine HCV genotype and as vaccines against HCV infection.
XX
PS      Example 1; Page 224; 340pp; English.
XX
CC      AAT16689-T16694 are a set of RT-PCR primers used for the identification
CC      of the cDNA sequence of the E1 (envelope-1) gene of 51 HCV isolates. The
CC      isolated sequences are useful for the prodn. of primers useful for
CC      detecting the presence of HCV in a sample, the primers are also useful
CC      for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines
CC      for immunising against HCV infection. The proteins may also be used to
CC      detect antibodies against HCV in serum, saliva, lymphocytes or other
CC      mononuclear cells. The antibodies may be used in the prevention of HCV
CC      infection
XX
SQ      Sequence 40 BP; 7 A; 9 C; 12 G; 12 T; 0 U; 0 Other;

Query Match      51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

PS      Example 1; Page 224; 340pp; English.
XX
CC      AAT16689-T16694 are a set of RT-PCR primers used for the identification
CC      of the cDNA sequence of the E1 (envelope-1) gene of 51 HCV isolates. The
CC      isolated sequences are useful for the prodn. of primers useful for
CC      detecting the presence of HCV in a sample, the primers are also useful
CC      for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines
CC      for immunising against HCV infection. The proteins may also be used to
CC      detect antibodies against HCV in serum, saliva, lymphocytes or other
CC      mononuclear cells. The antibodies may be used in the prevention of HCV
CC      infection
XX
SQ      Sequence 40 BP; 7 A; 9 C; 12 G; 12 T; 0 U; 0 Other;

Query Match      51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3  GGTACCCAGCAGCCGGCCTTGAA 27
Db      27  GGCACATCAATAGCAGCGCCTTGAA 3

RESULT 37
AAT16690/c
ID      AAT16690 standard; cDNA; 40 BP.
XX
AC      AAT16690;
XX
DT      02-OCT-1996 (first entry)
XX
DE      Hepatitis C virus E1 gene RT-PCR primer.
XX
KW      HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
KW      hepatitis; reverse transcriptase polymerase chain reaction; RT-PCR; ss.

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```

XX      Synthetic.
XX      OS
XX      WO9605315-A2.
XX      PN
XX      22-FEB-1996.
XX      PD
XX      15-AUG-1995; 95WO-US010398.
XX      PF
XX      15-AUG-1994; 94US-00290665.
XX      PR
XX      (USSH ) US SEC DEPT HEALTH.
XX      PA
XX      Bukh J, Miller RH, Purcell RH;
XX      PI
XX      WPI; 1996-139709/14.
XX      DR
XX      DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
XX      determine HCV genotype and as vaccines against HCV infection.
XX      PT
XX      Example 1; Page 224; 340pp; English.
XX      PS
XX      AAT16689-T16694 are a set of RT-PCR primers used for the identification
XX      of the cDNA sequence of the E1 (envelope-1) gene of 51 HCV isolates. The
XX      isolated sequences are useful for the prodn. of primers useful for
XX      detecting the presence of HCV in a sample, the primers are also useful
XX      for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines
XX      for immunising against HCV infection. The proteins may also be used to
XX      detect antibodies against HCV in serum, saliva, lymphocytes or other
XX      mononuclear cells. The antibodies may be used in the prevention of HCV
XX      infection
XX      CC
XX      SQ      Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;

Query Match      51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3  GGTACCCAGCAGCCGGCCTTGAA 27
Db      40  GGCACATCAATAGCAGCGCCTTGAA 16

RESULT 38
ADF08491/c
ID      ADF08491 standard; DNA; 40 BP.
XX
AC      ADF08491;
XX
DT      12-FEB-2004 (first entry)
XX
DE      Hepatitis C virus (HCV) genomic DNA PCR primer #4.
XX
KW      Hepatitis C virus; HCV; inducible promoter; HCV infection; PCR; primer;
KW      ss.
XX
OS      Hepatitis C virus.
XX
PN      US2003148267-A1.
XX      PD
XX      07-AUG-2003.
XX
PF      08-NOV-2002; 2002US-00292129.
XX
PR      09-NOV-2001; 2001US-0345405P.
XX
PA      (SCHM/) SCHMIDT E V.
PA      (CHUN/) CHUNG R T.
XX
PI      Schmidt EV, Chung RT;
XX
PW      WPI; 2003-897533/82.
XX

```

PT Identifying a compound that increases the mutation rate of hepatitis C
 PT virus (HCV) comprises detecting an increase in HCV quasi-species produced
 PT by the cell in the presence of the candidate compound.

XX Example 10; SEQ ID NO 8; 35pp; English.

XX
 CC The invention relates to a method for identifying a compound that
 CC increases the mutation rate of hepatitis C virus (HCV), comprising
 CC detecting an increase in HCV quasi-species produced by the cell in the
 CC presence of the candidate compound by e.g. sequencing HCV nucleic acid
 CC molecules isolated from the test cell. The method involves providing a
 CC test cell containing a nucleic acid molecule comprising a first
 CC nucleotide sequence consisting of an infectious hepatitis C viral genome
 CC or its DNA copy, a second nucleotide consisting of a ribozyme or its DNA
 CC copy and an inducible promoter operably linked to the first and second
 CC nucleotide sequences, where the ribozyme is configured to remove a 3'
 CC sequence unnecessary for replication of the hepatitis C viral genome from
 CC a transcript initiated by the promoter, inducing the inducible promoter,
 CC contacting the test cell with a candidate compound and detecting an
 CC increase in HCV quasi-species produced by the cell in the presence of the
 CC candidate compound compared to that in the absence of the compound, where
 CC an increase in the HCV quasi-species indicates that the compound increases
 CC the mutation rate of HCV. The method is useful in identifying compounds
 CC that may be used for treating HCV infection. This sequence represents a
 CC PCR primer used to amplify an HCV genomic DNA region, used in the method
 CC of the invention.

XX SQ Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 51.3%; Score 15,4; DB 10; Length 40;

Best Local Similarity 76.0%; Pred. No. 1.5e+04;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCCGCAGCGCCGCTTGAA 27

Db 40 GGCACATCAATAGCAGCGCTTGAA 16

RESULT 39

AAL31882

ID AAL31882 standard; DNA; 50 BP.

XX AC AAL31882;

XX DT 24-JAN-2002 (first entry)

XX DE Human SNP oligonucleotide #5090.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US035498.

XX PR 28-DEC-1999; 99US-0173419P.

XX PR 27-DEC-2000; 2000US-00173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.

XX Claim 1; Page 2851; 4143pp; English.

XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
 CC protein coupled receptors and thioesterases. The present sequence is one
 CC such oligonucleotide. The oligonucleotides and the peptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of the proteins listed above.
 CC Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms

XX SQ Sequence 50 BP; 11 A; 17 C; 16 G; 6 T; 0 U; 0 Other;

Query Match 51.3%; Score 15,4; DB 4; Length 50;

Best Local Similarity 76.0%; Pred. No. 1.5e+04;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCGGTACCCCGCAGCGCGCTTG 25

Db 22 GAGGCACAGCAGCGCGCGCTTG 46

RESULT 40

ADL96717

ID ADL96717 standard; DNA; 25 BP.

XX AC ADL96717;

XX DT 20-MAY-2004 (first entry)

XX DE M. paratuberculosis DNA PCR primer #57.

XX M. paratuberculosis; PCR; milk; faeces; blood;

KW M. paratuberculosis infection; John's disease; polypeptide purification;
 KW primer; ss; ds.

XX OS Mycobacterium avium subsp. paratuberculosis.

XX US2003175725-A1.

XX PD 18-SEP-2003.

XX PF 30-APR-2002; 2002US-00137113.

XX PR 06-MAR-2002; 2002US-0362396P.

XX PA (KAPU/) KAPUR V.

XX BANN/) BANNANTINE J P.

XX PI Kapur V, Bannantine JP;

XX WPI; 2003-863842/80.

XX New isolated nucleic acids and encoded polypeptides useful for detecting
 PT Mycobacterium paratuberculosis, and as antibacterial vaccines.

XX Example 16; SEQ ID NO 108; 38pp; English.

XX The invention relates to Mycobacterium avium subsp. paratuberculosis (M.
 CC paratuberculosis) nucleic acid molecules. A nucleic acid of the invention

CC combined with a second nucleic acid will generate an amplification
CC product from M. paratuberculosis but not from human, Pseudomonas
CC aeruginosa, Streptomyces viridochromogenes, mouse, cat or Xanthomonas
CC campestris. The nucleic acids and other sequences specific for
CC Mycobacterium paratuberculosis are used to detect M. paratuberculosis in
CC e.g. milk, faeces or blood. The polypeptides encoded by these sequences,
CC and antibodies directed against them, are also used to detect M.
CC paratuberculosis by immunoassay. The nucleic acids and the polypeptides
CC are also used as vaccines to prevent infection (John's disease) by M.
CC paratuberculosis. The antibodies are also useful for polypeptide
CC purification. This sequence represents a PCR primer used to amplify an M.
CC paratuberculosis nucleic acid of the invention.

XX
SQ Sequence 25 BP; 6 A; 10 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 11; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ACCCCAGCAGCCCGCCTTG 25
|||
Db 6 ACTCCAGCAGCCCGCCTCG 25

Search completed: November 18, 2005, 11:52:28
Job time : 207.578 secs

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Result No.	Score	Query			ID	Description
		Match	Length	DB		
C 1	15.8	52.7	50	1	AUI04878	AUI04878 AUI04878
C 2	15.4	51.3	43	9	CL211120	CL211120 W191D04 G
C 3	15	50.0	50	1	AUI02519	AUI02519 AUI02519
C 4	14.8	49.3	50	1	AUI05799	AUI05799 AUI05799
C 5	14.6	48.7	50	1	AUI02973	AUI02973 AUI02973
C 6	14.6	48.7	50	1	AUI02977	AUI02977 AUI02977
C 7	14.6	48.7	50	1	AUI02978	AUI02978 AUI02978
C 8	14.6	48.7	50	1	AUI04624	AUI04624 AUI04624
C 9	14.2	47.3	39	8	AZ810583	AZ810583 2M0076G19
C 10	14	46.7	38	8	AZ487251	AZ487251 1M0316A18
C 11	14	46.7	43	1	AS457556	AS457556 vk83e07.8
C 12	14	46.7	43	8	BH892666	BH892666 3526 1.22
C 13	14	46.7	43	9	CC940831	CC940831 01S0615-0
C 14	14	46.7	45	8	AZ503949	AZ503949 1M0343L24
C 15	13.8	46.0	36	8	BH909575	BH909575 SALX_0545
C 16	13.8	46.0	50	1	AUI03064	AUI03064 AUI03064
C 17	13.8	46.0	50	1	AUI03065	AUI03065 AUI03065
C 18	13.8	46.0	50	1	AUI03067	AUI03067 AUI03067
C 19	13.8	46.0	50	1	AUI04872	AUI04872 AUI04872
C 20	13.8	46.0	50	1	AUI04893	AUI04893 AUI04893
C 21	13.8	46.0	50	1	AUI04917	AUI04917 AUI04917
C 22	13.6	45.3	46	9	CL529006	CL529006 HIVE5A08.
C 23	13.6	45.3	46	9	AUI05070	AUI05070 AUI05070
C 24	13.4	44.7	28	1	AUI168501	AUI168501 ow90q01.s

```
RESULT 2
LOCUS      CL211120
DEFINITION W191D04 GGTc Gene Trap Library GV04C04 Mus musculus cDNA clone
ACCESSION  CL211120
VERSION    CL211120.2
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 43)
AUTHORS   Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,B.M., Vauti,F.,
          Arnold,H.H., Schnutten,F., Wurst,W., Von Melchner,H. and Ruiz,P.
TITLE     A large-scale, gene-driven mutagenesis approach for the functional
          analysis of the mouse genome
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
MEDLINE    22810117
PUBMED     12904583
COMMENT    On Jun 30, 2004 this sequence version replaced gi:40728021.
          Contact: GGTc
          German Genetrap Consortium (GGTC)
          Email: info@genetrap.de
          Roabsetago gene trap. Sequence tag generated by 5'RACE. Additional
          sequence information can be found at:
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          clone_id=W191D04' ES cell line harboring insertion mutation of
          target gene is available at:
          'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
          1' Inhouse Sequence Identifier: 11106
          Class: Gene Trap.
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            /sex="Male"
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            /cell_line="ES cells 129S2 (formerly 129/SvPas)"
            /clone_lib="GGTC Gene Trap Library GV04C04"
            /note="Vector: ROSAbetago"
ORIGIN
Query Match      51.3%; Score 15.4; DB 9; Length 43;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CGGTACCCAGCAGCCGCGCTTGA 26
    |||||
Db 17 GCGGACCCAGCGCCACCTTGA 42

RESULT 3
LOCUS      AU102519/c
DEFINITION AU102519 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION  CAS01336, mRNA sequence.
VERSION    AU102519.1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE    21270072
PUBMED     11375929
COMMENT    Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yezuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).
FEATURES   source
            Location/Qualifiers
            1..50
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="COLF5975"
            /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      49.3%; Score 14.8; DB 1; Length 50;
Best Local Similarity 88.9%; Pred. No. 2.5e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
JOURNAL      Mapping of mRNA start sites
MEDLINE      EMBO Rep. 2 (5), 388-393 (2001)
PUBMED      21270072
COMMENT      Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yezuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).
FEATURES   source
            Location/Qualifiers
            1..50
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CAS01336"
            /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      50.0%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 2.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 6 ACCCCAGCAGCCGCGCTTGAAG 28
    |||||
Db 45 ACCCGAGCAGCCCGCCAGCCAG 23

RESULT 4
LOCUS      AU105799/c
DEFINITION AU105799 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION  COLF5975, mRNA sequence.
VERSION    AU105799
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE    21270072
PUBMED     11375929
COMMENT    Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yezuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).
FEATURES   source
            Location/Qualifiers
            1..50
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="COLF5975"
            /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      49.3%; Score 14.8; DB 1; Length 50;
Best Local Similarity 88.9%; Pred. No. 2.5e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 2 CCGTACCCAGCAGCCCGGCCTTGAAGAA 30

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0316 row: A column: 18
 Seq primer: CACACAGGAACAGTCATGACC
 Class: plasmid ends
 High quality location stop: 38.

FEATURES

source

```

1..38
  Location/Qualifiers
    .organism="Mus musculus"
    .mol_type="genomic DNA"
    .strain="C57BL/6J"
    .db_xref="taxon:10090"
    .clone="UUGC1M0316A18"
    .sex="Male"
    /clone_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  
```

ORIGIN

```

Query Match      46.7%; Score 14; DB 8; Length 38;
Best Local Similarity 66.7%; Pred. No. 5e+05;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

```

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
    ||| ||| ||| ||| ||| ||| |||
Db 3 GCGCCACCACTGCACACCAACCCCTGAAAA 32

```

RESULT 11

AA547556/c

LOCUS

```

DEFINITION      AA547556 43 bp mRNA linear EST 05-AUG-1997
                  vk83e07.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
                  IMAGE:961284 5' similar to TR:G517115 G517115 MRNA ;, mRNA
                  sequence.

```

ACCESSION AA547556

VERSION AA547556.1

KEYWORDS GI:2308847

SOURCE Mus musculus (house mouse)

ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)

```

REFERENCE

AUTHORS

```

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,f., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

```

TITLE

The WashU-HHMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:550076

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 High quality sequence stop: 1.

FEATURES

source

```

1..43
  Location/Qualifiers
    .organism="Mus musculus"
    .mol_type="mRNA"
    .strain="C57BL/6J x DBA/2J F1"
    .db_xref="taxon:10090"
    .clone="IMAGE:961284"
    .tissue_type="embryo"
    .dev_stage="2-cell"
    /lab_host="DH10B"
    /clone_lib="Knowles Solter mouse 2 cell"
    /note="Organ: embryo; Vector: pBluescribe (modified);
    Site 1: MluI; Site 2: SalI; Cloned unidirectionally from
    mRNA prepared from 13,500 2-cell stage embryos. Primer:
    SalI (df): 5'-CGGTCGACGCGACCGGTTTTTTTTTTT-3'. cDNAs
    were cloned into the MluI/SalI sites of a modified
    pBluescribe vector using commercial linkers (NEB).
    Average insert size: 1.2 kb."
  
```

ORIGIN

```

Query Match      46.7%; Score 14; DB 1; Length 43;
Best Local Similarity 77.3%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy 4 GTACCCCGACGAGCCGCGCTTG 25
    ||| ||| ||| ||| ||| ||| |||
Db 43 GTGCCCTAGCTGCCCTTCCTTG 22

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RESULT 12

BH892666

LOCUS

```

DEFINITION      BH892666 43 bp DNA linear GSS 14-AUG-2002
                  3526_122_1 A12.2EL_x_1 3526 - RescueMu Grid K Zea mays genomic,
                  genomic survey sequence.

```

ACCESSION BH892666

VERSION BH892666.1

KEYWORDS GSS

SOURCE Zea mays

ORGANISM

```

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 43)

```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

```

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 3526_122_1 row: 28
 Class: transposon-tagged.
 Location/Qualifiers

FEATURES

source

1..43

/organism="Zea mays"

```

/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3526 - RescueMu Grid X"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmbd.iastate.edu' and follow the links for 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter 2000-2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 46.7%; Score 14; DB 8; Length 43;
Best Local Similarity 77.3%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 8 CCCAGCAGCCGCGCTTGAGAA 29
    ||||| ||||| ||||| |||||
Db 20 CCCAGAGCGCGAAATTGAGAA 41

RESULT 13
LOCUS CC940831 43 bp DNA linear GSS 18-AUG-2003
DEFINITION 01S0615-06B1-A12 UniformMu MutTAIL Library Zea mays genomic clone
ACCESSION CC940831
VERSION 01S0615-06B1-A12, genomic survey sequence.
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 43)
AUTHORS Latschew,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE Sequence tagged transposon insertions from the UniformMu maize
population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
01S0615-06, Primer set: B
Class: transposon insertion site.
Location/Qualifiers
1..43
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="01S0615-06B1-A12"
/notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

/mol_type="genomic DNA"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3526 - RescueMu Grid X"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmbd.iastate.edu' and follow the links for 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter 2000-2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 46.7%; Score 14; DB 9; Length 43;
Best Local Similarity 66.7%; Pred. No. 5e+05;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GCGTACCCAGCAGCGCGCTTGAGAA 30
    ||||| ||||| ||||| |||||
Db 9 GAGGACACTCAGCCCCCGCCACCTTGGAGCA 38

RESULT 14
LOCUS AZ503949 45 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0343L24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0343L24 R, genomic survey sequence.
ACCESSION AZ503949
VERSION AZ503949.1 GI:10685265
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 45)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0343 row: L column: 24
Seq primer: CACACAGGAAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
1..45
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0343L24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

ORIGIN

Query Match 46.7%; Score 14; DB 8; Length 45;
 Best Local Similarity 77.3%; Pred. No. 5e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGGTACCCAGCAGCCGCGCC 22
 |||||
 Db 9 GCGGTTCCCGCAGCGGCTGCC 30
 |||||

RESULT 15

BH909575/c

LOCUS

DEFINITION BH909575 36 bp DNA linear GSS 04-SEP-2002
 SALK_054521.15.30.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_054521.15.30.x, genomic
 survey sequence.

ACCESSION

BH909575

VERSION

BH909575.1

GI:22722508

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

1 (bases 1 to 36)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)

CONTACT: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 5' end of
 Atg53460.

Class: TDNA tagged.

Location/Qualifiers

1..36

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_054521.15.30.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 46.0%; Score 13.8; DB 8; Length 36;
 Best Local Similarity 72.0%; Pred. No. 5.9e+05;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GTACCCAGCAGCCGCGCTTGAG 28
 |||||

Db 31 GTACCCATAAGCCAGCATTGGAG 7
 |||||

RESULT 16

AU103064

LOCUS

DEFINITION AU103064 50 bp mRNA linear EST 28-JAN-2004
 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HRC00745, mRNA sequence.

ACCESSION

AU103064

VERSION

AU103064.1

GI:13552585

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE

21270072

PUBMED

11375929

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES

source

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HRC00745"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match

46.0%; Score 13.8; DB 1; Length 50;

Best Local Similarity

72.0%; Pred. No. 6.1e+05;

Matches

18; Conservative

0; Mismatches

7; Indels

0; Gaps

0;

QY

1 GCGGTACCCAGCAGCCGCGCTTG 25
 |||||

Db

26 GAGGTCCCCCGCGCGCGGCGCTG 50
 |||||

FEATURES

source

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HRC00745"

/clone_lib="Sugano Homo sapiens cDNA library"

HRC01582, mRNA sequence.

ACCESSION

AU103065

VERSION

AU103065.1

GI:13552586

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE

21270072

PUBMED

11375929

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

```

FEATURES
  source      Location/Qualifiers
              1..50
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="HRC01582"
              /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy  1  GCGGTACCCAGCAGCCGCGCTTG 25
Db   24 GAGGTCCCGCGCGCGCGGCGCTG 48

RESULT 18
LOCUS   AU101067
DEFINITION AU103067 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
VERSION   HRC09549, mRNA sequence.
ACCESSION AU103067.1 GI:13552588
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
          Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites

TITLE     Query Match      46.0%; Score 13.8; DB 1; Length 50;
          Best Local Similarity 72.0%; Pred. No. 6.1e+05;
          Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE   21270072
PUBMED    11375929
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yszuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES
  source      Location/Qualifiers
              1..50
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="HEP00153"
              /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy  1  GCGGTACCCAGCAGCCGCGCTTG 25
Db   40 GCGGTATCCAGCGCGGCTCGGCGCTG 16

RESULT 20
LOCUS   AU104893/c
DEFINITION AU104893 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
VERSION   HRC08321, mRNA sequence.
ACCESSION AU104893
VERSION   AU104893.1 GI:13554414
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
          Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites

TITLE     Query Match      46.0%; Score 13.8; DB 1; Length 50;
          Best Local Similarity 72.0%; Pred. No. 6.1e+05;
          Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE   21270072
PUBMED    11375929
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yszuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES
  source      Location/Qualifiers
              1..50
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="HRC09549"
              /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy  1  GCGGTACCCAGCAGCCGCGCTTG 25
Db   26 GAGGTCCCGCGCGCGGCGGCGCTG 50

RESULT 19
LOCUS   AU104872/c
DEFINITION AU104872 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
VERSION   HEP00153, mRNA sequence.
ACCESSION AU104872
VERSION   AU104872.1 GI:13554393

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC08321"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCGCGCTTG 25
    ||||| || ||||| |||||
Db 40 GCGGTATCCAGCGGCTCGGCGCTG 16

RESULT 21
AUI04917/c
LOCUS      AUI04917 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION ADSE00422, mRNA sequence.
ACCESSION  AUI04917
VERSION     AUI04917.1 GI:13554438
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADSE00422"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCGCGCTTG 25
    ||||| || ||||| |||||
Db 37 GCGGTATCCAGCGGCTCGGCGCTG 13

RESULT 22
CL529006
LOCUS      CL529006 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HIV55A08 fwd HIV-vector integration sites in human IMR90 primary
lung fibroblasts Homo sapiens genomic clone HIV55A08.fwd, genomic
survey sequence.
ACCESSION  CL529006
VERSION     CL529006.1 GI:47422217
KEYWORDS   GSS.

/organism="Homo sapiens (human)"
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
Mitchell,R.S., Beitzel, B.F., Schroder,A.R.W., Shinn,P., Chen,H.,
Berry, C.C., Ecker,J.R. and Bushman,F.
Retroviral DNA Integration: ASLV, HIV and MLV Show Distinct Target
Site Preferences
Unpublished (2004)
Contact: Frederic Bushman
Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1630
Fax: 858 554 0341
Email: bushman@salk.edu
Class: PCR with specific primers.
Location/Qualifiers
1..46
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="HIV55A08.fwd"
/clone_lib="HIV-vector integration sites in human IMR90
primary lung fibroblasts"
/notes="Human primary lung fibroblasts (IMR90) were
infected with an HIV-based vector. DNA was isolated and
cleaved with restriction enzymes; linkers were ligated
onto the cleaved DNA and DNAs were amplified using one
primer that bound to the linker DNA and one that bound to
the HIV cDNA. Junctions between integrated HIV proviruses
and cellular DNA were cloned and sequenced."

ORIGIN
Query Match      45.3%; Score 13.6; DB 9; Length 46;
Best Local Similarity 80.0%; Pred. No. 7.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 10 CAGCAGCCGCGCTTGAAGA 29
    ||||| ||||| |||||
Db 25 CAGCAGGCTGGCAATGAAGA 44

RESULT 23
AUI05070
LOCUS      AUI05070 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION KAT06679, mRNA sequence.
ACCESSION  AUI05070
VERSION     AUI05070.1 GI:13554591
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADSE00422"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCGCGCTTG 25
    ||||| || ||||| |||||
Db 37 GCGGTATCCAGCGGCTCGGCGCTG 13

RESULT 22
CL529006
LOCUS      CL529006 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HIV55A08 fwd HIV-vector integration sites in human IMR90 primary
lung fibroblasts Homo sapiens genomic clone HIV55A08.fwd, genomic
survey sequence.
ACCESSION  CL529006
VERSION     CL529006.1 GI:47422217
KEYWORDS   GSS.

```

```

149-156 (1997)
FEATURES
  source
    Location/Qualifiers
      1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="KAT06679"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
  Query Match      45.3%; Score 13.6; DB 1; Length 50;
  Best Local Similarity 67.9%; Pred. No. 7.3e+05;
  Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAG 28
    |||||
Db 23 GAGGTTTCCACCGCGCGCGCGGAG 50
    |||||

RESULT 24
AII168501/c
LOCUS
DEFINITION
  ow90g01.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA
  clone IMAGE:1654128 3' similar to TR:Q14521 Q14521 GIANT LARVAE
  HOMOLOGUE. ; mRNA sequence.
ACCESSION
  AII168501
VERSION
  AII168501.1 GI:3701671
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 28)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  This clone is available royalty-free through LNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Trace considered overall poor quality
  Insert Length: 890 Std Error: 0.00
  Seq primer: -40ml3 fwd. ET from Amersham
  High quality sequence stop: 1.
  Location/Qualifiers
    1..28
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:1654128"
      /sex="male"
      /dev_stages="20 week-post conception fetus"
      /lab_host="DH10B (ampicillin resistant)"
      /clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
      /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
      with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
      This is a subcloned version of the original Soares fetal
      liver spleen INFLS library. 1st strand cDNA was primed
      with a Pac I - oligo(dT) primer [5',
      AACTGGAAGAATTATTAAGATCTTTTCTTTTCTTTT 3'],
      double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Pac I and cloned into the Pac I
      and Eco RI sites of the modified pT7T3 vector. Library
      went through one round of normalization. Library
      constructed by Bento Soares and M.Patima Bonaldo."
ORIGIN
  Query Match      44.7%; Score 13.4; DB 1; Length 28;
  Best Local Similarity 93.3%; Pred. No. 8.4e+05;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 11 AGCAGCCCGCGCTTG 25
    |||||
Db 24 AGCAGCCCGCGCTTG 10
    |||||

RESULT 25
BG717269/c
LOCUS
DEFINITION
  60269583F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4821885 5',
  mRNA sequence.
ACCESSION
  BG717269
VERSION
  BG717269.1 GI:13996456
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 36)
  NIH-MGC http://mgs.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
  cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
  Toshiyuki and Piero Carninci (RIKEN)
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LNL at:
  http://image.llnl.gov
  Plate: LUAM10729 row: e column: 22
  High quality sequence stop: 36.
  Location/Qualifiers
    1..36
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:4821885"
      /lab_host="DH10B"
      /clone_lib="NIH_MGC_97"
      /note="Organ: testis; Vector: pBluescriptR (modified
      pBluescript KS+); Site 1: BamHI, Site 2: SalI-XhoI
      (GTCGAG); Oligo-dT primed using primer
      5'-TTTTTTTTTTTNN-3', size-selected for average
      insert size 2.2 kb and normalized to R0T 5. This is a
      primary library enriched for full-length clones and
      constructed using the Cap-trapper method (Carninci, in
      preparation). Library constructed by M. Brownstein
      (NIH/NHGRI, National Institutes of Health). Note: this is
      a NIH_MGC Library."
ORIGIN
  Query Match      44.7%; Score 13.4; DB 4; Length 36;
  Best Local Similarity 73.9%; Pred. No. 8.5e+05;
  Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GCGGTACCCAGCAGCCGCGCTT 23
    |||||
Db 29 GCGGACCCCAAGCGCGCGGCT 7
    |||||

RESULT 26
H99826/c
LOCUS
DEFINITION
  Yx28d12.s1 Soares melanocyte 2NdhM Homo sapiens cDNA clone
  IMAGE:263063 3' similar to SP:BI3_MOUSE P28662 BRAIN PROTEIN I3 ;,
  mRNA sequence.
ACCESSION
  H99826
VERSION
  H99826.1 GI:1124494
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 43)
Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE
JOURNAL
COMMENT

The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNLN
This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 732 Std Error: 0.00
Seq primer: m13 -40 forward
High quality sequence stop: 1.

FEATURES
source

1..43
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3872705"
/db_xref="taxon:9606"
/clone="IMAGE:263063"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NbHM"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5' TGTTACCAATCTGAGTGGAGCGCGCCAGTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 44.7%; Score 13.4; DB 7; Length 43;
Best Local Similarity 73.9%; Pred. No. 8.6e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CCCAGCAGCCCGCGCTTGAAGA 29
| ||||| ||| |||||
Db 43 CTCAGCACCACCCACCTGCAGA 21

RESULT 27
CC022113/c
LOCUS
DEFINITION
3591.1.28.1.C03.2ELY_1.3591 - RescueMu Grid P Zea mays genomic,
genomic survey sequence.

ACCESSION
CC022113
VERSION
CC022113.1 GI:29436186
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 47)
REFERENCE
AUTHORS
Walbot, V.

TITLE
JOURNAL
COMMENT

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3591.1.28.1 row: 15
Class: transposon-tagged.

FEATURES
Location/Qualifiers
1..47
source
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 44.7%; Score 13.4; DB 8; Length 47;
Best Local Similarity 73.9%; Pred. No. 8.7e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGTACCCCGCAGCCCGCCTT 24
| ||||| ||| |||||
Db 44 CCGTGCCTCCCGCGCGCAGCCTT 22

RESULT 28
AJ590023
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
562D09, genomic survey sequence.

ACCESSION
AJ590023
VERSION
AJ590023.1 GI:37939647
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1
REFERENCE
AUTHORS
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G.,
Lepiniec, L., Caboche, M., and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

EMBO Rep. 3 (12), 1152-1157 (2002)
2363535
12446565
2 (bases 1 to 47)
Balzerque, S.
Direct Submission
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES
 source
 1..47
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassillewskija"
 /db_xref="taxon:3702"
 /clone="562D09"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 misc_feature
 1..47
 /note="T-DNA flanking sequence
 left border"

ORIGIN

Query Match 44.7%; Score 13.4; DB 9; Length 47;
 Best Local Similarity 70.8%; Pred. No. 8.7e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GTACCCAGCAGCGCGCTTGAA 27
 ||||| ||||| ||||| ||||| |||||
 Db 23 GTACCTCGCGCGGCATTA 46

RESULT 29
 AZ868876/c
 LOCUS 29 bp DNA linear GSS 21-FEB-2001
 DEFINITION 2M0180F17R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC2M0180F17 R, genomic survey sequence.

ACCESSION AZ868876
 VERSION AZ868876.1 GI:13072628
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 29)

REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0180 row: F column: 17

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

FEATURES

source

1..29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC2M0180F17"

/sex="Male"
 /ldb_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into cells chemically-competent E. coli XL10-Gold (Stratagene) and selected for ampicillin resistance."

ORIGIN

Query Match 44.0%; Score 13.2; DB 8; Length 29;
 Best Local Similarity 83.3%; Pred. No. 1e+06; 3; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 AGCAGCCCGCGCTTGAA 28
 ||||| ||||| ||||| ||||| |||||
 Db 25 AGCAGCGCGCGCTGGA 8

RESULT 30
 W05202

LOCUS

DEFINITION 37 bp mRNA linear EST 23-APR-1996
 2442R01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:295249 5' similar to SW:GSGS_BOVIN P30670 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-5 SUBUNIT. [1] ; mRNA sequence.

ACCESSION W05202

VERSION W05202.1 GI:1277934

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 37)

REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL

COMMENT Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.REGA+ET

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1..37
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:1240170"
 /db_xref="taxon:9606"
 /clone="IMAGE:295249"
 /sex="male"

/dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFLS"
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
 1st strand cDNA was primed with a Pac I - oligo(dT) primer
 [5' ACTCGAGAAATTAATTAAGATCTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Donaldo."

ORIGIN

Query Match 44.0%; Score 13.2; DB 7; Length 37;
 Best Local Similarity 69.2%; Pred. No. 1e+06;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 TACCCAGAGCCCGCGCTTGAAGAA 30
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2 TCCTCCAGCGCGCGCTATGAAGA 27

RESULT 31

CG774406
 LOCUS 1123018G05.2EL_Y1 1123 - RescueMu Grid L Zea mays genomic, GSS 29-OCT-2003
 DEFINITION survey sequence.

ACCESSION CG774406
 VERSION CG774406.1 GI:38030394
 KEYWORDS GSS.

SOURCE

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 40)

REFERENCE

AUTHORS Walbot.V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.

Plate: 1123018 row: 12

Class: transposon-tagged.

FEATURES

source

1..40
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1123 - RescueMu Grid L"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI, Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 44.0%; Score 13.2; DB 9; Length 40;
 Best Local Similarity 69.2%; Pred. No. 1e+06;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCGGTACCCAGCAGCCCGGCTTGA 26
 | | | | | | | | | | | | | | | | | | | | | |
 Db 4 GTGGTCTCCAGCAGCAGGATCTGGA 29

RESULT 32

BZ586362

LOCUS

BZ586362 3590.1.16.1.D07.2EL_Y 1 3590 - RescueMu Grid M Zea mays genomic, GSS 17-DEC-2002

DEFINITION genomic survey sequence.

ACCESSION BZ586362

VERSION BZ586362.1 GI:27221423

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 41)

REFERENCE Walbot.V.

AUTHORS Maize genomic sequences found using engineered RescueMu transposon
 TITLE Unpublished (2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.

Plate: 3590.1.16.1 column: 4

Class: transposon-tagged.

FEATURES

source

1..41
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="3590 - RescueMu Grid M"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI, Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid M was grown at University of Arizona in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 44.0%; Score 13.2; DB 8; Length 41;
 Best Local Similarity 69.2%; Pred. No. 1e+06;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCGGTACCCAGCAGCCCGGCTTGA 26
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5 GTGGTCTCCAGCAGCAGGATCTGGA 30

RESULT 33

```

CC182796/c
LOCUS      CC182796              45 bp   mRNA   linear   GSS 08-MAY-2003
DEFINITION XG533 BayGenomics Gene Trap Library pGTLxf Mus musculus cDNA, mRNA
sequence.
ACCESSION  CC182796
VERSION     CC182796.1   GI:30426696
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 45)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL     BayGenomics.
COMMENT     http://baygenomics.ucsf.edu/
            Unpublished (2001)
            Contact: BayGenomics
            Bay Area Functional Genomics Consortium (BayGenomics)
            Email: info@baygenomics.ucsf.edu
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from BayGenomics. Annotation
            information available from
            http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
            CEIL.LIN&KEY=XG533
            Class: Gene Trap.
            Location/Qualifiers
            1..45
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="129 ola"
            /db_xref="taxon:10090"
            /sex="Male"
            /cell_type="Embryonic stem cell"
            /clone_lib="BayGenomics Gene Trap Library pGTLxf"
            /note="Vector: pGTLxf"

ORIGIN
Query Match      44.0%; Score 13.2; DB 8; Length 45;
Best Local Similarity 83.3%; Pred. No. 1e+06;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  7  CCCGACGACCGCGCCTT 24
    ||| ||||| ||||| |||||
Db   45  CCACGACGACCGACCTT 28

RESULT 34
LOCUS      AI019594/c              46 bp   mRNA   linear   EST 16-JUN-1998
DEFINITION ua91a06.r1 Soares mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:1364818 5' similar to SW:BBP_HUMAN Q00341 HIGH DENSITY
LIPOPROTEIN BINDING PROTEIN ;, mRNA sequence.
ACCESSION  AI019594
VERSION     AI019594.1   GI:3233930
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 46)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
COMMENT     Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
            The WashU-HMI Mouse EST Project
            Unpublished (1996)
            Contact: Marra M/Mouse EST Project
            WashU-HMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810

```

```

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:898038
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..46
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1364818"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary_gland_NbMMG"
/note="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGCAATGTTTGTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

ORIGIN
Query Match      44.0%; Score 13.2; DB 1; Length 46;
Best Local Similarity 83.3%; Pred. No. 1e+06;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  3  GGTACCCCGACGACCGCG 20
    ||| ||||| ||||| |||||
Db   19  GGCACCCCGCGACGCGCG 2

RESULT 35
LOCUS      AL585781/c              46 bp   mRNA   linear   EST 28-FEB-2001
DEFINITION AL585781 BP Chicken Embryo Library Gallus gallus cDNA clone
ROS029H11, mRNA sequence.
ACCESSION  AL585781
VERSION     AL585781.1   GI:13164514
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
ORGANISM    Gallus gallus
REFERENCE   1 (bases 1 to 46)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
JOURNAL     Phasianinae; Gallus.
COMMENT     Murray,F.
            BP Chicken Embryo Library
            Unpublished (2001)
            Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            Seq primer: T3.
            Location/Qualifiers
            1..46
            /organism="Gallus gallus"
            /mol_type="mRNA"
            /db_xref="taxon:9031"
            /clone="ROS029H11"

```

/tissue type="Embryo"
 /dev stage="5 days old"
 /lab host="DH10B"
 /clone lib="BP Chicken Embryo Library"
 /note="Vector: pBJUESCRIPT SK; Site 1: NotI; Site 2: SalI;
 Cloned unidirectionally. Primer: Oligo dt. 5' adaptor
 sequence: 5' TCAGCTCGAG 3'; 3' adaptor sequence: 5'
 GCGCGCGCTTTTTTTTTTTTTTTT 3"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 46;
 Best Local Similarity 69.2%; Pred. No. 1e+06;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4 GTACCCAGCAGCGCGCTTGAAGA 29

Db 46 GAACCCACCTGCTGTCATGAAGA 21

RESULT 36

AA238784/c

LOCUS AA238784 46 bp mRNA linear EST 03-MAR-1997
 DEFINITION wx2zh02.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692883 5'
 similar to SW:NEB4_HUMAN P46934 NEDD-4 RELATED PROTEIN ; mRNA
 sequence.

ACCESSION AA238784

VERSION AA238784.1 GI:1862822

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 46)

REFERENCE

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE

The WashU-HMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:426443

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1..46
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:692883"
 /tissue type="Liver"
 /lab host="DH10B"
 /clone lib="Soares mouse NML"
 /note="Vector: pTT3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTTCACCAATCTGAGTGGGAGCGCGGATCTTTTTTTTTTTT 3'];
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pTT73 vector. Library
 constructed and normalized by Bento Soares and M.Fatima

Bonaldo."

ORIGIN

Query Match 44.0%; Score 13.2; DB 7; Length 46;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Query Match 44.0%; Score 13.2; DB 1; Length 46;
 Best Local Similarity 69.2%; Pred. No. 1e+06;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 TACCCAGCAGCGCGCTTGAAGAA 30

Db 36 TCCATCAGGAGCAGCGCTTCATAA 11

RESULT 37

H38217/c

LOCUS

H38217 46 bp mRNA linear EST 16-AUG-1995
 DEFINITION YP58c07.sl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
 IMAGE:191628 3' similar to SP:KGUA_PIG P31006 GUANYLATE KINASE ;
 mRNA sequence.

ACCESSION H38217

VERSION H38217.1 GI:907716

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 46)

REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1641

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: Promega -21ml3

High quality sequence stop: 1.

Location/Qualifiers

1..46

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3761417"

/db_xref="taxon:9606"

/clone="IMAGE:191628"

/sex="male"

/dev stage="20 week-post conception fetus"

/lab host="DH10B (ampicillin resistant)"

/clone lib="Soares fetal liver spleen lNFLS"

/notes="Organ: Liver and Spleen; Vector: pTT3D (Pharmacia)

with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer

[5' AACTGGAGAATTAATAAGATCTTTTTTTTTTTT 3']

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pTT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 44.0%; Score 13.2; DB 7; Length 46;

Best Local Similarity 75.0%; Pred. No. 1e+06;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GTACCCAGCAGCCGGCCT 23
Db 46 GGAGCCAGNANCCGGCCT 27

RESULT 38
BX629147/C
LOCUS BX629147.1 linear mRNA EST 08-AUG-2003
DEFINITION BX629147 NAP1 Anopheles gambiae cDNA clone ANGNP2364C01T7, mRNA sequence.
ACCESSION BX629147
VERSION BX629147.1 GI:33558282
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anophelinae.

REFERENCE 1 (bases 1 to 48)
AUTHORS Lobo, N.L., Gardner, M., Romans, P. and Collins, F.H.
TITLE Anopheles gambiae EST, Center for Tropical Disease Research and Training
JOURNAL Unpublished (2003)
COMMENT Contact: Frank H. Collins
Center for Tropical Disease Research and Training
University of Notre Dame
Notre Dame, IN 46556, USA
Tel: 574-631-9245
Fax: 574-631-3996
Email: frank.h.collins.75@nd.edu.

FEATURES
source
1..48
/organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
/clone="ANGNP2364C01T7"
/lab_host="E. coli DH10B"
/clone_lib="NAP1"
/note="Vector: pT7T3D-Pac (Pharmacia); Site 1: NotI; Site 2: EcoRI; ESTs sequenced from the T7 priming site that reads from the 5' end of cDNA. The NAP1 is a directionally cloned and normalized, oligo-T primed cDNA library constructed from a mixture of Anopheles gambiae developmental stages according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN
Query Match 44.0%; Score 13.2; DB 5; Length 48;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGGCCTTGA 27
Db 40 GCGGTTCCCAGCGCTGTCCTTGA 14

RESULT 39
BH902004
LOCUS BH902004.1 linear DNA GSS 04-SEP-2002
DEFINITION SALK_091114.48.90.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_091114.48.90.x, genomic survey sequence.
ACCESSION BH902004
VERSION BH902004.1 GI:22712885
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.

REFERENCE 1 (bases 1 to 48)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..48
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_091114.48.90.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 44.0%; Score 13.2; DB 8; Length 48;
Best Local Similarity 69.2%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 TACCCAGCAGCCGGCCTTGAAGAA 30
Db 10 TAATCAAGCATTCAGCCCTTAAGAA 35

RESULT 40
RA739463
LOCUS RA739463 linear mRNA EST 14-JAN-1998
DEFINITION vv54a11.r1 Soares_thymus_2NBMT Mus musculus cDNA clone IMAGE:1226204 5' similar to SW:GBG5_BOVIN P30670 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-5 SUBUNIT. ;, mRNA sequence.

ACCESSION RA739463
VERSION RA739463.1 GI:2775649
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 49)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:651796

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers

1..49
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1226204"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
/clone_lib="Soares_thymus_2NbMT"
/note="Vector: pVT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pVT3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 49;
Best Local Similarity 59.2%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 3 GGTACCCAGAGCGCGCTTGAG 28
||| ||||| ||| |||
Db 22 GGTGTCCAGAGCTCCGCGTGAG 47

Search completed: November 18, 2005, 21:12:48
Job time : 1436.98 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 58.289 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-6
Perfect score: 30
Sequence: 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1	US-07-989-160-6
2	18.2	60.7	26	4	US-09-268-311-9
3	18.2	60.7	26	4	US-09-154-219-9
4	16.6	55.3	48	1	US-08-592-411-11
5	16.6	55.3	48	1	US-08-591-501-11
6	16.4	54.7	30	1	US-08-244-010-1
7	16.2	54.0	28	4	US-09-268-311-11
8	16.2	54.0	28	4	US-09-268-311-13
9	16.2	54.0	28	4	US-09-154-219-11
10	16.2	54.0	28	4	US-09-154-219-13
11	16.2	54.0	33	1	US-07-640-476-20
12	16	53.3	25	4	US-09-396-196G-25759
13	15.8	52.7	25	4	US-09-396-196G-109792
14	15.6	52.0	25	4	US-09-396-196G-125627
15	15.6	52.0	32	2	US-08-403-852D-43
16	15.6	52.0	32	3	US-08-510-646B-45
17	15.6	52.0	32	3	US-09-231-818-43
18	15.6	52.0	32	4	US-09-635-359B-43
19	15.6	52.0	43	1	US-08-464-136-43
20	15.6	52.0	43	1	US-08-440-787A-42
21	15.6	52.0	43	2	US-08-349-131-43
22	15.6	52.0	43	3	US-08-470-297A-43
23	15.6	52.0	43	3	US-08-367-685-42
24	15.6	52.0	43	5	PCT-US91-07149-42
25	15.6	52.0	43	5	PCT-US91-07149-43
26	15.4	51.3	25	4	US-09-396-196G-25761
27	15.4	51.3	40	1	US-08-086-428B-104

C 28	15.4	51.3	40	1	US-08-086-428B-106	Sequence 106, App
C 29	15.4	51.3	40	2	US-08-468-570-104	Sequence 104, App
C 30	15.4	51.3	40	2	US-08-468-570-106	Sequence 106, App
C 31	15.4	51.3	40	2	US-08-290-665A-208	Sequence 208, App
C 32	15.4	51.3	40	2	US-08-290-665A-210	Sequence 210, App
C 33	15.4	51.3	40	4	US-08-466-601A-104	Sequence 104, App
C 34	15.4	51.3	40	4	US-08-466-601A-106	Sequence 106, App
C 35	15.4	51.3	40	5	PCT-US95-10398-208	Sequence 208, App
C 36	15.4	51.3	40	5	PCT-US95-10398-210	Sequence 210, App
C 37	15.2	50.7	25	4	US-09-396-196G-91572	Sequence 91572, A
C 38	15.2	50.7	25	4	US-09-396-196G-91573	Sequence 91573, A
C 39	14.8	49.3	32	4	US-09-673-198-23	Sequence 23, Appl
C 40	14.6	48.7	27	3	US-08-998-099-161	Sequence 161, App
C 41	14.6	48.7	44	1	US-08-471-791-37	Sequence 37, Appl
C 42	14.6	48.7	44	5	PCT-US91-01746-37	Sequence 37, Appl
C 43	14.6	48.7	48	1	US-08-471-791-35	Sequence 35, Appl
C 44	14.6	48.7	48	5	PCT-US91-01746-35	Sequence 35, Appl
C 45	14.4	48.0	29	4	US-09-304-232-405	Sequence 405, App

ALIGNMENTS

RESULT 1
US-07-989-160-6
; Sequence 6, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-989-160-6

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

RESULT 2

US-09-268-311-9
; Sequence 9, Application US/09268311
; Patent No. 6482923
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF3981
; CURRENT APPLICATION NUMBER: US/09/268,311
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 60/059,133
; EARLIER FILING DATE: 1997-09-17
; EARLIER APPLICATION NUMBER: 09/154,219
; EARLIER FILING DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-268-311-9

Query Match 60.7%; Score 18.2; DB 4; Length 26;
Best Local Similarity 87.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTT 23
Db 2 GCGGTACCCAGCAGCTCCCGGCTT 24

RESULT 3

US-09-154-219-9
; Sequence 9, Application US/09154219
; Patent No. 6635443
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398
; CURRENT APPLICATION NUMBER: US/09/154,219
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/059,133
; EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-219-9

Query Match 60.7%; Score 18.2; DB 4; Length 26;
Best Local Similarity 87.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTT 23
Db 2 GCGGTACCCAGCAGCTCCCGGCTT 24

RESULT 4

US-08-592-411-11
; Sequence 11, Application US/08592411
; Patent No. 5726032
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for the Efficient Production of
; TITLE OF INVENTION: 7-ADCA via 2-(Carboxyethylthio)acetyl-7-ADCA and

; TITLE OF INVENTION: 3-(Carboxymethylthio)propionyl-7-ADCA
; NUMBER OF SEQUENCES: 17
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/08/592,411
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: oligonucleotide 11
; US-08-592-411-11

Query Match 55.3%; Score 16.6; DB 1; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 ACCCCAGCAGCCGCGCTTGAAG 28
Db 18 ACCGCGCGCGCGCGCTTGAAG 40

RESULT 5

US-08-591-501-11
; Sequence 11, Application US/08591501
; Patent No. 5795733
; GENERAL INFORMATION:
; APPLICANT: BOVENBERG, ROELOF ARY LANS
; APPLICANT: KOEKMAN, BERTUS PIETER
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: VAN DER LAAN, JAN METSKE
; APPLICANT: VERWEIJ, JAN
; APPLICANT: DE VROOM, ERIK
; TITLE OF INVENTION: PROCESS FOR THE EFFICIENT PRODUCTION OF
; TITLE OF INVENTION: 7-ADCA VIA 3-(CARBOXYETHYLTHIO) PROPIONYL-7-ADCA
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,501
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 24615-20065.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs


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; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-219-11

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Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCT 23
Db 6 GGTACCCCGAGCGCTCCCGGCTT 26

RESULT 10
US-09-154-219-13
; Sequence 13, Application US/09154219
; Patent No. 6635443
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanguo
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398
; CURRENT APPLICATION NUMBER: US/09/154,219
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/059,133
; EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-219-13

Query Match          54.0%; Score 16.2; DB 4; Length 28;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCT 23
Db 6 GGTACCCCGAGCGCTCCCGGCTT 26

RESULT 11
US-07-640-476-20/c
; Sequence 20, Application US/07640476
; Patent No. 5376536
; GENERAL INFORMATION:
; APPLICANT: QUAX, WILHELMUS
; APPLICANT: LUITEN, RUDOLF G.M.
; APPLICANT: SCHUURHUIZEN, PAUL W.
; APPLICANT: MRABET, NADIR
; TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES AND
; TITLE OF INVENTION: THEIR USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/640,476
; FILING DATE: 19910110
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kate H. Murashige
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20009.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-7250
; TELEFAX: (415) 327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
US-07-640-476-20

Query Match          54.0%; Score 16.2; DB 1; Length 33;
Best Local Similarity 72.4%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGTACCCCGAGCGCCGCGCTTGAAGAA 30
Db 32 CGGACTCCATCATCTCGACCTTCAGAA 4

RESULT 12
US-09-396-196G-25759/c
; Sequence 25759, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25759
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-25759

Query Match          53.3%; Score 16; DB 4; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GTACCCCGAGCGCCGCGCTTGA 27
Db 25 GTAGCCCGAGCATGCCGAGCTTGA 2

RESULT 13
US-09-396-196G-109792/c
; Sequence 109792, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
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;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 109792
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: mus musculus
US-09-396-196G-109792

Query Match 52.7%; Score 15.8; DB 4; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CAGCAGCCCGGCTTGAAG 28
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DB 20 CAGCAGCTGGCCTTGAAG 2

RESULT 14
US-09-396-196G-125627
;; Sequence 125627, Application US/09396196G
;; Patent No. 6821724
;; GENERAL INFORMATION:
;; APPLICANT: Michael Mittmann
;; APPLICANT: David Mack
;; APPLICANT: David Lockhart
;; APPLICANT: Affymetrix, Inc.
;; TITLE OF INVENTION: Methods of Genetic Analysis
;; FILE REFERENCE: 3101.1
;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 125627
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: mus musculus
US-09-396-196G-125627

Query Match 52.0%; Score 15.6; DB 4; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CCCAGCAGCCCGGCTTGAAGA 29
||||| ||||| ||||| ||||| |||||
DB 3 CCCAGCAGCTCAGCCTGGCAGA 24

RESULT 15
US-08-403-852D-43/c
;; Sequence 43, Application US/08403852D
;; Patent No. 5891695
;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanche, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy-Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
;; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSES: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington

;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,852D
;; FILING DATE: 10-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-403-852D-43

Query Match 52.0%; Score 15.6; DB 2; Length 32;
Best Local Similarity 62.5%; Pred. No. 2.9e+03;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGGTACCCAGCAGCCGGCCTTG 25
||||| ||||| ||||| ||||| |||||
DB 32 CGGTACCCAGSAGSGGGGCTTS 9

RESULT 16
US-08-510-646B-45/c
;; Sequence 45, Application US/08510646B
;; Patent No. 6077699
;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanche, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy-Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
;; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSES: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/510,646B

;
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-510-646B-45

Query Match 52.0%; Score 15.6; DB 3; Length 32;
Best Local Similarity 62.5%; Pred. No. 2.9e+03;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCGGCGCTTG 25
Db 32 CGGTACCCAGSAGSGGGCTTS 9

RESULT 17
US-09-231-818-43/c
; Sequence 43, Application US/09231818
; Patent No. 6171846

;
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; Biosynthesis Of Streptogramins, Nucleotide Sequences
; Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,818
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,852
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-231-818-43

Query Match 52.0%; Score 15.6; DB 3; Length 32;
Best Local Similarity 62.5%; Pred. No. 2.9e+03;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCGGCGCTTG 25
Db 32 CGGTACCCAGSAGSGGGCTTS 9

RESULT 18
US-09-635-359B-43/c
; Sequence 43, Application US/09635359B
; Patent No. 6670157
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; Biosynthesis Of Streptogramins, Nucleotide Sequences
; Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/635,359B
; FILING DATE: 09-AUG-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/231,818
; FILING DATE: 15-JAN-1999
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-03000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-635-359B-43

Query Match 52.0%; Score 15.6; DB 4; Length 32;
Best Local Similarity 62.5%; Pred. No. 2.9e+03;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGGTACCCAGCAGCCGCGCTTG 25
DB 32 CGGTACCCAGSAGSGGCTTS 9

RESULT 19
US-08-464-136-43/c
; Sequence 43, Application US/08464136
; Patent No. 5698426
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 SO. FLOWER STREET, SUITE 200
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,136
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-136-43

Query Match 52.0%; Score 15.6; DB 1; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGGTACCCAGCAGCCGCGCTTGAGAA 30
DB 42 CGGTACCCAGCTTAATCGCCTTGAGAA 13

RESULT 20
US-08-440-787A-42/c
; Sequence 42, Application US/08440787A

; Patent No. 5770434
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; NUMBER OF SEQUENCES: 174
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,787A
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-440-787A-42

Query Match 52.0%; Score 15.6; DB 1; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGGTACCCAGCAGCCGCGCTTGAGAA 30
DB 42 CGGTACCCAGCTTAATCGCCTTGAGAA 13

RESULT 21
US-08-349-131-43/c
; Sequence 43, Application US/08349131
; Patent No. 5871974
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 SO. FLOWER STREET, SUITE 200
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,131

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;
; FILING DATE: 435
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,648
; FILING DATE:
; APPLICATION NUMBER: US/07/767,136
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-349-131-43

Query Match 52.0%; Score 15.6; DB 2; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAAA 13

RESULT 22
US-08-470-297A-43/c
; Sequence 43, Application US/08470297A
; Patent No. 6027933
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; HETEROOMIC RECEPTORS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES LLP
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,297A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-470-297A-43

Query Match 52.0%; Score 15.6; DB 3; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
```

```
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAAA 13

RESULT 23
US-08-367-685-42/c
; Sequence 42, Application US/08367685
; Patent No. 6258530
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; RANDOMIZED PEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,685
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,494
; FILING DATE:
; APPLICATION NUMBER: US/07/767,436
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 9072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-367-685-42

Query Match 52.0%; Score 15.6; DB 3; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAAA 13

RESULT 24
PCT-US91-07141-42/c
; Sequence 42, Application PC/TUS9107141
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; RANDOMIZED PEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
```

STATE: California
COUNTRY: United States
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07141
FILING DATE: 19910927
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 9072
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US91-07141-42

Query Match 52.0%; Score 15.6; DB 5; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03; Mismatches 0; Indels 9; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 9; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
||| ||||| ||| ||||| |||||
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAGAA 13

RESULT 25
PCT-US91-07149-43/c
Sequence 43, Application PC/TUS9107149
GENERAL INFORMATION:
APPLICANT: HUSE, WILLIAM D.
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
TITLE OF INVENTION: HETEROMERIC RECEPTORS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 SO. FLOWER STREET, SUITE 200
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07149
FILING DATE: 19910927
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8882
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear

Query Match 52.0%; Score 15.6; DB 5; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03; Mismatches 0; Indels 9; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 9; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
||| ||||| ||| ||||| |||||
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAGAA 13

RESULT 26
PCT-US91-07149-43
Sequence 43, Application US/09396196G
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25761
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-25761

Query Match 51.3%; Score 15.4; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.4e+03; Mismatches 6; Indels 6; Gaps 0;
Matches 19; Conservative 0; Mismatches 6; Indels 6; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGTG 25
||| ||||| ||||| ||||| |||||
Db 25 GCGGTACCCAGCATGCCGAGCTTG 1

RESULT 27
US-08-086-428B-104/c
Sequence 104, Application US/08086428B
Patent No. 5514539
GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

STATE: California
COUNTRY: United States
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07141
FILING DATE: 19910927
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 9072
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US91-07141-42

Query Match 52.0%; Score 15.6; DB 5; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03; Mismatches 0; Indels 9; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 9; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
||| ||||| ||| ||||| |||||
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAGAA 13

RESULT 26
PCT-US91-07149-43
Sequence 25761, Application US/09396196G
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25761
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-25761

Query Match 51.3%; Score 15.4; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.4e+03; Mismatches 6; Indels 6; Gaps 0;
Matches 19; Conservative 0; Mismatches 6; Indels 6; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGTG 25
||| ||||| ||||| ||||| |||||
Db 25 GCGGTACCCAGCATGCCGAGCTTG 1

RESULT 27
US-08-086-428B-104/c
Sequence 104, Application US/08086428B
Patent No. 5514539
GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-086-428B-104

Query Match 51.3%; Score 15.4; DB 1; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCGAGCGCCGGCTTGAA 27
Db 40 GGCACATCAATAGCAGCGCTTGAA 16

RESULT 28

US-08-086-428B-106/c
Sequence 106, Application US/08086428B
Patent No. 5514539

GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,428B
FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-086-428B-106

Query Match 51.3%; Score 15.4; DB 1; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCGAGCGCCGGCTTGAA 27
Db 27 GGCACATCAATAGCAGCGCTTGAA 3

RESULT 29

US-08-468-570-104/c
Sequence 104, Application US/08468570
Patent No. 5871962

GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-570-104

Query Match 51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCGAGCGCCGGCTTGAA 27
Db 40 GGCACATCAATAGCAGCGCTTGAA 16

RESULT 30

US-08-468-570-106/c
Sequence 106, Application US/08468570
Patent No. 5871962

GENERAL INFORMATION:
APPLICANT: BURKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE

Query Match 51.3%; Score 15.4; DB 2; Length 40;
 Best Local Similarity 76.0%; Pred. No. 3.6e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCGCGCTTGAA 27
 |||||
 Db 27 GGCACATCAATAGCAGCGCTTGAA 3

RESULT 33
 US-08-466-601A-104/c
 ; Sequence 104, Application US/08466601A
 ; Patent No. 6572864
 ; GENERAL INFORMATION:
 ; APPLICANT: BUKH, J., MILLER, R.H. AND
 ; APPLICANT: PURCELL, R.H.
 ; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
 ; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
 ; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
 ; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
 ; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
 ; NUMBER OF SEQUENCES: 160
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,601A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 2026-4070US2
 ; FILING DATE: 29-JUN-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RICHARD W. BORK
 ; REGISTRATION NUMBER: 36,459
 ; REFERENCE/DOCKET NUMBER: 2026-4070US2
 ; TELEPHONE: (212) 751-6849
 ; TELEFAX: (212) 751-6849
 ; TELEX: 421792
 ; INFORMATION FOR SEQ ID NO: 104:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 40 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-466-601A-104

Query Match 51.3%; Score 15.4; DB 3; Length 40;
 Best Local Similarity 76.0%; Pred. No. 3.6e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCGCGCTTGAA 27
 |||||
 Db 40 GGCACATCAATAGCAGCGCTTGAA 16

RESULT 34
 US-08-466-601A-106/c
 ; Sequence 106, Application US/08466601A
 ; Patent No. 6572864
 ; GENERAL INFORMATION:

; APPLICANT: BUKH, J., MILLER, R.H. AND
 ; APPLICANT: PURCELL, R.H.
 ; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
 ; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
 ; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
 ; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
 ; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
 ; NUMBER OF SEQUENCES: 160
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,601A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/086,428
 ; FILING DATE: 29-JUN-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RICHARD W. BORK
 ; REGISTRATION NUMBER: 36,459
 ; REFERENCE/DOCKET NUMBER: 2026-4070US2
 ; TELEPHONE: (212) 751-6849
 ; TELEFAX: (212) 751-6849
 ; TELEX: 421792
 ; INFORMATION FOR SEQ ID NO: 106:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 40 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-466-601A-106

Query Match 51.3%; Score 15.4; DB 4; Length 40;
 Best Local Similarity 76.0%; Pred. No. 3.6e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCGCGCTTGAA 27
 |||||
 Db 27 GGCACATCAATAGCAGCGCTTGAA 3

RESULT 35
 PCT-US95-10398-208/c
 ; Sequence 208, Application PC/TUS9510398
 ; GENERAL INFORMATION:
 ; APPLICANT: BUKH, J., MILLER, R.H. AND
 ; APPLICANT: PURCELL, R.H.
 ; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
 ; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
 ; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
 ; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
 ; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
 ; NUMBER OF SEQUENCES: 263
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:

; GENERAL INFORMATION:

```

; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-10398-210

Query Match 51.3%; Score 15.4; DB 5; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGTACCCCGACGACCGCGCTTGAA 27
DB 27 GGCACATCATAGACGCGCTTGAA 3
|||||
|||||

RESULT 37
US-09-396-196G-91572/c
; Sequence 91572, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91572
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-91572

Query Match 50.7%; Score 15.2; DB 4; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CAGCAGCCCGCGCTTGAGA 29
DB 24 CAGCATCCGACACTTGAGA 5
|||||
|||||

RESULT 38
US-09-396-196G-91573/c
; Sequence 91573, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-91573

Query Match      50.7%; Score 15.2; DB 4; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CAGCAGCCCGCGCTTGAAGA 29
    ||||| ||| |||||
Db 21 CAGCATCCACACTTGAAGA 2

RESULT 39
US-09-673-198-23
; Sequence 23, Application US/09673198
; Patent No. 6806076
; GENERAL INFORMATION:
; APPLICANT: MIYAKE, Koichiro; HASHIMOTO, Shinichi; MOTOYAMA Hiroaki;
; APPLICANT: OZAKI, Akio; SETO, Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji
; TITLE OF INVENTION: A process for producing isoprenoid compounds by
; TITLE OF INVENTION: microorganisms and a method for screening compounds with
; TITLE OF INVENTION: antibiotic or weeding activity
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/673,198
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: JP98/103101
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: JP98/221910
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: JP99/035739
; PRIOR FILING DATE: 1999-02-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-673-198-23

Query Match      49.3%; Score 14.8; DB 4; Length 32;
Best Local Similarity 73.1%; Pred. No. 6.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGA 26
    ||||| ||| |||||
Db 1 GGGGATCTCGCCAGCCAGCGCTTGA 26

RESULT 40
US-08-998-099-161/c
; Sequence 161, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18

; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized Hammerhead Ribozyme
; OTHER INFORMATION: The letter "n" represents stem II region of a HH ribozyme.
US-08-998-099-161

Query Match      48.7%; Score 14.6; DB 3; Length 27;
Best Local Similarity 77.3%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCCGGCC 22
    ||||| ||| |||||
Db 23 GCGTTTCATCATCAGCCCGGCC 2

Search completed: November 18, 2005, 11:22:00
Job time : 58.289 secs
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 403.232 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-6

Perfect score: 30

Sequence: 1 GCGGTACCCAGCAGCCGGCTTGAAGAA 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2:	/cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq.*
3:	/cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq.*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq.*
6:	/cgn2_6/ptodata/1/pubpna/PCTUS PUBCOMB.seq.*
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11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq.*
13:	/cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq.*
14:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
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20:	/cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
21:	/cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
22:	/cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23:	/cgn2_6/ptodata/1/pubpna/US10_NEW PUB.seq.*
24:	/cgn2_6/ptodata/1/pubpna/US10_NEW PUB.seq.*
25:	/cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
26:	/cgn2_6/ptodata/1/pubpna/US11_NEW PUB.seq.*
27:	/cgn2_6/ptodata/1/pubpna/US60_NEW PUB.seq.*
28:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	US-08-469-172-6	Sequence 6, Appli
2	30	100.0	30	US-10-788-779-6	Sequence 6, Appli
3	18.2	60.7	26	US-09-796-844-9	Sequence 9, Appli
4	18.2	60.7	26	US-10-645-702-9	Sequence 9, Appli
5	18.2	60.7	26	US-10-686-639-9	Sequence 9, Appli

6	18.2	60.7	26	24	US-10-645-702-9	Sequence 9, Appli
7	16.8	56.0	25	22	US-10-719-900-167892	Sequence 167892,
8	16.8	56.0	25	22	US-10-719-900-189296	Sequence 189296, A
9	16.2	54.0	25	16	US-10-098-263B-28065	Sequence 28065, A
10	16.2	54.0	25	16	US-10-098-263B-41023	Sequence 41023, A
11	16.2	54.0	28	11	US-09-796-844-11	Sequence 11, Appl
12	16.2	54.0	28	11	US-09-796-844-13	Sequence 13, Appl
13	16.2	54.0	28	11	US-10-645-702-11	Sequence 11, Appl
14	16.2	54.0	28	20	US-10-645-702-13	Sequence 13, Appl
15	16.2	54.0	28	20	US-10-686-639-11	Sequence 11, Appl
16	16.2	54.0	28	20	US-10-686-639-13	Sequence 13, Appl
17	16.2	54.0	28	24	US-10-645-702-11	Sequence 11, Appl
18	16.2	54.0	28	24	US-10-645-702-13	Sequence 13, Appl
19	16.2	54.0	38	10	US-09-923-760-2	Sequence 2, Appli
20	16	53.3	25	22	US-10-809-189-25759	Sequence 25759, A
21	16	53.3	25	9	US-09-949-145-26	Sequence 26, Appl
22	15.8	52.7	19	10	US-09-880-313A-54	Sequence 54, Appl
23	15.8	52.7	19	10	US-09-880-313A-140	Sequence 140, App
24	15.8	52.7	25	22	US-10-809-189-109792	Sequence 109792,
25	15.8	52.7	39	18	US-10-375-913-39	Sequence 39, Appl
26	15.8	52.7	39	26	US-11-110-001-39	Sequence 39, Appl
27	15.8	52.7	39	26	US-11-110-002-39	Sequence 39, Appl
28	15.6	52.0	25	22	US-10-719-900-48747	Sequence 48747, A
29	15.6	52.0	25	22	US-10-719-900-48748	Sequence 48748, A
30	15.6	52.0	25	22	US-10-809-189-125627	Sequence 125627,
31	15.6	52.0	25	24	US-10-719-956-186720	Sequence 186720,
32	15.6	52.0	25	24	US-10-719-956-220107	Sequence 220107,
33	15.6	52.0	25	24	US-10-719-956-254406	Sequence 254406,
34	15.6	52.0	25	24	US-10-719-956-273121	Sequence 273121,
35	15.6	52.0	25	24	US-10-719-956-627239	Sequence 627239,
36	15.6	52.0	25	24	US-10-719-956-627240	Sequence 627240,
37	15.6	52.0	32	21	US-10-716-803-43	Sequence 43, Appl
38	15.6	52.0	43	9	US-09-727-311-42	Sequence 42, Appl
39	15.6	52.0	43	22	US-10-767-869-43	Sequence 43, Appl
40	15.4	51.3	20	10	US-09-880-313A-243	Sequence 243, App
41	15.4	51.3	25	22	US-10-719-900-468543	Sequence 468543,
42	15.4	51.3	25	22	US-10-719-900-675526	Sequence 675526,
43	15.4	51.3	25	22	US-10-719-900-763075	Sequence 763075,
44	15.4	51.3	25	22	US-10-809-189-25761	Sequence 25761, A
45	15.4	51.3	25	22	US-10-956-157-292888	Sequence 292888,

ALIGNMENTS

RESULT 1
US-08-469-172-6
; Sequence 6, Application US/08469172
; Publication No. US200300543A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-469-172-6

Query Match 100.0%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

RESULT 2
US-10-788-779-6
; Sequence 6, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-788-779-6

Query Match 100.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

RESULT 3
US-09-796-844-9
; Sequence 9, Application US/09796844
; Publication No. US20040096935A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/09/796,844
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-844-9

Query Match 60.7%; Score 18.2; DB 11; Length 26;
Best Local Similarity 87.0%; Pred. No. 7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTT 23
Db 2 GCGGTACCCAGCAGCCGCGCTT 24

RESULT 4
US-10-645-702-9
; Sequence 9, Application US/10645702
; Publication No. US20040115698A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
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; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-9
```

```
Query Match          60.7%; Score 18.2; DB 20; Length 26;
Best Local Similarity 87.0%; Pred. No. 7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 GCGGTACCCAGCAGCCCGGCTT 23
    ||||||| |||||
Db 2 GCGGTACCCAGCAGCCCGGCTT 24
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RESULT 5

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US-10-686-639-9
; Sequence 9, Application US/10686639
; Publication No. US20040175790A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398
; CURRENT APPLICATION NUMBER: US/10/686,639
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US/09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-686-639-9
```

```
Query Match          60.7%; Score 18.2; DB 20; Length 26;
Best Local Similarity 87.0%; Pred. No. 7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 1 GCGGTACCCAGCAGCCCGGCTT 23
    ||||||| |||||
Db 2 GCGGTACCCAGCAGCCCGGCTT 24
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RESULT 6

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US-10-645-702-9
; Sequence 9, Application US/10645702
; Publication No. US20050181372A9
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
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```
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-9
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Query Match          60.7%; Score 18.2; DB 24; Length 26;
Best Local Similarity 87.0%; Pred. No. 7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 1 GCGGTACCCAGCAGCCCGGCTT 23
    ||||||| |||||
Db 2 GCGGTACCCAGCAGCCCGGCTT 24
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RESULT 7

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US-10-719-900-167892
; Sequence 167892, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 167892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-167892
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Query Match          56.0%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy 11 AGCAGCCCGGCTTGAAGAA 30
    ||||||| |||||
Db 1 AGCAGCCCGGCTATAGAGAA 20
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RESULT 8

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US-10-719-900-189296
; Sequence 189296, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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```
; SEQ ID NO 189296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-189296

Query Match          56.0%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 AGCAGCCCGGCTTGAAGAA 30
    ||||| ||||| |||||
Db 1 AGGAGCCTGGCTTGAAGAA 20

RESULT 9
US-10-098-263B-28065
; Sequence 28065, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 28065
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-263B-28065

Query Match          54.0%; Score 16.2; DB 16; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGGCC 22
    ||||| ||||| |||||
Db 4 CGGTACCCAGCAGCCCGGCC 24

RESULT 10
US-10-098-263B-41023
; Sequence 41023, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 41023
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-263B-41023

Query Match          54.0%; Score 16.2; DB 16; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGGCC 22
    ||||| ||||| |||||
Db 3 CGGTACCCAGCAGCCCGGCC 23

us-09-796-844-11
; Sequence 11, Application US/09796844
; Publication No. US20040096935A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanguu
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/09/796,844
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-844-11

Query Match          54.0%; Score 16.2; DB 11; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCTT 23
    ||||| ||||| |||||
Db 6 GGTACCCAGCAGCCCGGCTT 26

RESULT 12
US-09-796-844-13
; Sequence 13, Application US/09796844
; Publication No. US20040096935A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanguu
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/09/796,844
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-844-13
```

```
US-09-796-844-13
Query Match          54.0%; Score 16.2; DB 11; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTACCCAGAGCCCGGCTT 23
   |||||
Db 6 GGTACCCAGAGCCCGGCTT 26

RESULT 13
US-10-645-702-11
; Sequence 11, Application US/10645702
; Publication No. US20040115698A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-11

Query Match          54.0%; Score 16.2; DB 20; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTACCCAGAGCCCGGCTT 23
   |||||
Db 6 GGTACCCAGAGCCCGGCTT 26

RESULT 14
US-10-645-702-13
; Sequence 13, Application US/10645702
; Publication No. US20040115698A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-11

Query Match          54.0%; Score 16.2; DB 20; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTACCCAGAGCCCGGCTT 23
   |||||
Db 6 GGTACCCAGAGCCCGGCTT 26

RESULT 15
US-10-686-639-11
; Sequence 11, Application US/10686639
; Publication No. US20040175790A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398
; CURRENT APPLICATION NUMBER: US/10/686,639
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US/09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-686-639-11

Query Match          54.0%; Score 16.2; DB 20; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTACCCAGAGCCCGGCTT 23
   |||||
Db 6 GGTACCCAGAGCCCGGCTT 26

RESULT 16
US-10-686-639-13
; Sequence 13, Application US/10686639
; Publication No. US20040175790A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398
; CURRENT APPLICATION NUMBER: US/10/686,639
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US/09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-686-639-13
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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-686-639-13

Query Match      54.0%; Score 16.2; DB 20; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCAGCCCGGCTT 23
Db 6 GGTACCCCGAGCAGCCCGGCTT 26

RESULT 17
US-10-645-702-11
; Sequence 11, Application US/10645702
; Publication No. US20050181372A9
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF39822
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-11

Query Match      54.0%; Score 16.2; DB 24; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCAGCCCGGCTT 23
Db 6 GGTACCCCGAGCAGCCCGGCTT 26

RESULT 18
US-10-645-702-13
; Sequence 13, Application US/10645702
; Publication No. US20050181372A9
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanguu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF39822
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-11

Query Match      54.0%; Score 16.2; DB 24; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCAGCCCGGCTT 23
Db 6 GGTACCCCGAGCAGCCCGGCTT 26

RESULT 19
US-09-923-760-2
; Sequence 2, Application US/09923760
; Publication No. US20030119054A1
; GENERAL INFORMATION:
; APPLICANT: Mrksich, Milan
; APPLICANT: Hodneland, Christian
; TITLE OF INVENTION: POLYPEPTIDE IMMOBILIZATION
; FILE REFERENCE: 7814/45
; CURRENT APPLICATION NUMBER: US/09/923,760
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer sequence, Exon1B, for F. solani cutinase gene
US-09-923-760-2

Query Match      54.0%; Score 16.2; DB 10; Length 38;
Best Local Similarity 72.4%; Pred. No. 4.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGTACCCCGAGCAGCCCGGCTTGAAGAA 30
Db 2 CGGTACCCCGAGCAGCCCGGCTTCTCTGTGAA 30

RESULT 20
US-10-809-189-25759/c
; Sequence 25759, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
```

; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25759
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-189-23759

Query Match 53.3%; Score 16; DB 22; Length 25;
Best Local Similarity 79.2%; Pred. No. 6e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4 GTACCCAGCAGCCGCGCTTGA 27
Db 25 GTAGCCAGCATGCGAGCTTGA 2

RESULT 21

US-09-949-145-26
; Sequence 26, Application US/0949145
; Patent No. US20020055622A1
; GENERAL INFORMATION:
; APPLICANT: New York Blood Center
; TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and Glyco
; FILE REFERENCE: Docket 454-31
; CURRENT APPLICATION NUMBER: US/09/949,145
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230660
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-145-26

Query Match 53.3%; Score 16; DB 9; Length 29;
Best Local Similarity 79.2%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GGTACCCAGCAGCCGCGCTTGA 26
Db 6 GGCACCCCTGCAGCATGCGCTTGA 29

RESULT 22

US-09-880-313A-54/c
; Sequence 54, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-880-313A-54

Query Match 52.7%; Score 15.8; DB 10; Length 19;

Best Local Similarity 89.5%; Pred. No. 7.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GTACCCAGCAGCCGCGGCC 22
Db 19 GTACCCCTGCAGCGCGGCC 1

RESULT 23

US-09-880-313A-140/c
; Sequence 140, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-880-313A-140

Query Match 52.7%; Score 15.8; DB 10; Length 19;
Best Local Similarity 89.5%; Pred. No. 7.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GTACCCAGCAGCCGCGGCC 22
Db 19 GTACCCCTGCAGCGCGGCC 1

RESULT 24

US-10-809-189-109792/c
; Sequence 109792, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109792
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-109792

Query Match 52.7%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 10 CAGCAGCCGCGCTTGAAG 28
Db 20 CAGCAGTCTGCGCTTGAAG 2

RESULT 25

US-10-375-913-39/c

```
; Sequence 39, Application US/10375913
; Publication No. US20030216550A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Ming-Qun
; APPLICANT: Ferrandon, Sebastien
; APPLICANT: Taron, Christopher
; APPLICANT: Colussi, Paul
; TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
; FILE REFERENCE: NEB-200-US
; CURRENT APPLICATION NUMBER: US/10/375,913
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,354
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 39
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: primer
; US-10-375-913-39

Query Match          52.7%; Score 15.8; DB 18; Length 39;
Best Local Similarity 89.5%; Pred. No. 6.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGC 21
Db 28 GGTACCCCGAGCGCGCGC 10

RESULT 26
US-11-110-001-39/c
; Sequence 39, Application US/11110001
; Publication No. US20050196804A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Ming-Qun
; APPLICANT: Ferrandon, Sebastien
; APPLICANT: Taron, Christopher
; APPLICANT: Colussi, Paul
; TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
; FILE REFERENCE: NEB-200-US
; CURRENT APPLICATION NUMBER: US/11/110,001
; CURRENT FILING DATE: 2005-04-20
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US/10/375,913
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 39
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: primer
; US-11-110-001-39

Query Match          52.7%; Score 15.8; DB 26; Length 39;
Best Local Similarity 89.5%; Pred. No. 6.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGC 21
Db 28 GGTACCCCGAGCGCGCGC 10

RESULT 27
US-11-110-002-39/c
; Sequence 39, Application US/11110002
; Publication No. US20050196841A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Ming-Qun
; APPLICANT: Ferrandon, Sebastien
; APPLICANT: Taron, Christopher
; APPLICANT: Colussi, Paul
; TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
; FILE REFERENCE: NEB-200-US
; CURRENT APPLICATION NUMBER: US/10/375,913
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,354
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 39
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: primer
; US-11-110-002-39

Query Match          52.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCTT 24
Db 3 GATAACCCGAGGAGCGCGCAT 24

RESULT 28
US-10-719-900-48747
; Sequence 48747, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48747
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-48747

Query Match          52.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCTT 24
Db 3 GATAACCCGAGGAGCGCGCAT 24

RESULT 29
US-10-719-900-48748
; Sequence 48748, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
```

```
; APPLICANT: Xu, Ming-Qun
; APPLICANT: Ferrandon, Sebastien
; APPLICANT: Taron, Christopher
; APPLICANT: Colussi, Paul
; TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
; FILE REFERENCE: NEB-200-US
; CURRENT APPLICATION NUMBER: US/11/110,002
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: US/10/375,913
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,354
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 39
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: primer
; US-11-110-002-39

Query Match          52.7%; Score 15.8; DB 26; Length 39;
Best Local Similarity 89.5%; Pred. No. 6.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGC 21
Db 28 GGTACCCCGAGCGCGCGC 10

RESULT 28
US-10-719-900-48747
; Sequence 48747, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48747
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-48747

Query Match          52.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCTT 24
Db 3 GATAACCCGAGGAGCGCGCAT 24

RESULT 29
US-10-719-900-48748
; Sequence 48748, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
```


Query Match 52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels

; AFFILIATION: AUE MEI ZHOU
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527.1
 ; CURRENT APPLICATION NUMBER: US/10/719,956

;
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 273121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-273121

Query Match 52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 CCAGCAGCCCGCCTTGAAGAA 30
|||||
Db 23 CCAGCAGCCAGGTCTTCAAGCA 2

RESULT 35
US-10-719-956-627239/c
; Sequence 627239, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 627239
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-627239

Query Match 52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 CCAGCAGCCCGCCTTGAAGAA 30
|||||
Db 22 CCAGCAGCCTGGTCTTCAAGCA 1

RESULT 36
US-10-719-956-627240/c
; Sequence 627240, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 627240
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-627240

Query Match 52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 CCAGCAGCCCGCCTTGAAGAA 30
|||||
Db 22 CCAGCAGCCAGGTCTTCAAGCA 1

RESULT 37
US-10-716-803-43/c
; Sequence 43, Application US/10716803
; Publication No. US20040229236A1
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; Blanche, Francis
; Crouzet, Joel
; Jacques, Nathalie
; Lacroix, Patricia
; Thibaut, Denis
; Zagorec, Monique
; Debussche, Laurent
; De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; Biosynthesis Of Streptogramins, Nucleotide Sequences
; Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/716,803
; FILING DATE: 20-Nov-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/635,359
; FILING DATE: 09-AUG-2000
; APPLICATION NUMBER: US 09/231,818
; FILING DATE: 15-JAN-1999
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Arrigo, Salvatore J.
; REGISTRATION NUMBER: 46,063
; REFERENCE/DOCKET NUMBER: 03806.0054-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-716-803-43

Query Match 52.0%; Score 15.6; DB 21; Length 32;
Best Local Similarity 62.5%; Pred. No. 8.6e+03;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGGCTTG 25
|||||
Db 32 CGGTACCCAGCAGCAGCGGCTTS 9

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 832.357 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-7

Perfect score: 30

Sequence: 1 GCGAATTCGGAGCCAGCGCACTGAAG 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

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2: gb_hlg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	6	I12900 Sequence 7
2	18.8	62.7	50	6	CQ848568 Sequence
3	16.2	54.0	23	6	AR030683 Sequence
4	16.2	54.0	23	6	AR076191 Sequence
5	16.2	54.0	23	6	AR124104 Sequence
6	16.2	54.0	23	6	E23386 DNA encodin
7	16.2	54.0	31	6	BD226997 Plasmid i
8	16.2	54.0	38	6	A37856 Sequence 26
9	16.2	54.0	38	6	AR069894 Sequence
10	16.2	54.0	38	6	AR099291 Sequence
11	16.2	54.0	38	6	AR124175 Sequence
12	16.2	54.0	38	6	AR442782 Sequence
13	15.4	51.3	41	6	AX515690 Sequence
14	15.4	51.3	41	6	AX518285 Sequence
15	15.2	50.7	24	6	CQ818454 Sequence
16	15.2	50.7	33	6	E30624 Antibody an
17	15.2	50.7	33	6	E31233 Device for
18	15.2	50.7	33	6	AR566423 Sequence
19	15	50.0	31	6	AS1539 Sequence 24

20	15	50.0	31	6	A51567 Sequence 27
21	15	50.0	31	6	AR084293 Sequence
22	15	50.0	31	6	CQ795411 Sequence
23	15	50.0	31	6	I95571 Sequence 26
24	14.8	49.3	26	6	AR307679 Sequence
25	14.8	49.3	27	6	AR003508 Sequence
26	14.8	49.3	27	6	AR070729 Sequence
27	14.8	49.3	27	6	AR118062 Sequence
28	14.8	49.3	27	6	I17115 Sequence 8
29	14.8	49.3	27	6	I62404 Sequence 8
30	14.8	49.3	27	6	I86716 Sequence 4
31	14.8	49.3	27	6	I86724 Sequence 12
32	14.8	49.3	30	6	AR049388 Sequence
33	14.8	49.3	30	6	AR095549 Sequence
34	14.6	48.7	32	6	CQ818101 Sequence
35	14.6	48.7	50	6	AR444529 Sequence
36	14.4	48.0	26	6	CQ857433 Sequence
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38	14.4	48.0	44	6	AR274129 Sequence
39	14.4	48.0	44	6	AR444946 Sequence
40	14.2	47.3	31	6	BD271888 Methods f
41	14.2	47.3	31	6	AX080183 Sequence
42	14.2	47.3	31	6	AX592510 Sequence
43	14.2	47.3	34	6	CQ756616 Sequence
44	14.2	47.3	39	6	AR009935 Sequence
45	14.2	47.3	39	6	I76260 Sequence 88

ALIGNMENTS

RESULT 1	I12900	Sequence 7 from patent US 5429923.	30 bp	DNA	linear	PAT 26-JUL-1995
LOCUS	I12900					
DEFINITION	Sequence 7 from patent US 5429923.					
ACCESSION	I12900					
VERSION	I12900.1	GI:910877				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 30)					
AUTHORS	Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.					
TITLE	Method for detecting hypertrophic cardiomyopathy associated mutations					
JOURNAL	Patent: US 5429923-A 7 04-JUL-1995;					
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source	1..30					
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Best Local Similarity	100.0%;	Pred. No. 0.034;				
Matches	30;	Conservative	0;	Mismatches	0;	Gaps
Indels	0;					
Qy	1	GCGAATTCGGAGCCAGCGCACTGAAG	30			
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RESULT 2	CQ848568	Sequence 28 from Patent WO2004065628.	50 bp	DNA	linear	PAT 19-AUG-2004
LOCUS	CQ848568					
DEFINITION	Sequence 28 from Patent WO2004065628.					
ACCESSION	CQ848568					
VERSION	CQ848568.1	GI:51469996				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					

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AUTHORS
Fu,G.
TITLE
Quantitative multiplex detection of nucleic acids
JOURNAL
Patent: WO 2004065628-A 28 05-AUG-2004;
Fu, Guoliang (GB)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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Best Local Similarity 76.7%; Pred. No. 2.5e+03;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GGGAAATTCGGAGCCAGCCAGCTGAAG 30
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Db 14 GAGAATTCGAGCATCCAGGTGCTCACTGAAG 43
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RESULT 3
AR030683 LOCUS 23 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5861294.
ACCESSION AR030683
VERSION AR030683.1 GI:5943897
KEYWORDS
ORGANISM Unknown.
REFERENCE
Unclassified.
1 (bases 1 to 23)
AUTHORS Cowart,M.Daniel., Halbert,D.N., Kerwin,J.F. Jr. and McNally,T.
TITLE Adenosine kinase polypeptides
JOURNAL Patent: US 5861294-A 20 19-JAN-1999;
FEATURES
Location/Qualifiers
source
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ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 23;
Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GAATTCGGAGCCAGCCAGCCG 23
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Db 1 GAATTCGTGGAGCCAAACCG 21
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RESULT 4
AR076191 LOCUS 23 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 5 from patent US 5958748.
ACCESSION AR076191
VERSION AR076191.1 GI:10002937
KEYWORDS
ORGANISM Unknown.
REFERENCE
Unclassified.
1 (bases 1 to 23)
AUTHORS Akira,S. and Kawai,T.
TITLE DNA coding for serine/threonine kinase
JOURNAL Patent: US 5958748-A 5 28-SEP-1999;
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Query Match 54.0%; Score 16.2; DB 6; Length 23;
Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
AUTHORS
Fu,G.
TITLE
Quantitative multiplex detection of nucleic acids
JOURNAL
Patent: WO 2004065628-A 28 05-AUG-2004;
Fu, Guoliang (GB)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
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Best Local Similarity 76.7%; Pred. No. 2.5e+03;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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RESULT 5
AR124104 LOCUS 23 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6171841.
ACCESSION AR124104
VERSION AR124104.1 GI:14109465
KEYWORDS
ORGANISM Unknown.
REFERENCE
Unclassified.
1 (bases 1 to 23)
AUTHORS Akira,S. and Kawai,T.
TITLE DNA coding for serine/threonine kinase
JOURNAL Patent: US 6171841-A 5 09-JAN-2001;
FEATURES
Location/Qualifiers
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Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GGGAAATTCGGAGCCAGCCAGCG 21
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Db 1 GGGAAATTCGGAGCCAGCGAGG 21
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RESULT 6
E23386 LOCUS 23 bp DNA linear PAT 18-JUN-2001
DEFINITION DNA encoding serine/threonine kinase.
ACCESSION E23386
VERSION E23386.1 GI:13024388
KEYWORDS JP 1999098984-A/3.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE
1 (bases 1 to 23)
AUTHORS Shizuo,S. and Taro,K.
TITLE DNA encoding serine/threonine kinase
JOURNAL Patent: JP 1999098984-A 3 13-APR-1999;
COMMENT
SCIENCE & TECH AGENCY
OS Unidentified
PN JP 1999098984-A/3
PD 13-APR-1999
PF 26-SEP-1997 JP 1997261589
PR
PI SHIZUO SHINRA,TARO KAWAI
PC C12N15/09,C12N1/21,C12N9/12/(C12N15/09,C12R1:91), (C12N1/21,
PC C12R1:19),
PC (C12N9/12,C12R1:19),C12N15/00, (C12N15/00,C12R1:91) CC
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CC Topology: Linear;
FH Key Location/Qualifiers
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ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 23;
Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 GGGAAATTCGGGAGCCAGCAGC 21
Db 1 GGGAAATTCGGGAGCCAGCAGC 21

RESULT 7
BD226997 31 bp DNA linear PAT 17-JUL-2003
LOCUS Plasmid inhibitor from Australia brown snake Pseudonaja textilis
DEFINITION textilis.
ACCESSION BD226997
VERSION BD226997.1 GI:33036767
KEYWORDS JP 2002514404-A/17.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 31)
AUTHORS Masci, P., Lavin, M.F. and Gaffney, P.J.
TITLE Plasmid inhibitor from Australia brown snake Pseudonaja textilis
JOURNAL Patent: JP 2002514404-A 17 21-MAY-2002;
THE UNIVERSITY OF QUEENSLAND, NATIONAL INSTITUTE OF BIOLOGICAL
STANDARDS AND CONTROL UNITED KINGDOM
COMMENT OS Artificial Sequence
PN JP 2002514404-A/17
PD 21-MAY-2002
PF 07-MAY-1999 JP 2000548371
PI 11-MAY-1998 AU PP 3450
PI PANTALEONE PAUL MASCI, MARTIN FRANCIS LAVIN, PATRICK JOSEPH PI
PI GAFFNEY
PC C12N15/09, A61K38/00, A61K38/43, A61K39/44, A61P7/04, A61P35/00, PC
A61P43/00,
PC C07K14/81, C12N15/00, A61K37/02, A61K37/465
CC Description of Artificial Sequence: gene-specific reverse CC
primer for Txln1
FH Key Location/Qualifiers
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FT /organism='Artificial Sequence'.
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ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 31;
Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGGAGCCAGCAGC 21
Db 4 GGGAAATTCAGAGCCAGCAGC 24

RESULT 8
A37856 38 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 26 from Patent WO9408014.
DEFINITION A37856
ACCESSION A37856
VERSION A37856.1 GI:2294536
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 38)
AUTHORS Blanc, V., Blanchet, F., Crouzet, J., Jacques, N., Lacroix, P.,
Thibaut, D., and Zagorec, M.
TITLE POLYPEPTIDES INVOLVED IN STREPTOGRAMIN BIOSYNTHESIS, NUCLEOTIDE
SEQUENCES CODING FOR SAID POLYPEPTIDES AND USE THEREOF
JOURNAL Patent: WO 9408014-A 26 14-APR-1994;
RHONE-POULENC RORER SA (FR)
COMMENT Other publication AU 4823993 940426

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Other publication CA 2145523 940414
Other publication ZA 9307102 940422
Other publication FI 951403 950324
Other publication FR 2696189 940401
Other publication JP 85016961 960227.
Location/Qualifiers
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Best Local Similarity 66.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGGAGCCAGCAGCAGCAGT 27
Db 11 GSGAGTTTCGCGCGCTGGGACGCGCACG 37

RESULT 9
AR069894 38 bp DNA linear PAT 18-FEB-2000
LOCUS Sequence 42 from patent US 5891695.
DEFINITION AR069894
ACCESSION AR069894
VERSION AR069894.1 GI:7220782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Blanc, V., Blanchet, F., Crouzet, J., Jacques, N., Lacroix, P.,
Thibaut, D., Zagorec, M., Debussche, L., and De Crecy-Lagard, V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 5891695-A 42 06-APR-1999;
FEATURES Location/Qualifiers
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Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGGAGCCAGCAGCAGCAGT 27
Db 11 GSGAGTTTCGCGCGCTGGGACGCGCACG 37

RESULT 10
AR099291 38 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 44 from patent US 6077699.
DEFINITION AR099291
ACCESSION AR099291
VERSION AR099291.1 GI:12809057
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Blanc, V., Blanchet, F., Crouzet, J., Jacques, N., Lacroix, P.,
Thibaut, D., Zagorec, M., Debussche, L., and De Crecy-Lagard, V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 6077699-A 44 20-JUN-2000;
FEATURES Location/Qualifiers
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Query Match	54.0%;	Score 16.2;	DB 6;	Length 38;	
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LOCUS	AR124175	38 bp	DNA	linear	PAT 16-MAY-2001
DEFINITION	Sequence 42 from patent US 6171846.				
ACCESSION	AR124175				
VERSION	AR124175.1	GI:14109536			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 . (bases 1 to 38)				
AUTHORS	Blanc,V., Blanche,F., Crouzet,J., Jacques,N., LaCroix,P., Thibaut,D., Zagorec,M., Debussche,L. and De Crecy-Lagard,V.				
TITLE	Polypeptides involved in the biosynthesis of streptogramins, nucleotide sequences coding for these polypeptides and their use				
JOURNAL	Patent: US 6171846-A 42 09-JAN-2001;				
FEATURES	Location/Qualifiers				
source	1 . 38				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	54.0%;	Score 16.2;	DB 6;	Length 38;	
Best Local Similarity	66.7%;	Pred. NO. 3.3e+04;			
Matches	18;	Conservative	3;	Mismatches	6; Indels 0; Gaps 0;
Qy	1	GGGAATTCCGGAGCCAGCGGCACTG	27		
Db	11	GSGAGTTCGCGCGSTGGGACGCACCG	37		
RESULT 12					
LOCUS	AR442782	38 bp	DNA	linear	PAT 20-FEB-2004
DEFINITION	Sequence 42 from patent US 6670157.				
ACCESSION	AR442782				
VERSION	AR442782.1	GI:42670186			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 . (bases 1 to 38)				
AUTHORS	Blanc,V., Blanche,F., Crouzet,J., Jacques,N., LaCroix,P., Thibaut,D., Zagorec,M., Debussche,L. and De Crecy-Lagard,V.				
TITLE	Polypeptides involved in the biosynthesis of streptogramins, nucleotide sequences coding for these polypeptides and their use				
JOURNAL	Patent: US 6670157-A 42 30-DEC-2003;				
FEATURES	Location/Qualifiers				
source	1 . 38				
ORIGIN	/organism="unknown"				
	/mol_type="genomic DNA"				
Query Match	54.0%;	Score 16.2;	DB 6;	Length 38;	
Best Local Similarity	66.7%;	Pred. NO. 3.3e+04;			
Matches	18;	Conservative	3;	Mismatches	6; Indels 0; Gaps 0;
Qy	1	GGGAATTCCGGAGCCAGCGGCACTG	27		
Db	11	GSGAGTTCGCGCGSTGGGACGCACCG	37		
RESULT 13					

AX515690/c	AX515690	Sequence 1888 from Patent WO02052044.	41 bp	DNA	linear	PAT 05-OCT-2002
LOCUS	AX515690					
DEFINITION	Sequence 1888 from Patent WO02052044.					
ACCESSION	AX515690					
VERSION	AX515690.1	GI:23563011				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1	Nakamura,Y., Sekine,A., Iida,A. and Saito,S.				
AUTHORS	Detection of genetic polymorphisms					
TITLE	Patent: WO 02052044-A 1888 04-JUL-2002;					
JOURNAL	Riken (JP)					
FEATURES	Location/Qualifiers					
source	1 . 41					
ORIGIN	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
Query Match	51.3%;	Score 15.4;	DB 6;	Length 41;		
Best Local Similarity	70.4%;	Pred. No. 7.4e+04;				
Matches	19;	Conservative	1;	Mismatches	7; Indels 0; Gaps 0;	
Qy	4	AATTGCGGAGCCAGCGGCACTGAAG	30			
Db	41	AACTACAGGAGCCAGGAGCGCTGCAG	15			
RESULT 14						
AX518285/c	AX518285	Sequence 4483 from Patent WO02052044.	41 bp	DNA	linear	PAT 05-OCT-2002
LOCUS	AX518285					
DEFINITION	Sequence 4483 from Patent WO02052044.					
ACCESSION	AX518285					
VERSION	AX518285.1	GI:23567718				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1	Nakamura,Y., Sekine,A., Iida,A. and Saito,S.				
AUTHORS	Detection of genetic polymorphisms					
TITLE	Patent: WO 02052044-A 4483 04-JUL-2002;					
JOURNAL	Riken (JP)					
FEATURES	Location/Qualifiers					
source	1 . 41					
ORIGIN	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
Query Match	51.3%;	Score 15.4;	DB 6;	Length 41;		
Best Local Similarity	70.4%;	Pred. No. 7.4e+04;				
Matches	19;	Conservative	1;	Mismatches	7; Indels 0; Gaps 0;	
Qy	4	AATTGCGGAGCCAGCGGCACTGAAG	30			
Db	41	AACTACAGGAGCCAGGAGCGCTGCAG	15			
RESULT 15						
CQ818454	CQ818454	Sequence 15 from Patent WO2004029088.	24 bp	DNA	linear	PAT 07-JUN-2004
LOCUS	CQ818454					
DEFINITION	Sequence 15 from Patent WO2004029088.					
ACCESSION	CQ818454					
VERSION	CQ818454.1	GI:48427099				
KEYWORDS	.					
SOURCE	synthetic construct					
ORGANISM	synthetic construct					
	other sequences; artificial sequences.					

REFERENCE 1
AUTHORS Roth,C.W., Brey,F.T., Holm,I., Graillies,M. and Rzhetsky,A.
TITLE Multidrug resistance proteins in drosophila and anopheles
JOURNAL Patent: WO 2004029088-A 15 08-APR-2004;
(CNRS) (FR) INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

FEATURES
source Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: primer"

ORIGIN
Query Match 50.7%; Score 15.2; DB 6; Length 24;
Best Local Similarity 85.0%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGAC 20
||||| | | | | |
Db 1 GGGAAATTCGGGAGCCAGAC 20

RESULT 16
E30624
LOCUS Antibody and nucleic acid encoding the same. linear PAT 18-JUN-2001
DEFINITION E30624
ACCESSION E30624
VERSION E30624.1 GI:13017190
KEYWORDS JP 1999332563-A/11.
SOURCE unidentified
ORGANISM unidentified
1 (bases 1 to 33)
REFERENCE Mitsuharu,O., Takayuki,K. and Ikuo,M.
AUTHORS Antibody and nucleic acid encoding the same
TITLE Patent: JP 1999332563-A 11 07-DEC-1999;
JOURNAL ASahi CHEM IND CO LTD
COMMENT OS Unidentified
PN JP 1999332563-A/11
PD 07-DEC-1999
PF 26-MAY-1998 JP 1998163034
PR MITSUOHARU ONO,TAKAYUKI KUSAKA,IKUO MORIMOTO
PC C12N15/02,A61K39/395,A61K39/395,C07K16/28,C12N15/09,C12P21/08,
PC C12N15/00,
PC C12N15/00
CC Key Location/Qualifiers
FH source 1..33
FT Location/Qualifiers
/organism="Unidentified".
/mol_type="Unidentified"
/db_xref="taxon:32644"

FEATURES
source Location/Qualifiers
1..33
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 50.7%; Score 15.2; DB 6; Length 33;
Best Local Similarity 85.0%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGAC 20
||||| | | | | |
Db 1 GGGAAATTCGGGAGCCAGAC 20

RESULT 17
E31233
LOCUS Sequence 24 from Patent EP0728842. linear PAT 10-MAR-1997
DEFINITION E31233
ACCESSION E31233
VERSION E31233.1 GI:2304360
KEYWORDS

KEYWORDS JP 1999332594-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 33)
AUTHORS Mitsuharu,O., Takayuki,K. and Ikuo,M.
TITLE Device for separating CD4-positive cells and separation method
JOURNAL Patent: JP 1999332594-A 11 07-DEC-1999;
ASAHI CHEM IND CO LTD
COMMENT OS Unidentified
PN JP 1999332594-A/11
PD 07-DEC-1999
PF 26-MAY-1998 JP 1998163023
PR MITSUOHARU ONO,TAKAYUKI KUSAKA,IKUO MORIMOTO
PC C12Q1/04,C07K16/28,C07K16/46,C12M1/34,G01N33/53 CC
FH Key Location/Qualifiers
FT source 1..33
/organism="Unidentified".
/mol_type="Unidentified"
/db_xref="taxon:32644"

FEATURES
source Location/Qualifiers
1..33
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 50.7%; Score 15.2; DB 6; Length 33;
Best Local Similarity 85.0%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGAC 20
||||| | | | | |
Db 1 GGGAAATTCGGGAGCCAGAC 20

RESULT 18
AR566423
LOCUS Sequence 3 from patent US 6768004. linear PAT 08-OCT-2004
DEFINITION AR566423
ACCESSION AR566423
VERSION AR566423.1 GI:53983440
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified
REFERENCE 1 (bases 1 to 33)
AUTHORS Muller,S. and Kohler,H.
TITLE Nucleotide sequences encoding variable regions of heavy and light chains of monoclonal antibody 1F7, an anti-idiotypic antibody reactive with anti-HIV antibodies
JOURNAL Patent: US 6768004-A 3 27-JUL-2004;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 50.7%; Score 15.2; DB 6; Length 33;
Best Local Similarity 85.0%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGAC 20
||||| | | | | |
Db 1 GGGAAATTCGGGAGCCAGAC 20

RESULT 19
A51539
LOCUS Sequence 24 from Patent EP0728842. linear PAT 10-MAR-1997
DEFINITION A51539
ACCESSION A51539
VERSION A51539.1 GI:2304360
KEYWORDS

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SOURCE      unidentified
ORGANISM    unclassified
REFERENCE   1 (bases 1 to 31)
AUTHORS     Audonnet,J.-C.,Bublout,M.J., Darteil,R.J., Duinat,C.V., Laplace,E.L.
            and Riviere,M.A.
TITLE       Live recombinant avian vaccine based on an avianherpes virus,
            against Gumboro disease
JOURNAL     Patent: EP 0728842-A 24 28-AUG-1996;
            RHONE MERIEUX (FR)
COMMENT     Other publication FR 2728794 960705
            Other publication CA 2166371 960701
            Other publication AU 4063095 960711.
FEATURES    source
            1..31
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      50.0%; Score 15; DB 6; Length 31;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGGAGCCGACGGCAC 25
Db 6 GAATTCGCGAAGAGAGAGGAAC 28

RESULT 20
A51567 LOCUS 31 bp DNA linear PAT 10-MAR-1997
DEFINITION Sequence 27 from Patent EP0719864.
ACCESSION A51567
VERSION A51567.1 GI:2304395
KEYWORDS
SOURCE      unidentified
            unclassified.
REFERENCE   1 (bases 1 to 31)
AUTHORS     Audonnet,J.F., Bublout,M.J., Darteil,R.J., Duinat,C.V., Laplace,E.L.
            and Riviere,M.A.
TITLE       Recombinant live avian vaccin, using an avian herpes virus as
            vector
JOURNAL     Patent: EP 0719864-A 27 03-JUL-1996;
            RHONE MERIEUX (FR)
COMMENT     Other publication FR 2728795 960705
            Other publication CA 2166367 960701
            Other publication AU 4071595 960711.
FEATURES    source
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            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      50.0%; Score 15; DB 6; Length 31;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGGAGCCGACGGCAC 25
Db 6 GAATTCGCGAAGAGAGAGGAAC 28

RESULT 21
AR084293 LOCUS 31 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 27 from patent US 5980906.
ACCESSION AR084293
VERSION AR084293.1 GI:10011064
KEYWORDS
SOURCE      Unknown.

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ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 31)
AUTHORS     Audonnet,J.-C.Francis., Bublout,M.Joseph.Marie., Darteil,R.Jean.,
            Duinat,C.Veronique., Laplace,E.Louise.Francedillaaise. and
            Riviere,M.Albert.Emile.
TITLE       Live recombinant avian vaccine using an avian herpesvirus as vector
JOURNAL     Patent: US 5980906-A 27 09-NOV-1999;
            Location/Qualifiers
            1..31
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match      50.0%; Score 15; DB 6; Length 31;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGGAGCCGACGGCAC 25
Db 6 GAATTCGCGAAGAGAGAGGAAC 28

RESULT 22
CQ795411 LOCUS 31 bp DNA linear PAT 19-APR-2004
DEFINITION Sequence 27 from Patent EP1403375.
ACCESSION CQ795411
VERSION CQ795411.1 GI:46407501
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Audonnet,J.C., Bublout,M., Darteil,R., Duinat,C., Laplace,E. and
            Riviere,M.
TITLE       Recombinant live avian vaccin, using avian herpes virus as vector
JOURNAL     Patent: EP 1403375-A 27 31-MAR-2004;
            MERIAL (FR)
FEATURES    source
            1..31
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="oligonucl otide servant d'amorce de PCR"
ORIGIN
Query Match      50.0%; Score 15; DB 6; Length 31;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGGAGCCGACGGCAC 25
Db 6 GAATTCGCGAAGAGAGAGGAAC 28

RESULT 23
I95571 LOCUS 31 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 26 from patent US 5733554.
ACCESSION I95571
VERSION I95571.1 GI:3940041
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 31)
AUTHORS     Audonnet,J.-C.Francedillaais., Bublout,M.Joseph.Marie.,
            Darteil,R.Jean., Duinat,C.Veronique.,
            Laplace,E.Louise.Francedillaaise. and Riviere,M.Albert.Emile.
TITLE       Avian herpesvirus-based live recombinant avian vaccine, in
            particular against Gumboro disease
JOURNAL     Patent: US 5733554-A 26 31-MAR-1998;

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FEATURES
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    /mol_type="unassigned DNA"

ORIGIN
  Query Match
  Best Local Similarity 50.0%; Score 15; DB 6; Length 31;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGAATTCGGAGCCGACGCGCAC 25
Db 6 GGAATTCGCAAGAGAGGAAC 28

RESULT 24
AR0307679
LOCUS AR0307679 26 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 26 from patent US 6551821.
ACCESSION AR0307679
VERSION AR0307679.1 GI:31698384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kandel,E.R., Santoro,B., Bartsch,D., Siegelbaum,S., Tibbe,G. and Grant,S.
TITLE Brain cyclic nucleotide gated ion channel and uses thereof
JOURNAL Patent: US 6551821-A 26 22-APR-2003;
FEATURES
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    /organism="unknown"
    /mol_type="genomic DNA"

ORIGIN
  Query Match
  Best Local Similarity 49.3%; Score 14.8; DB 6; Length 26;
  Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ATTCGGAGCCGACGCGCATGTGAAG 30
Db 1 ATGTTCCGAGCAGAAGCGGTGGAG 26

RESULT 25
AR003508
LOCUS AR003508 27 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5744310.
ACCESSION AR003508
VERSION AR003508.1 GI:3964767
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C.
TITLE Bax promoter sequence and screening assays for indentifying agents that regulate bax gene expression
JOURNAL Patent: US 5744310-A 4 28-APR-1998;
FEATURES
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    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
  Query Match
  Best Local Similarity 49.3%; Score 14.8; DB 6; Length 27;
  Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCGACGCGCACTG 27
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26

RESULT 26
AR070729
LOCUS AR070729 27 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 8 from patent US 5908750.
ACCESSION AR070729
VERSION AR070729.1 GI:7221617
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C., Miyashita,T., Hariigai,M. and Hanada,M.
TITLE Screening assays for identifying agents that regulate the expression of genes involved in cell death
JOURNAL Patent: US 5908750-A 8 01-JUN-1999;
FEATURES
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ORIGIN
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  Best Local Similarity 49.3%; Score 14.8; DB 6; Length 27;
  Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCGACGCGCACTG 27
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26

RESULT 27
AR118062
LOCUS AR118062 27 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6140484.
ACCESSION AR118062
VERSION AR118062.1 GI:14098968
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Bitler,C.,Mastroni., Bowersox,S.Scott., Crea,R., Demo,S.Dunham., Horne,W.A. and Zhou,M.
TITLE Bax .omega. protein and methods
JOURNAL Patent: US 6140484-A 1 31-OCT-2000;
FEATURES
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    Location/Qualifiers
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    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
  Query Match
  Best Local Similarity 49.3%; Score 14.8; DB 6; Length 27;
  Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCGACGCGCACTG 27
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26

RESULT 28
I17115
LOCUS I17115 27 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 8 from patent US 5484710.
ACCESSION I17115
VERSION I17115.1 GI:1252023
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
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AUTHORS Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
TITLE Method of down-regulating a gene linked to a P-53 responsive element
JOURNAL Patent: US 5484710-A 8 16-JAN-1996;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 2 GGAATTCCGCGGAGCCAGCGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26
RESULT 29
162404
LOCUS I62404 27 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 8 from patent US 5659024.
ACCESSION I62404
VERSION I62404.1 GI:2480352
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
TITLE Promoters that regulate the expression of genes involved in cell death
JOURNAL Patent: US 5659024-A 8 19-AUG-1997;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 2 GGAATTCGCGGAGCCAGCGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26
RESULT 30
186716
LOCUS I86716 27 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5702897.
ACCESSION I86716
VERSION I86716.1 GI:3206434
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C. and Sato,T.
TITLE Interaction of proteins involved in a cell death pathway
JOURNAL Patent: US 5702897-A 4 30-DEC-1997;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGCGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26
RESULT 31
186724
LOCUS I86724 27 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 12 from patent US 5702897.
ACCESSION I86724
VERSION I86724.1 GI:3206442
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C. and Sato,T.
TITLE Interaction of proteins involved in a cell death pathway
JOURNAL Patent: US 5702897-A 12 30-DEC-1997;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 2 GGAATTCGCGGAGCCAGCGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26
RESULT 32
AR049388
LOCUS AR049388 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 25 from patent US 5824513.
ACCESSION AR049388
VERSION AR049388.1 GI:6005427
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Katz,L., Donadio,S. and McAlpine,J.B.
TITLE Recombinant DNA method for producing erythromycin analogs
JOURNAL Patent: US 5824513-A 25 20-OCT-1998;
FEATURES Location/Qualifiers
source 1. .30
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 49.3%; Score 14.8; DB 6; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 2 GGAATTCGCGGAGCCAGCGGCACTG 27
Db 2 GGAATTCGCGGTGATGGACGGGTCCG 27
RESULT 33
AR095549
LOCUS AR095549 30 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 25 from patent US 6004787.
ACCESSION AR095549
VERSION AR095549.1 GI:10023513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C. and Sato,T.
TITLE Interaction of proteins involved in a cell death pathway
JOURNAL Patent: US 5702897-A 4 30-DEC-1997;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"

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REFERENCE 1 (bases 1 to 30)
AUTHORS Katz,L., Donadio,S. and McAlpine,J.B.
TITLE Method of directing biosynthesis of specific polyketides
JOURNAL Patent: US 6004787-A 25 21-DEC-1999;
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        /mol_type="unassigned DNA"
ORIGIN
Query Match 49.3%; Score 14.8; DB 6; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GGAATTCGGGAGCCAGCGGCACTG 27
Db 2 GGAATTCGGTGGCATGCGGCACTG 27
RESULT 34
CQ818101
LOCUS CQ818101 32 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 128 from Patent WO2004044004.
ACCESSION CQ818101
VERSION CQ818101.1 GI:48426915
KEYWORDS
    synthetic construct
    synthetic construct
    other sequences; artificial sequences.
ORIGIN
REFERENCE 1
AUTHORS Jakobsen,B.K., Andersen,T.B., Molloy,P.E., Li,Y. and Boulter,J.M.
TITLE T cell receptor display
JOURNAL Patent: WO 2004044004-A 128 27-MAY-2004;
Avidex Limited (GB)
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"
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Query Match 48.7%; Score 14.6; DB 6; Length 32;
Best Local Similarity 69.0%; Pred. No. 1.7e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2 GGAATTCGGGAGCCAGCGGCACTGAAG 30
Db 1 GGAATTCATCGATGCAGAGGAAGTGGAG 29
RESULT 35
AR444529
LOCUS AR444529 50 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 940 from patent US 6670464.
ACCESSION AR444529
VERSION AR444529.1 GI:42672308
KEYWORDS
    Unknown.
    SOURCE Unknown.
    ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: US 6670464-A 940 30-DEC-2003;
FEATURES
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        /mol_type="genomic DNA"
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Query Match 48.7%; Score 14.6; DB 6; Length 50;
REFERENCE 1 (bases 1 to 31)
AUTHORS Sha,N., Walinton,J. and Patel,N.
TITLE Gene composition and method
JOURNAL Patent: JP 2000245487-A 426 12-SEP-2000;
AFIMETRICS INC
COMMENT
    OS Unknown
    PN JP 2000245487-A/426
    PD 12-SEP-2000
    PF 27-JAN-2000 JP 2000019392
    PR 27-JAN-1999 US 09/238,402
    PI NIRA SHA, JANET WALINTON, NIRA PATEL
    CC C12N15/09, C12Q1/68, C12N15/00
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ORIGIN
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Best Local Similarity 83.3%; Pred. No. 2e+05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGAAATTCGGGAGCCAG 18
Db 25 GGGAAATTCRGGGACCAG 8
RESULT 37
BD002760
LOCUS BD002760 31 bp DNA linear PAT 31-JAN-2002
DEFINITION Gene composition and method.
ACCESSION BD002760
VERSION BD002760.1 GI:18630721
KEYWORDS
    unidentified
    SOURCE unidentified
    ORGANISM unclassified.
REFERENCE 1 (bases 1 to 31)
AUTHORS Sha,N., Walinton,J. and Patel,N.
TITLE Gene composition and method
JOURNAL Patent: JP 2000245487-A 426 12-SEP-2000;
AFIMETRICS INC
COMMENT
    OS Unknown
    PN JP 2000245487-A/426
    PD 12-SEP-2000
    PF 27-JAN-2000 JP 2000019392
    PR 27-JAN-1999 US 09/238,402
    PI NIRA SHA, JANET WALINTON, NIRA PATEL
    CC C12N15/09, C12Q1/68, C12N15/00
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ORIGIN

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Best Local Similarity 69.0%; Pred. No. 1.7e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GGGAAATTCGGGAGCCAGCGGCACTGAA 29
Db 2 GGGAAAGCGCATATCTCTGGCGGCACGCA 30
RESULT 36
CQ857433/C
LOCUS CQ857433 26 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 161 from Patent WO2004069211.
ACCESSION CQ857433
VERSION CQ857433.1 GI:51851714
KEYWORDS
    synthetic construct
    synthetic construct
    other sequences; artificial sequences.
ORIGIN
REFERENCE 1
AUTHORS Houtzager,E., Vijn,I.M., Sijmons,P.C., Valinotti,T., Mudge,G. and Fadel,A.
TITLE Affinity proteins for controlled application of cosmetic substances
JOURNAL Patent: WO 2004069211-A 161 19-AUG-2004;
L-Mabs B.V. (NL)
FEATURES
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    source
        1..26
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Description of Artificial Sequence: primer Pr817"
ORIGIN
Query Match 48.0%; Score 14.4; DB 6; Length 26;
Best Local Similarity 83.3%; Pred. No. 2e+05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGAAATTCGGGAGCCAG 18
Db 25 GGGAAATTCRGGGACCAG 8
RESULT 37
BD002760
LOCUS BD002760 31 bp DNA linear PAT 31-JAN-2002
DEFINITION Gene composition and method.
ACCESSION BD002760
VERSION BD002760.1 GI:18630721
KEYWORDS
    unidentified
    SOURCE unidentified
    ORGANISM unclassified.
REFERENCE 1 (bases 1 to 31)
AUTHORS Sha,N., Walinton,J. and Patel,N.
TITLE Gene composition and method
JOURNAL Patent: JP 2000245487-A 426 12-SEP-2000;
AFIMETRICS INC
COMMENT
    OS Unknown
    PN JP 2000245487-A/426
    PD 12-SEP-2000
    PF 27-JAN-2000 JP 2000019392
    PR 27-JAN-1999 US 09/238,402
    PI NIRA SHA, JANET WALINTON, NIRA PATEL
    CC C12N15/09, C12Q1/68, C12N15/00
    FT Key
    FT source
    FT Location/Qualifiers
    FT 1..31
    FT /organism='Unknown'.
    FT Location/Qualifiers
    FT 1..31
    FT /organism="unidentified"
    FT /mol_type="genomic DNA"
    FT /db_xref="taxon:32644"
ORIGIN

```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 206.578 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-7

Perfect score: 30

Sequence: 1 GGGAAATTCGGCGAGCCAGCGCACTGAAG 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167256

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002as.*

7: geneseqn2002bs.*

8: geneseqn2003as.*

9: geneseqn2003bs.*

10: geneseqn2003cs.*

11: geneseqn2003ds.*

12: geneseqn2004as.*

13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	2	AaQ91127 Beta-card
2	30	100.0	30	9	ACA63117 Human bet
3	30	100.0	30	13	ADRO5303 Human bet
4	18.8	62.7	50	13	ADQ31570 Multiplex
5	17.2	57.3	31	3	Aaz58040 Porcine r
6	16.8	56.0	35	3	Aaz54807 Neisseria
7	16.2	54.0	23	2	Aat48848 Rat brain
8	16.2	54.0	23	2	Aax01108 PCR prime
9	16.2	54.0	23	2	Aax34658 Sense pri
10	16.2	54.0	31	3	Aaz29034 Txln 1 ge
11	16.2	54.0	33	8	ABZ99945 Human gua
12	16.2	54.0	36	6	AAS98482 Human pro
13	16.2	54.0	39	6	AAL55433 Specific
14	16.2	54.0	39	6	ABQ76067 Anticance
15	16.2	54.0	39	8	ABV75124 Mutant HG
16	16.2	54.0	39	12	Aai80425 Anti-cumo
17	15.8	52.7	29	3	AAAl1359 Human Myx
18	15.8	52.7	41	6	ABZ47699 Human ATP
19	15.8	52.7	41	6	ABZ45104 Human ATP
20	15.6	52.0	25	9	ACI97483 Human mic

c	21	15.6	52.0	25	9	ACK28325	Human mic
c	22	15.6	52.0	41	3	Aaz54975	Neisseria
	23	15.4	51.3	34	3	AAA30422	Single-do
	24	15.2	50.7	24	12	ADN97120	Primer of
	25	15.2	50.7	33	2	AAQ90440	RT-PCR pr
	26	15.2	50.7	33	3	Aaz44213	Murine CD
	27	15.2	50.7	33	3	Aaz58671	Anti-CD4
	28	15.2	50.7	33	3	AAA39128	Murine mo
	29	15.2	50.7	33	5	AAH41120	Murine im
	30	15.2	50.7	33	6	AAL48649	Murine Ma
	31	15.2	50.7	40	3	Aaz96102	Polynucle
	32	15	50.0	28	13	ADS18341	Murine TR
	33	15	50.0	29	6	ABA03393	Sindbis v
	34	15	50.0	31	2	AAT35896	Marek's d
	35	15	50.0	31	2	AAT39333	Marek's d
	36	15	50.0	31	2	AAT35930	Marek dis
	37	15	50.0	31	12	ADM41163	PCR prime
	38	15	50.0	45	13	ADRI3841	Human her
	39	14.8	49.3	27	2	AAT62767	Human bax
	40	14.8	49.3	27	2	AAT03167	Human Bax
	41	14.8	49.3	27	2	AAT48489	Bax Omega
	42	14.8	49.3	27	2	AAV25511	Primer fo
	43	14.8	49.3	27	2	AAZ19765	Human tru
	44	14.8	49.3	30	2	AAQ46803	pALeryAW4
	45	14.8	49.3	36	10	ADD35981	Single ch

ALIGNMENTS

RESULT 1

AAQ91127

ID AAQ91127 standard; cdna; 30 BP.

XX

AC AAQ91127;

XX

DT 19-FEB-1996 (first entry)

XX

DE Beta-cardiac myosin heavy chain PCR primer C'.

XX

KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;

KW diagnosis; primer; mutation; detection; ss.

XX

OS Synthetic.

XX

PN US5429923-A.

XX

PD 04-JUL-1995.

XX

PF 11-DEC-1992; 92US-00989160.

XX

PR 11-DEC-1992; 92US-00989160.

XX

PA (HARD) HARVARD COLLEGE.

PA

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA

PA (GCHO-) GEN HOSPITAL SHENYANG MILITARY AREA.

PI

PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX

XX WPI; 1995-245715/32.

XX

XX Non-invasive method for diagnosis of hypertrophic cardio-mycopathy -

XX

XX Example 1; Col 10; 22pp; English.

XX

XX AaQ91121-Q91130 are nested PCR primers used for the amplification and

XX identification of beta-cardiac myosin heavy-chain RNA. They are used in a

XX new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),

XX the method involves detecting the presence or absence of specific HC-

XX associated mutations in the beta-cardiac myosin heavy-chain obtained from

XX a blood sample. The method may be used to diagnose familial or sporadic

XX HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 30 BP; 8 A; 7 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGAAATTCGGAGCCAGCGCACTGAAG 30

Db 1 GGGAAATTCGGAGCCAGCGCACTGAAG 30

RESULT 2

ACA63117

ID ACA63117 standard; DNA; 30 BP.

XX ACA63117;

AC ACA63117;

DT 28-AUG-2003 (first entry)

XX Human beta cardiac myosin heavy chain PCR primer C'.

DE Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;

XX familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;

KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;

KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;

KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

OS US2003054343-A1.

XX 20-MAR-2003.

XX 06-JUN-1995; 95US-00469172.

XX 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

PI WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with

XX hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or

XX hemophilia, by detecting a mutation in an amplified product of a beta

XX cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

PS The invention relates to detecting the presence or absence of a mutation

XX associated with hypertrophic cardiomyopathy (sporadic or familial, SHC

XX and FHC) comprises detecting a mutation associated with hypertrophic

XX cardiomyopathy in an amplified product of a beta cardiac myosin heavy

XX chain DNA. The mutations associated with SHC/FHC are detected in the

XX myosin gene isolated from blood, by detecting mis-matched areas in RNA-

XX DNA hybrid double strands (RNA from the normal gene, DNA from the suspect

XX sample). FHC associated point mutation can be classified and used to

XX determine life expectancy in affected individuals e.g. using a Kaplan-

XX Meier curve for the classified type of FHC causing point mutation. Also

XX included are an RNA probe comprising ribonucleotides arranged in a

XX sequence which is complementary to at least a portion of beta-cardiac

XX myosin heavy-chain DNA and a set of DNA oligonucleotide primers for

XX amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a nested PCR primer used to amplify a region of the beta cardiac
 CC myosin heavy chain cDNA containing an FHC-associated mutation

XX Sequence 30 BP; 8 A; 7 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGAAATTCGGAGCCAGCGCACTGAAG 30

Db 1 GGGAAATTCGGAGCCAGCGCACTGAAG 30

RESULT 3

ADR05303

ID ADR05303 standard; DNA; 30 BP.

XX ADR05303;

AC ADR05303;

XX 21-OCT-2004 (first entry)

XX Human beta cardiac myosin heavy chain mutation detection primer C'.

DE Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;

XX familial hypertrophic cardiomyopathy;

KW sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

OS US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

PI WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to

XX diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac

XX myosin heavy-chain DNA and detecting the mutation in the amplified

XX product.

XX Claim 18; SEQ ID NO 7; 22pp; English.

PS The invention relates to detecting the presence or absence of a mutation

XX associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,

XX SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,

XX comprising amplifying beta-cardiac myosin heavy-chain DNA forming an

XX amplified product, and detecting the presence or absence of a mutation

XX associated with hypertrophic cardiomyopathy in the amplified product,

XX thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also

XX included are a set of DNA oligonucleotide primers for amplifying beta-

XX cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
 CC oligonucleotide primers being useful for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
 CC cardiomyopathy-associated mutation) and a kit for facilitating the
 CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
 CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
 CC heavy chain DNA, where the RNA probe is capable of detecting a
 CC hypertrophic cardiomyopathy-associated mutation, a second container
 CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
 CC instructions for using the components of the kit to detect the presence
 CC or absence of a hypertrophic cardiomyopathy-associated mutation in
 CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
 CC detecting the presence or absence of a mutation associated with
 CC hypertrophic cardiomyopathy for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
 CC having hypertrophic cardiomyopathy relies on the presence of typical
 CC clinical symptoms and the demonstration of unexplained ventricular
 CC hypertrophy. The present invention is non-invasive and based, at least in
 CC part, on the discovery that hypertrophic cardiomyopathy is caused by
 CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
 CC reveals that there are no extensive studies involving a large number of
 CC families which established that this particular disease or disorder was
 CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
 CC The present sequence is a PCR primer used to amplify a region of the beta
 CC cardiac myosin heavy chain having a disease-related point mutation.

Sequence 30 BP; 8 A; 7 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 13; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGAGGACGACGCGACTGAAG 30
 |||||
 DB 1 GGGAAATTCGGAGGACGACGCGACTGAAG 30

RESULT 4

ADQ31570
 ID ADQ31570 standard; DNA; 50 BP.

XX ADQ31570;

DT 21-OCT-2004 (first entry)

DE Multiplex detection of human SNPs, primer F7C.

XX Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP;
 KW single nucleotide polymorphism.

XX Homo sapiens.

XX US2004146866-A1.

XX 29-JUL-2004.

PF 24-JAN-2003; 2003US-00349780.

PR 24-JAN-2003; 2003US-00349780.

XX (FUGG/) FU G.

XX Fu G;

XX WPI; 2004-552653/53.

XX Analyzing multiple targets in polynucleotide, by providing multiple
 PT primers with target nucleic acids, digesting nucleic acid products with
 PT cognate restriction enzymes, amplifying digested products, and detecting
 PT amplified products.

XX Example 1; SEQ ID NO 28; 65pp; English.

CC The invention relates analysing multiple targets in polynucleotide,
 CC involves providing a set or sets of multiple primers with target nucleic
 CC acids in separate reactions of primer extension or amplification, where
 CC the reactions produce nucleic acid products in that each nucleic acid
 CC fragments comprise at least one restriction site, digesting nucleic acid
 CC products of the separate reactions on the restriction sites with cognate
 CC restriction enzymes, joining digested products derived from the separate
 CC reactions together, where randomly joining nucleic acid fragments from
 CC the separated reactions are created, amplifying the joined products, and
 CC detecting the amplified products. Also included are an oligonucleotide
 CC primer for detecting target nucleic acid sequence (comprising a 3'
 CC complementary portion and 5' non-complementary enzyme site, where the 5'
 CC restriction site acts as detection marker in the process of detecting
 CC target nucleic acid sequence, where the detection signal generated from
 CC enzymatic manipulation on restriction site of reaction product is
 CC indicative of the presence of target nucleic acid sequence) and a kit for
 CC use in analysis and detection of multiple targets in a polynucleotide
 CC (comprising a set or sets of multiple primers, universal primers,
 CC restriction enzymes, DNA ligase, DNA polymerase, ddNTP, buffers for all
 CC in a polynucleotide and for genotyping mutations, preferably single
 CC nucleotide polymorphisms (SNPs), and for analysing differential gene
 CC expression profiles, genomic methylation patterns and any specific
 CC nucleic acids from any source. The method enables analysis of multiple
 CC targets quantitatively. An experiment was performed, using the method of
 CC the invention, where 8 SNPs were detected in human genomic DNA,
 CC simultaneously. The present sequence is a primer used in the above
 CC experiment.

Sequence 50 BP; 16 A; 10 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 62.7%; Score 18.8; DB 13; Length 50;

Best Local Similarity 76.7%; Pred. No. 2.2e+02;
 Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGAGGACGACGCGACTGAAG 30
 |||||
 DB 14 GAGAAATTCGAGATCCAGGTGTCACTGAAG 43

RESULT 5

AAZ58040

ID AAZ58040 standard; DNA; 31 BP.

XX AAZ58040;

XX 06-AUG-2003 (revised)

DT 25-APR-2000 (first entry)

XX Porcine reproductive and respiratory syndrome virus ORF3 3' primer.

XX PRRS; racoonpox virus; vaccine; homology vector 934-64.2; PCR primer;
 KW ss.

XX Porcine reproductive and respiratory syndrome virus.

OS WO200003030-A2.

XX 20-JAN-2000.

PF 09-JUL-1999; 99WO-US015565.

XX 10-JUL-1998; 98US-00113750.

XX (SCHE) SCHERING-PLOUGH LTD.

XX Cochran MD, Junker DE;

XX WPI; 2000-171150/15.

XX New recombinant racoonpox virus containing foreign DNA inserted into a
 PT non-essential region within the HindIII U genomic region, useful as a

PT vaccine against pathogens in mammalian and avian species.

XX Disclosure; Page 55; 164pp; English.

XX

CC The present sequence is that of downstream primer 9/97.10 used in the PCR

CC amplification of open reading frame 3 (ORF3) of swine reproductive and

CC respiratory syndrome virus (PPRS). It is based on the 3' end of the PPRS

CC ORF3, and introduces an EcoRI site at the 3' end of the gene. The PCR

CC product was used in the construction of homology vector 934-64.2, which

CC incorporates a beta-glucuronidase marker gene and the PPRS ORF3 gene

CC flanked by raccoonpox virus (RPV) DNA, and was constructed for the

CC purpose of inserting foreign DNA into recombinant RPV. Recombinant RPVs

CC of the invention have foreign DNA inserted into non-essential regions of

CC the RPV genome. They can be included in vaccines against animal

CC pathogens, useful for immunising animals (especially avian species or

CC mammals, including humans) against animal pathogens (claimed), e.g.

CC feline pathogens (claimed) or human pathogens such as hepatitis B virus,

CC human immunodeficiency virus, human influenza etc. (Updated on 06-AUG-

CC 2003 to correct OS field.)

XX

SQ Sequence 31 BP; 6 A; 9 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 57.3%; Score 17.2; DB 3; Length 31;

Best Local Similarity 73.3%; Pred. No. 1e+03;

Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGCAGCGCACTGAAG 30

Db 2 GGGAAATTCCTATCGCCGTACGCGCACTGAGG 31

RESULT 6

AAZ54807

ID AAZ54807 standard; DNA; 35 BP.

XX

AC AAZ54807;

XX

DT 21-MAR-2000 (first entry)

DE

DE Neisseria species ORF cloning PCR primer #192.

XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;

KW antibacterial; gene therapy; PCR primer; ss.

XX

OS Synthetic.

OS Neisseria sp.

PN WO9957280-A2.

XX

PD 11-NOV-1999.

XX

PF 30-APR-1999; 99WO-US009346.

XX

PR 01-MAY-1998; 98US-0083758P.

PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.

PR 02-SEP-1998; 98US-0099062P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103794P.

PR 09-OCT-1998; 98US-0103796P.

PR 25-FEB-1999; 99US-0121528P.

XX

PA (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

XX

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;

PI Tettelin H, Venter JC;

XX

DR WPI; 2000-062150/05.

XX

PT Novel Neisserial polypeptides predicted to be useful antigens for

PT vaccines and diagnostics.

XX Example 16; Page 145; 1453pp; English.

XX

CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941

CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides

CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent

CC PCR primers used in the exemplification of the present inventions. The

CC polypeptides, the polynucleotides, antibodies and compositions of the

CC invention can be used as vaccines, as diagnostic reagents, and as

CC immunogenic compositions. The polypeptides can be used in the manufacture

CC of medicaments for treating or preventing infection due to Neisserial

CC bacteria (e.g. meningitis and septicaemia), to detect the presence of

CC Neisseria bacteria, or to raise antibodies. They may also be used to

CC screen for agonists or antagonists, which may themselves have use as

CC antibacterial agents. The polynucleotides of the invention may also be

CC used in gene therapy protocols

XX

SQ Sequence 35 BP; 16 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 56.0%; Score 16.8; DB 3; Length 35;

Best Local Similarity 75.0%; Pred. No. 1.6e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GAATTCGGGAGCCAGCAGCGCACTGAAG 30

Db 7 GAATTCGCACAGCAAAACGGTTTGAAG 34

RESULT 7

AAZ48848

ID AAT48848 standard; DNA; 23 BP.

XX

AC AAT48848;

XX

DT 30-MAR-1997 (first entry)

DE

DE Rat brain adenosine kinase outer forward primer.

XX

KW Adenosine kinase; agonist; antagonist; monoclonal antibody;

KW polymerase chain reaction; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO9640937-A2.

XX

PD 19-DEC-1996.

XX

PF 31-MAY-1996; 96WO-US008097.

XX

PR 07-JUN-1995; 95US-00480019.

XX

PA (ABBO) ABBOTT LAB.

XX

PI Cowart MD, Halbert DN, Kerwin JP, McNally T;

XX

DR WPI; 1997-052334/05.

XX

PT Rat brain, and human placenta short and long forms of adenosine kinase -

PT used, e.g. for assaying for AK (ant)agonists or for prodn. of monoclonal

PT antibodies against AK.

XX

PS Disclosure; Page 52; 75pp; English.

XX

CC Nested PCR primers (AAT48848-51) were designed to obtain a full-length

CC coding sequence for rat brain adenosine kinase (AK). These primers bind

CC to the 5' and 3' untranslated regions of the gene. Rat brain cDNA was

CC initially amplified with outer primers (AAT48848, AAT48850) and then with

CC the inner primers (AAT48849, AAT48851). The PCR fragment was cloned into

CC pGEM-T and inserts from multiple clones were sequenced. A full-length

CC consensus sequence (AAT48843) coding for rat brain AK (AAW08369) was obtd

XX

SQ Sequence 23 BP; 6 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

RESULT 9
AAX34658

XX 11-MAY-1998; 98AU-00003450.
XX (UYOU) UNIV QUEENSLAND.
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
PA (MASC-) MASC P P.
PA (LAVI/) LAVIN M P.
PA (GAFF/) GAFFNEY P J.
XX Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
XX WPI; 2000-039073/03.
XX Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
PT agents.
XX
XX Example 2; Page 61; 112pp; English.
XX
XX The present DNA sequence is the Txln 1 gene specific reverse primer, R1.
CC This is specifically designed, increasing the GC content, to determine
CC the 5' and 3' untranslated regions (UTR) of the Txln cDNA, from the
CC Australian brown snake, Pseudonaja textilis textilis. It includes an
CC EcoRI restriction site and a stop codon
XX
XX Sequence 31 BP; 8 A; 9 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 54.0%; Score 16.2; DB 3; Length 31;
Best Local Similarity 85.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGAAATTCGCGAGCCACAGC 21
DB 4 GGGAAATTCGAGCCACAGC 24
RESULT 11
ABZ99545
ID ABZ99545 standard; DNA; 33 BP.
XX AC ABZ99545;
XX 27-JUN-2003 (first entry)
XX Human guanosine monophosphate reductase GMPR2 PCR primer 2.
XX Human; guanosine monophosphate reductase; GMPR2; tumour; PCR; primer; ss.
XX Homo sapiens.
XX CN1380407-A.
XX 20-NOV-2002.
XX 12-APR-2001; 2001CN-00105966.
XX 12-APR-2001; 2001CN-00105966.
XX (IMMU-) INST IMMUNOLOGY NO 2 MILITARY MEDICAL CO.
XX Zhang J, Zhang W, Wan T;
XX WPI; 2003-230990/23.
XX New human-phosphoguanosine reductase, its coding sequence and
PT application.
XX Example 2; Page 19; 30pp; Chinese.
XX The invention relates to a novel human guanosine monophosphate reductase
CC GMPR2, and the polynucleotide encoding it. The zymological activity and
CC the relationship of GMPR2 and tumour cell multiplication and cell
CC differentiation are verified. The invention also discloses the strategy
CC of resisting GMPR2 for diagnosing and curing diseases, specially for

CC diagnosing and curing the diseases of tumour. The present sequence
CC represents a PCR primer used to amplify the human GMPR2 of the invention
XX
XX Sequence 33 BP; 8 A; 9 C; 9 G; 7 T; 0 U; 0 Other;
Query Match 54.0%; Score 16.2; DB 8; Length 33;
Best Local Similarity 72.4%; Pred. No. 2.8e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 GGAATTCGCGAGCCAGCGCACTGAAG 30
DB 1 GGAATTCGCGAGCCAGCGCTCACTGAAG 29
RESULT 12
AAS98482/c
ID AAS98482 standard; cDNA; 36 BP.
XX AC AAS98482;
XX 12-MAR-2002 (first entry)
XX Human protective DNA sequence CNI-00738 open reading frame DNA #41.
XX Human; protective sequence; cell death; central nervous system; stroke;
XX ischaemia; open reading frame; ORF; cerebral herniation; septic embolism;
XX cerebral oedema; meningitis; protozoal infection; malaria; CNI-00733; ss;
XX metazoal infection; vascular disease; eye; macular degeneration; trauma;
XX diabetic retinopathy; epidural haematoma; tumour; degenerative disease;
XX nutritional condition; environmental condition; metabolic condition;
XX CNI-00736; CNI-00738; CNI-00742; CNI-00748; cancer; gene therapy.
XX Homo sapiens.
XX WO200181361-A1.
XX 01-NOV-2001.
XX 09-APR-2001; 2001WO-US011501.
XX 11-APR-2000; 2000US-00547938.
XX (COGE-) COGENT NEUROSCIENCE INC.
XX Portbury SD, Puranam K, Katz LC, Lo DC, Barney S, Thomas MB;
XX WPI; 2002-066433/09.
XX P-PSDB; AAU73320.
XX Polypeptides and polynucleotides comprising protective sequences useful
PT for preventing, delaying or rescuing a cell from death in disease,
PT condition or disorders such as Alzheimer's disease, stroke, tumors,
PT trauma.
XX Claim 2; Fig 6AR; 228pp; English.
XX The invention relates to an isolated polypeptide encoded by a protective
CC sequence, which is a polynucleotide comprising sequences which, when
CC introduced into a cell either predisposed to undergo cell death or in the
CC process of undergoing cell death, prevent delay or rescue the cell from
CC death, relative to a corresponding cell into which exogenous nucleic
CC acids have been introduced. The sequences of the invention are useful for
CC diagnosing a protective sequence-mediated condition, disorder or disease
CC in an individual. The treatable disorders are preferably of the central
CC nervous system of humans including ischaemia-related conditions such as
CC stroke, cerebral herniation, septic embolism, cerebral oedema, infections
CC such as meningitis, protozoal infections such as malaria, metazoal
CC infections such as echinococcosis, vascular diseases such as ischaemic
CC encephalopathy, conditions involving the eye such as macular
CC degeneration, diabetic retinopathy, trauma such as epidural haematoma,
CC tumours such as primary intracranial tumours, degenerative diseases such
CC as Alzheimer's disease and nutritional, environmental and metabolic
CC conditions. Sequences AAS98409-AAS98544 represent human protective

CC sequence DNA and open reading frames of the polynucleotides
XX
SQ Sequence 36 BP; 4 A; 13 C; 7 G; 12 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 6; Length 36;
Best Local Similarity 72.4%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCCGGAGCCAGACGCGCACTGAAG 30

Db 33 GGAATCTCGGAGGAGGAGCGGCACAAAGAAG 5

RESULT 13

AAL55433

ID AAL55433 standard; DNA; 39 BP.

XX

AC AAL55433;

XX

DT 22-MAY-2003 (first entry)

XX

DE Specific tumour cell proliferation related PCR primer, SEQ ID No 3.

XX

KW Recombination virus; proliferating; tumour cell; anti-oncogene;

KW proliferation; telomerase promoter; therapy; tumour; PCR; primer; ss.

XX

OS Unidentified.

XX

PN WO2003006640-A1.

XX

PD 23-JAN-2003.

XX

PF 12-JUL-2002; 2002WO-CN000493.

XX

PR 12-JUL-2001; 2001CN-00126113.

XX

PA (QIAN/) QIAN Q.

XX

PI Qian Q, Wu M, Shan S;

XX

DR WPI; 2002-464081/22.

XX

PT Telomerase promoter-controlled recombinant viruses proliferating
PT specifically in tumor cells to highly express antioncogene to kill tumor
PT cells by synergism, applicable in treating tumor.

XX

PS Example 1; Page 22; 56pp; Chinese.

XX

CC The invention relates to a recombination virus proliferating in a tumour
CC cell, which can express an anti-oncogene with high efficiency. The
CC invention also relates to the method of its proliferation. A telomerase
CC promoter controlling the transcription of at least one necessary gene for
CC a recombination virus proliferating, can make the virus optionally
CC proliferate in a tumour cell, which has the activity of telomerase and
CC basically does not proliferate in a normal cell without the activity of a
CC telomerase. The recombination virus can be used in therapy of many kinds
CC of tumours. This polynucleotide sequence represents a PCR primer relating
CC to the specific proliferation in a tumour cell of the invention

XX

SQ Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 6; Length 39;

Best Local Similarity 72.4%; Pred. No. 2.9e+03;

Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCCGGAGCCAGACGCGCACTGAAG 30

Db 1 GGAATCTCGGAGGAGGAGCGGCACAAAGAAG 29

RESULT 14

ABQ76067

ID ABQ76067 standard; DNA; 39 BP.

XX
AC ABQ76067;
XX
DT 30-SEP-2002 (first entry)
XX
DE Anticancer gene-associated PCR primer #3.
XX
KW Proliferation; anticancer gene; tumour cell; telomerase; promoter;
XX early virus gene; PCR; primer; ss.
XX
OS Unidentified.
XX
PN CN1339584-A.
XX
PD 13-MAR-2002.
XX
PF 12-JUL-2001; 2001CN-00126113.
XX
PR 12-JUL-2001; 2001CN-00126113.
XX
PA (QIAN/) QIAN Q.
XX
PI Qian Q, Wu M, Cen X;
XX
DR WPI; 2002-464081/50.
XX
XX
PT Telomerase promoter-controlled recombinant viruses proliferating
PT specifically in tumor cells to highly express antioncogene to kill tumor
PT cells by synergism, applicable in treating tumor.
XX
PS Example 1; Page 10; 25pp; Chinese.
XX
CC
CC This invention describes a novel recombinant virus for specific
CC proliferation and efficient expression of an anticancer gene in tumour
CC cells. By inserting a telomerase promoter in the upstream area of an
CC early virus gene, the recombinant virus is made to proliferate
CC selectively in tumour cells with telomerase activity rather than in
CC normal cells without telomerase activity. This recombinant virus may be
CC used to treat several kinds of tumours. This sequence represents a PCR
CC primer used to illustrate the method described in the disclosure of the
CC invention
XX
SQ Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 6; Length 39;

Best Local Similarity 72.4%; Pred. No. 2.9e+03;

Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCCGGAGCCAGACGCGCACTGAAG 30

Db 1 GGAATCTCGGAGGAGGAGCGGCACAAAGAAG 29

RESULT 15

ABV75124/c

ID ABV75124 standard; DNA; 39 BP.

XX

AC ABV75124;

XX

DT 19-FEB-2003 (first entry)

XX

DE Mutant HGFL constructing mutagenic oligonucleotide.

XX

KW HGFL; RON; MSP; transmembrane; glycoprotein; receptor tyrosine kinase;

KW hepatotropic; liver; hepatocyte growth factor-like protein; human;

KW macrophage stimulating protein; mutagenic; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO200283074-A2.

XX

PD 24-OCT-2002.

XX 15-APR-2002; 2002WO-US011724.
XX
XX 13-APR-2001; 2001US-0283789P.
XX
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
XX Waltz SE, Leonis MA, Degan SJ;
XX
XX WPI; 2003-067549/06.
XX
XX Pharmacological composition useful in prevention and treatment of hepatic
XX disorders comprises heterodimeric transmembrane glycoprotein receptor
XX tyrosine kinase inhibitor.
XX
XX Example 1; Page 36; 66pp; English.
XX
XX The invention relates to a pharmaceutical composition that comprises
XX heterodimeric transmembrane glycoprotein (RON) receptor tyrosine kinase
XX inhibitor with at least one additional component selected from carriers,
XX adjuvants, emulsifiers, solubilizers and stabilizers. The compositions
XX decrease the action of RON receptor tyrosine kinase in the liver
XX physiology. The composition can be used in the treatment of hepatobiliary
XX damage e.g. acute and chronic liver failure; for preventing hepatobiliary
XX damage due to exposure to hepatotoxic agent (preferably anesthetic,
XX neuropsychotropics, anticonvulsants, analgesics, antimicrobials,
XX hormones, cardiovascular drugs, immunosuppressives, radiation and
XX antineoplastic agents). It is also useful in the treatment and prevention
XX of injury and diseases of liver, biliary tract, bile ducts, gall bladder
XX and other related hepatobiliary system; to treat patient at risk of
XX developing liver damage due to drug overdose, accidental exposure to
XX infected blood samples, aggressive chemotherapy or liver transplantation.
XX Sequences ABV75114-125 represent mutagenic oligonucleotides used for
XX creating mutant forms of the human hepatocyte growth factor-like protein
XX (HGFL), also known as macrophage stimulating protein (MSP)
XX
XX Sequence 39 BP; 2 A; 10 C; 18 G; 9 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 8; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CGCGAGCGCAGCGCAGCTGA 28
|||||
Db 26 CGCGAGCAGCGCGCTGA 6
|||||

RESULT 16
ADI80425
ID ADI80425 standard; DNA; 39 BP.
XX
XX AC ADI80425;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Anti-tumour recombinant virus related primer, SEQ ID No 3.
XX
XX KW recombinant virus; tumour cell; antibody; cytostatic; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2004007703-A1.
XX
XX PD 22-JAN-2004.
XX
XX PF 15-JUL-2003; 2003WO-CN000565.
XX
XX PR 15-JUL-2002; 2002CN-00136028.
XX
XX PA (SINO-) SINO GENE BIOTECHNOLOGY LTD.
XX
XX PI Qian Q, Yang Q;
XX

DR WPI; 2004-122938/12.
XX
XX Recombinant viruses for expressing anti-tumor antibody or its fragment
XX with high efficiency in tumor cells to kill or inhibit proliferation and
XX transfer of tumors, useful in drug compositions to treat tumors.
XX
XX PT Disclosure; SEQ ID NO 3; 79pp; Chinese.
XX
XX The invention relates to a novel recombinant virus that is capable of
XX specific replication in tumour cells, comprising a nucleotide sequence
XX encoding an antibody or its fragment for treating a tumour. The invention
XX further relates to: application of the virus for killing or inhibiting
XX tumour cells after external infection of such cells with an effective
XX dose of the virus; treating human tumours by external or internal
XX infection of the tumour cells to limit their replication and upgrowth
XX with selectivity after expressing a dose of the antibody or its fragment,
XX if necessary, for direct killing of copies of the encoded nucleotide sequence
XX formation of tumour, its growth and transfer; use of the virus to inhibit
XX proliferation of tumour cells; use of virus producing remedies for
XX treating a tumour; and drug compositions containing the recombinant virus
XX and pharmaceutically-acceptable carriers. The recombinant virus has
XX cytostatic activity. The viruses are applicable for killing or inhibiting
XX tumour cells when used in drug compositions to treat tumours. This
XX polynucleotide sequence represents a primer used in the exemplification
XX of the invention.
XX
XX Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 12; Length 39;
Best Local Similarity 72.4%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGAGCGCAGCGCAGCTGAAG 30
|||||
Db 1 GGAATTCGCGCGCAGATCTCAGACG 29
|||||

RESULT 17
AAAI1359
ID AAAl1359 standard; DNA; 29 BP.
XX
XX AC AAAl1359;
XX
XX DT 16-NOV-2000 (first entry)
XX
XX DE Human Myx cDNA primer #6.
XX
XX KW Human; Myx; Mad; c-myc; tumour; cancer; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN CN1248626-A.
XX
XX PD 29-MAR-2000.
XX
XX PF 09-AUG-1999; 99CN-00113968.
XX
XX PR 09-AUG-1999; 99CN-00113968.
XX
XX PA (UYFU-) UNIV FUDAN.
XX
XX PI Yu L, Fu Q, Zhao Y;
XX
XX WPI; 2000-483210/43.
XX
XX Novel human gene coding sequence, its coded polypeptide and preparation
XX process thereof.
XX
XX Example 4; Page 7; 13pp; Chinese.
XX
XX Primers AAAl1358-AAI1359 were used to PCR amplify the cDNA (AAAl1353)
XX encoding the human Myx protein (AAV93137) for subcloning into the

expression vector pcDNA3. This is used for the production and purification of the protein from Chinese Hamster Ovary (CHO) host cells. Myx is a member of the Mad family of proteins which interact with c-myc. The sequence was isolated from a lambda gt10 cDNA library. The cDNA and protein can be used for further researching action of Mad family proteins in the treatment of tumours

```
Q Sequence 29 BP; 5 A; 9 C; 9 G; 6 T; 0 U; 0 Other;
Query Match 52.7%; Score 15.8; DB 3; Length 29;
Best Local Similarity 74.1%; Pred. NO. 4.1e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

Qy 1 GGGAAATTCGGGAGGCCAGACGGCACTG 27
|||||
Db 3 GGGAAATTCATAGCCAGGCGCCGCCG 29

RESULT 18
ABZ47699/C
ID ABZ47699 standard; DNA: 41 BP.

AC ABZ47699;

DT 26-JUN-2003 (first entry)

Human ATP-binding cassette ABCC8 gene polymorphic site, #4483.

Human; drug metabolising enzyme; gene; drug metabolism; chromosome 11;
 polymorphic site; drug evaluation; drug screening; genotyping;
 genetic profiling; therapeutic customisation; adverse reaction;
 clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
 Homo sapiens.
 QS

Key	Location/Qualifiers
variation	replace(21,C)
FT	/*tag= a
FT	/standard name= "single nucleotide polymorphism (SNP)"

PN WO200252044-A2.

04-JUL-2002.

AA 27-DEC-2001: 2001WO-JP011592.

PR 27-DEC-2000; 2000JP-00399443.

PR 02-MAY-2001; 2001JP-00135256.
PR 27-AUG-2001; 2001JP-00256862.

PA (RIKE) RIKEN KK.

XX PI Nakamura Y. Seki

XX
DR
WPI: 2002-583571/62.

Identifying individuals

PT detecting at least one polymorphism in the drug metabolizing enzyme

PS Claim 23; Page 148; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide

PT Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.

PS Claim 23; Page 95; 2785pp; English.

XX Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolizing enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy

XX SQ Sequence 41 BP; 5 A; 15 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 52.7%; Score 15.8; DB 6; Length 41;
Best Local Similarity 74.1%; Pred. No. 4.3e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 AATTGCGGAGCCAGCGGCACTGAAG 30
Db 41 AACTACAGAGCCAGGCACTGCAG 15
|||||
|||||

RESULT 20
AC197483
ID AC197483 standard; DNA; 25 BP.

XX AC AC197483;

XX DT 14-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 97474.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.
PR (AFFY-) AFFYMETRIX INC.

PA Mittmann MP;

XX PI

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 97474; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 8 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 52.0%; Score 15.6; DB 9; Length 25;
Best Local Similarity 81.8%; Pred. No. 5e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGAATTGCGGAGCCAGCGGC 23
Db 2 GGAATTGCGGAACCAAGAGGCG 23
|||||
|||||

RESULT 21
ACK28325/c
ID ACK28325 standard; DNA; 25 BP.

XX AC ACK28325;

XX DT 14-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 128306.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PF 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.
 XX Mittmann MP;
 XX WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 PS Claim 1; SEQ ID NO 128306; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 52.0%; Score 15.6; DB 9; Length 25;
 Best Local Similarity 81.8%; Pred. No. 5e+03;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 2 GGAATTTCGGAGCCAGCAGGC 23
 |||||
 Db 24 GGAATTTCGGACCAAGAGGC 3
 |||||
 RESULT 22
 AAZ54975/c
 ID AAZ54975 standard; DNA; 41 BP.
 XX
 AC AAZ54975;
 XX
 DT 21-MAR-2000 (first entry)
 XX
 DE Neisseria species ORF cloning PCR primer #360.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
 KW antibacterial; gene therapy; PCR primer; ss.
 XX
 OS Synthetic.
 OS Neisseria sp.
 XX
 PN WO9957280-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US0009346.
 XX
 PR 01-MAY-1998; 98US-0083758P.
 PR 31-JUL-1998; 98US-0094869P.
 PR

PR 02-SEP-1998; 98US-0098994P.
 PR 02-SEP-1998; 98US-0099062P.
 PR 09-OCT-1998; 98US-0103749P.
 PR 09-OCT-1998; 98US-0103794P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 25-FEB-1999; 99US-0121528P.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
 PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
 PI Tettelin H, Venter JC;
 XX
 DR WPI; 2000-062150/05.
 XX
 PT Novel Neisserial polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics.
 PS Example 16; Page 150; 1453pp; English.
 XX
 CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAZ74253 to AAZ75941
 CC represent novel Neisseria meningitis and N. gonorrhoea polynucleotides
 CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to Neisserial
 CC bacteria (e.g. meningitis and septicaemia), to detect the presence of
 CC Neisseria bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols
 XX
 SQ Sequence 41 BP; 14 A; 10 C; 8 G; 9 T; 0 U; 0 Other;
 Query Match 52.0%; Score 15.6; DB 3; Length 41;
 Best Local Similarity 70.0%; Pred. No. 5.2e+03;
 Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 1 GGGAAATTCGGAGCCAGCAGCGCACTGAAG 30
 |||||
 Db 41 GGGTTTTGGCTGAACACACGCGCAATCAGG 12
 |||||
 RESULT 23
 AAA30422
 ID AAA30422 standard; DNA; 34 BP.
 XX
 AC AAA30422;
 XX
 DT 21-SEP-2000 (first entry)
 XX
 DE Single-domain VH phage PCR oligonucleotide pET-21aVH3'XhoI.
 XX
 KW Mouse; phage display; anti-inflammatory; antibody therapy;
 KW inflammatory bowel disease; rheumatoid arthritis; septic shock;
 KW multiple sclerosis; chronic inflammation; allograft rejection; panning;
 KW tumour necrosis factor alpha; TNF; CDR3;
 KW complementarity determining region; hybridoma; PCR primer; ss.
 XX
 OS Mus sp.
 XX
 PN WO200029004-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 02-NOV-1999; 99WO-IL000581.
 XX
 PR 18-NOV-1998; 98IL-00127127.
 PR
 PA (PEPT-) PEPTOR LTD.

XX Plaksin D;
XX WPI; 2000-387610/33.
XX Small functional units of antibody heavy chain variable regions useful
XX for diagnosis and treatment of disease.
XX Example 3; Page 21; 48pp; English.
XX The present sequence is an oligonucleotide designated pET-21aVH3'XhoI
XX which was used for large scale production of VH single-domain molecules.
XX A phage library was generated from a gene isolated from a mouse
XX hybridoma. Phage clones contained a random sequence coding for 9 amino
XX acids in the third hypervariable loop (CDR3). CDR3 typically makes most
XX antigen contacts in antibody combining sites. Phage clones capable of
XX binding a specific antigen, e.g. Tumour necrosis factor alpha (TNFalpha),
XX were selected by library panning. The present sequence was used to
XX reamplify plasmid DNA from positive-binding clones in order to insert
XX cloning sites for subcloning into the T7 promoter-based pET-21a
XX expression vector. Protein was expressed at high levels in BL21 cells
XX upon IPTG induction and accumulated in intracellular inclusion bodies
XX which could then be isolated and purified. Single-domain VH proteins can
XX be used to treat or diagnose disorders associated with the antigens that
XX they bind to. For example, disorders in which TNF plays a role include
XX inflammatory bowel disease, rheumatoid arthritis, septic shock, multiple
XX sclerosis, chronic inflammation and allograft rejection
XX Sequence 34 BP; 6 A; 10 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 51.3%; Score 15.4; DB 3; Length 34;
Best Local Similarity 76.0%; Pred. No. 6.3e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GGGAAATTCGGAGCGGACGCGCAC 25
Db 1 GGGAAATTCCTGAGCTATGCGGCAC 25
RESULT 24
ADN97120
ID ADN97120 standard; DNA; 24 BP.
XX ADN97120;
XX 01-JUL-2004 (first entry)
XX Primer of the invention #9.
XX Multiple drug resistance protein; MRP; Drosophila melanogaster;
XX Anopheles gambiae; insecticide; ss; primer.
XX Synthetic.
XX WO2004029088-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-EP012400.
XX 26-SEP-2002; 2002US-0413469P.
XX (INSP) INST PASTEUR.
XX (CNRS) CENT NAT RECH SCI.
XX Roth CW, Brey PT, Holm I, Graillies M, Rzhetsky A;
XX WPI; 2004-305150/28.
XX New polynucleotide sequence encoding multiple drug resistance proteins
XX from Drosophila melanogaster or Anopheles gambiae, useful in developing
XX effective insecticides.

PS Disclosure; SEQ ID NO 15; 58pp; English.
XX The present invention relates to a purified polynucleotide or its
XX fragment and comprises a sequence encoding multiple drug resistance
XX proteins (MRPs) from Drosophila melanogaster or Anopheles gambiae. The
XX polynucleotide is useful in developing effective insecticides. The
XX present sequence represents a primer of the invention.
XX Sequence 24 BP; 7 A; 4 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 12; Length 24;
Best Local Similarity 85.0%; Pred. No. 7.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GGGAAATTCGGAGCGGACGCGCAC 20
Db 1 GGGAAATTCGGGTGGAGACAGAC 20
RESULT 25
AAQ90440
ID AAQ90440 standard; DNA; 33 BP.
XX AAQ90440;
XX 02-FEB-1996 (first entry)
XX RT-PCR primer for the production of anti-idiotypic antibodies.
XX Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
XX complementarity determining region, ss.
XX Mus sp.
XX JP07101999-A.
XX 18-APR-1995.
XX 06-OCT-1993; 93JP-00272950.
XX 06-OCT-1993; 93JP-00272950.
XX (HAGI/) HAGIWARA Y.
XX WPI; 1995-182987/24.
XX Novel anti-idiotypic antibody against an human anticancer monoclonal
XX antibody - and DNA sequences encoding the antibody, useful in
XX pharmacology, medicine and biochemical fields.
XX Example 5; Page 11; 28pp; Japanese.
XX AAQ90435-Q90441 are RT-PCR primers used for the production of anti-
XX idiotypic antibody clones of Idio3, Idio17, Idio20, Idio27 and Idio33
XX against a human anticancer monoclonal antibody. These antibodies and DNA
XX encoding them are useful in pharmacological, medical and biochemical
XX fields of research
XX Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 2; Length 33;
Best Local Similarity 85.0%; Pred. No. 7.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GGGAAATTCGGAGCGGACGCGCAC 20
Db 1 GGGAAATTCATGGAGACAGAC 20
RESULT 26
AAZ44213
ID AAZ44213 standard; DNA; 33 BP.
XX

AC AA244213;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 DE Murine CD4/CD34 recognising antibody PCR primer 7.
 XX
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine; PCR primer; ss.
 XX
 OS Mus sp.
 XX
 PN WO9961629-A1.
 XX
 PD 02-DEC-1999.
 XX
 PF 24-MAY-1999; 99WO-JP002711.
 XX
 PR 25-MAY-1999; 98JP-00159957.
 PR 26-MAY-1999; 98JP-00163023.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 PA (ASAH) ASAH MEDICAL CO LTD.
 XX
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 XX
 DR WPI; 2000-086720/07.
 XX
 PT Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells.
 XX
 PS Example 2; Page 87; 11pp; Japanese.
 XX
 CC This invention describes a novel device (I) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful
 CC for the separation of CD4 or CD34 positive cells, which is useful for the
 CC collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 CC detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. AA244207-
 CC 244230 represent PCR primers used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 50.7%; Score 15.2; DB 3; Length 33;
 Best Local Similarity 85.0%; Pred. No. 7.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGGAAATTCGGAGCCAGAC 20
 DB 1 GGGAAATTCGGAGCCAGAC 20
 RESULT 27
 AA258671
 ID AA258671 standard; DNA; 33 BP.
 AC
 XX AA258671;
 XX
 DT 17-APR-2000 (first entry)
 XX
 DE Anti-CD4 antibody 4H5 constructing primer.
 KW CD4 antigen; anti-human; antibody; 4H5; drug; PCR primer; ss.
 XX
 OS Mus sp.
 XX
 PN JP11332563-A.
 XX
 PD 07-DEC-1999.
 XX

PF 26-MAY-1998; 98JP-00163034.
 XX
 PR 26-MAY-1998; 98JP-00163034.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI; 2000-091351/08.
 XX
 PT An antibody and the nucleic acid coding the antibody.
 XX
 PS Example 5; Page 9; 25pp; Japanese.
 XX
 CC The invention provides an antibody having affinity to CD4 antigen. The
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and
 CC application for drugs. It is highly safe in human dose. Sequences
 CC AA258665-688 represent PCR primers used in the course of the invention
 CC for constructing the anti-CD4 antibody 4H5
 XX
 SQ Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 50.7%; Score 15.2; DB 3; Length 33;
 Best Local Similarity 85.0%; Pred. No. 7.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGGAAATTCGGAGCCAGAC 20
 DB 1 GGGAAATTCGGAGCCAGAC 20
 RESULT 28
 AAA39128
 ID AAA39128 standard; DNA; 33 BP.
 XX
 AC AAA39128;
 XX
 DT 05-SEP-2000 (first entry)
 XX
 DE Murine monoclonal antibody 1F7 light chain PCR primer SEQ ID NO:3.
 XX
 KW 1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;
 KW AIDS; anti-HIV; human immunodeficiency virus; detection;
 KW acquired immunodeficiency syndrome; PCR primer; ss.
 XX
 OS Mus sp.
 XX
 PN US6057421-A.
 XX
 PD 02-MAY-2000.
 XX
 PF 03-DEC-1997; 97US-00984277.
 XX
 PR 30-NOV-1994; 94US-00351193.
 XX
 PA (IMMP-) IMMPPERON INC.
 XX
 PI Muller S, Kohler H;
 XX
 DR WPI; 2000-338622/29.
 XX
 PT Variable heavy and light chain regions of murine monoclonal antibody 1F7,
 XX useful for treating HIV infection and AIDS.
 PS Disclosure; Col 5; 45pp; English.
 XX
 CC The present invention describes the variable heavy and light chain
 CC regions (I) of murine monoclonal antibody (mAb) 1F7. AA91014 to AA91016
 CC represent specifically claimed amino acid sequences of the variable light
 CC chain, and AA91017 to AA91019 represent specifically claimed amino acid
 CC sequence of the variable heavy chain. The antibodies are used for
 CC treatment of HIV (human immunodeficiency virus) infection and AIDS
 CC (acquired immunodeficiency syndrome). They are also used for detecting
 CC HIV in serum and for stimulating HIV antigen related and committed B
 CC cells to produce broadly reactive and neutralising antibodies by

CC clonotypic stimulation. The present sequence represents a PCR primer used
 CC in the amplification of the murine monoclonal antibody 1F7

XX Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
 SQ Query Match 50.7%; Score 15.2; DB 3; Length 33;
 Best Local Similarity 85.0%; Pred. No. 7.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGAC 20
 ||||| |||||
 Db 1 GGGAAATTCATGGAGACAGAC 20

RESULT 29

AAH41120
 ID AAH41120 standard; DNA; 33 BP.

AC AAH41120;

XX 17-AUG-2001 (first entry)

DE Murine immunoglobulin, IgkappaVL-B, PCR primer.

XX Murine; immunoglobulin E; monoclonal antibody; IGE; PCR primer; ss.

XX Mus musculus.

XX JP2001074737-A.

XX 23-MAR-2001.

XX 03-SEP-1999; 99JP-00249805.

XX 03-SEP-1999; 99JP-00249805.

XX (ASAK) ASAHI BREWERIES LTD.

XX WPI; 2001-311336/33.

XX Anti-human IGE monoclonal antibody.

XX Example 6; Page 6; 13pp; Japanese.

XX The present invention relates to anti-human immunoglobulin E (IGE)
 CC monoclonal antibody selected the monoclonal antibodies 4D3, 1A7, 3E8,
 CC 4D10, and 11D10, which combine specifically to human IGE. The monoclonal
 CC antibody can be used for the detection of human IGE. The present sequence
 CC was used in an example from the present invention

XX Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 5; Length 33;
 Best Local Similarity 85.0%; Pred. No. 7.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGAC 20
 ||||| |||||
 Db 1 GGGAAATTCATGGAGACAGAC 20

RESULT 30

AAL48649
 ID AAL48649 standard; DNA; 33 BP.

AC AAL48649;

XX 11-OCT-2002 (first entry)

XX Murine Mab 1F7 light chain PCR primer #1.

DE Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
 XX complementarity determining region; framework-determining region; FR;

KW heavy chain; light chain; HIV infection; PCR; primer; ss.

XX Mus sp.

XX WO200255668-A2.

XX 18-JUL-2002.

XX 11-JAN-2002; 2002WO-US000927.

XX 11-JAN-2001; 2001US-00759112.

XX (IMMP-) IMPHERON INC.

XX Muller S, Kohler H;

XX WPI; 2002-590668/63.

XX New polynucleotide encoding a complementarity- or framework-determining
 PT region of an anti-idiotypic antibody that binds to human or primate anti-
 PT human immunodeficiency virus (HIV) antibodies, for use in vaccines
 PT against HIV.

XX Example; Page 16; 27pp; English.

XX The present invention relates to coding sequences of the murine 1F7 anti-
 CC idiotypic antibody complementarity-determining region (CDR) or framework-
 CC determining region (FR). The antibody binds to human or primate anti-
 CC human immunodeficiency virus (HIV) antibodies and can be used in the
 CC treatment of HIV infection. The present sequence is a PCR primer used to
 CC isolate a 1F7 coding sequence

XX Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 6; Length 33;
 Best Local Similarity 85.0%; Pred. No. 7.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGAC 20

||||| |||||
 Db 1 GGGAAATTCATGGAGACAGAC 20

RESULT 31

AAZ96102

ID AAZ96102 standard; DNA; 40 BP.

XX AAZ96102;

XX 10-APR-2000 (first entry)

XX Polynucleotide sequence including binding site for BamHI.

DE Ligand binding; restriction enzyme; nucleic acid determination;
 KW pharmaceutical; BamHI; ss.

XX Synthetic.

XX WO9963077-A2.

XX 09-DEC-1999.

XX 04-JUN-1999; 99WO-US012516.

XX 04-JUN-1998; 98US-0087905P.

XX 03-JUN-1999; 99US-00324672.

XX (TWTE-) TM TECHNOLOGIES INC.

XX Lane MJ, Benight AS, Faldasz BD;

XX WPI; 2000-116369/10.

PT Modulating polynucleotide ligand binding site affinity using
PT determination of the flanking duplex sequences.

PS Example 1; Page 44; 62pp; English.

XX
XX
XX The invention provides a method for determining the sequence of
CC polynucleotide flanking regions that modulate ligand binding
CC characteristics of an adjacent binding site. The method comprises: (i)
CC providing a number of different duplex polynucleotides, each having the
CC same polynucleotide ligand binding site and a randomly synthesized
CC sequence flanking the binding site; (ii) exposing the duplex to a ligand
CC selective for the binding site; (iii) isolating duplexes which bind or do
CC not bind the ligand, and (iv) determining the nucleotide composition of
CC the flanking duplex sequence by sequencing the duplex sequence adjacent
CC to the binding site. The invention is used to modulate the ligand-binding
CC characteristics of any nucleotide sequence. The invention is less costly
CC and more efficient than prior art techniques that moderate ligand binding
CC using small molecule pharmaceuticals. Sequences AA295762-296170 represent
CC polynucleotide sequences including the binding site for the restriction
CC enzyme BamHI and used in the course of the invention

XX Sequence 40 BP; 8 A; 3 C; 21 G; 8 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 3; Length 40;

Best Local Similarity 71.4%; Pred. No. 7.8e+03;

Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GAATTCGGGAGCCAGCGGCTGAG 30

DB 13 GAAGCGAGGAGGTAGCGGTCTGAGG 40

RESULT 32

ADS18341

ID ADS18341 standard; DNA; 28 BP.

XX ADS18341;

XX 02-DEC-2004 (first entry)

XX Murine TREM-like DNA specific RT-PCR primer, TREM 2 #2.

XX TREM; triggering receptor expressed on myeloid cell; TLT-1;
KW TREM-like transcript-1; septic shock; cancer; infectious disease; stroke;
KW heart disease; myocardial infarction; arteriosclerosis;
KW clotting disorder; bleeding disorder; platelet insufficiency;
KW TLT-1 associated disorder; gene therapy; antibacterial;
KW immunosuppressive; cytostatic; antimicrobial; cerebroprotective;
KW vasotropic; cardiant; antiarteriosclerotic; haemostatic; murine; RT-PCR;
KW reverse transcription; primer; ss.

XX Mus musculus.

XX US2004180409-A1.

XX 16-SEP-2004.

XX 16-MAR-2004; 2004US-00802441.

XX 16-MAR-2003; 2003US-0455370P.

XX (MCVI/) MCVICAR D.

PA (WASH/) WASHINGTON A V.

PA (QUIG/) QUIGLEY L.

XX MCVicar D, Washington AV, Quigley L;

XX WPI; 2004-661507/64.

XX New TREM-like transcript-1 nucleic acid molecules, useful for preventing
PT and treating a disorder, e.g. septic shock, cancer, infectious disease,
PT stroke, heart disease, arteriosclerosis, or bleeding disorders.

PS Example; SEQ ID NO 10; 71pp; English.

XX
XX The present invention relates to a triggering receptor expressed on
CC myeloid cell (TREM)-like transcript-1 (TLT-1) polypeptides and the
CC encoding polynucleotides, where the TLT-1 polypeptide can modulate
CC platelet function. The invention is useful for preventing, diagnosing and
CC treating a disorder, e.g. septic shock, cancer, infectious disease,
CC stroke, heart disease, myocardial infarction, arteriosclerosis, clotting
CC disorders, bleeding disorders, platelet insufficiency or a TLT-1
CC associated disorder. The invention is also useful in gene therapy. The
CC present sequence is the murine TREM DNA specific reverse transcription
CC (RT)-PCR primer. This sequence is used in the exemplification of the
CC invention.

SQ Sequence 28 BP; 6 A; 7 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 50.0%; Score 15; DB 13; Length 28;

Best Local Similarity 78.3%; Pred. No. 9.2e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 CGCGGAGCCAGCGGCTGAG 30

DB 1 CGCGGATCTGACTGGACTTAAG 23

RESULT 33

ABA03393

ID ABA03393 standard; DNA; 29 BP.

XX ABA03393;

XX 12-FEB-2002 (first entry)

XX Sindbis virus nonstructural protein gene PCR primer nsP3P.

XX Alphavirus-based vector; nonstructural protein 2; nsP2; replicon;
KW eukaryotic layered initiation system; noncytopathic; gene therapy;
KW persistent replication; recombinant protein expression; gene delivery;
KW PCR primer; ss.

XX Sindbis virus.

XX WO200181553-A1.

XX 01-NOV-2001.

XX 25-APR-2001; 2001WO-US013255.

XX 25-APR-2000; 2000US-0199579P.

XX (CHIR) CHIRON CORP.

XX Dubensky TW, Polo JM, Perri S, Belli BA;

XX WPI; 2002-049274/06.

XX New nucleic acid having altered alphavirus nonstructural protein 2 gene
PT which when operably incorporated into alphavirus replicon particle has
PT noncytopathic phenotype and persistently replicates in mammalian cell.

XX Example 2; Page 24; 64pp; English.

XX The present invention relates to an isolated nucleic acid having an
CC altered alphavirus (AV) nonstructural protein 2 (nsP2) gene which when
CC incorporated into an AV replicon particle (ARP) has a reduced level of
CC vector-specific RNA synthesis, increases the time required to reach 50%
CC inhibition of host cell-directed macromolecular synthesis when expressed
CC in mammalian cells and persistently replicates when introduced into
CC mammalian cells, as compared to wild-type ARP. The sequence can be used
CC to deliver a selected heterologous sequence to a vertebrate or insect
CC cell, where it can produce AV replicon particles and make a desired
CC protein, for example erythropoietin, basic fibroblast growth factor,
CC factor VIII, vascular endothelial growth factor and tissue plasminogen

CC activator (tPA). The recombinant AV vectors are useful for directing the
 CC expression of one or more heterologous gene products in the absence of
 CC vector induced cytopathology. The present sequence is a PCR primer used
 CC in the construction of a vector containing the Sindbis virus nsp2 gene

SQ Sequence 29 BP; 7 A; 10 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 50.0%; Score 15; DB 6; Length 29;
 Best Local Similarity 78.3%; Pred. No. 9.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGCGAGCCAGCGGCAC 25
 |||||
 Db 6 GAATTCGGCGGTATACCGCAC 28
 |||||

RESULT 34

AAT35896
 ID AAT35896 standard; DNA; 31 BP.

AC AAT35896;

DT 18-MAR-1997 (first entry)

DE Marek disease virus PCR primer MB048.

XX HVT; turkey herpes virus; THV; UL41; Marek disease virus; MDV RNA1.8;
 KW promoter; live avian vaccine; Gumboro disease; PCR primer;
 KW polymerase chain reaction; infectious bursal disease virus; IBDV; ss.

OS Synthetic.

XX WO9621034-A1.

PN 11-JUL-1996.

PD 29-DEC-1995; 95WO-FR001763.

PF 30-DEC-1994; 94FR-00016016.

PR (INNR) RHONE MERIEUX SA.

PI Audonnet J, Bublot MJM, Darteil R, Duinat CV, Laplace ELF;
 PI Riviere MA;

XX WPI; 1996-334009/33.

DR Live avian vaccine based on Marek disease virus - has sequence encoding
 PT antigenic polypeptide inserted into the UL13 gene.

XX Example 11; Page 22; 75pp; French.

XX Primers MB047 and MB048 (see AAT35895 and AAT35896) were used in a PCR to
 CC amplify a 163 bp fragment from DNA extracted from lymphocytes harvested
 CC from chickens infected by Marek disease virus (MDV) strain RB1B. The PCR
 CC product was subsequently used in the construction of a plasmid in which a
 CC VP2/MCMV-IE/RNA 1.8 kb/MDV GB double cassette was inserted into the UL41
 CC site of herpesvirus of turkeys. The final construct was useful as a viral
 CC vaccine to protect poultry against MDV

SQ Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 15; DB 2; Length 31;
 Best Local Similarity 78.3%; Pred. No. 9.3e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGCGAGCCAGCGGCAC 25
 |||||
 Db 6 GAATTCGGAAGAGAGAGGAAC 28
 |||||

RESULT 35

AAT39333

ID AAT39333 standard; DNA; 31 BP.

XX AAT39333;

XX 25-MAR-2003 (revised)

DT 21-APR-1997 (first entry)

XX Marek's disease virus 1.8 kb RNA gene upstream sequence primer MB048.

DE Herpes virus of turkey; open reading frame; ORF; homology; vector;
 XX avian herpes virus; recombinant viral vaccine; intergenic region; IBDV;
 KW cytomegalovirus immediate early promoter; UL55 gene; repeat region; ILTV;
 KW antigen; infectious bursal disease virus; Marek's disease virus; MDV;
 KW infectious laryngotracheitis virus; avian anaemia virus; vaccination;
 KW infectious bronchitis virus; IBV; poultry; Gumboro disease;
 KW Newcastle disease; ss.

OS Synthetic.

XX EP719864-A2.

XX 03-JUL-1996.

PD 28-DEC-1995; 95EP-00402970.

PF 30-DEC-1994; 94FR-00016017.

PR (INNR) RHONE MERIEUX SA.

PI Audonnet J, Bublot MJM, Darteil RJ, Duinat CV, Laplace ELF;
 PI Riviere MAE;

XX WPI; 1996-364150/37.

DR Live recombinant avian vaccine - comprises herpes virus as vector and
 PT having sequence encoding antigenic polypeptide inserted between UL55 gene
 PT and repeat region.

XX Example 13; Col 15; 50pp; French.

XX The invention relates to the generation of live recombinant avian
 CC vaccines using an avian herpes virus as the vector, esp. using the BamHI
 CC I fragment of herpes virus of turkeys (AAT39309). The fragment contains 6
 CC open reading frames (ORF) and 3 intergenic regions. The ORFs encode
 CC proteins having homology to other avian herpes viruses. The recombinant
 CC vectors are generated by inserting genes encoding proteins of interest
 CC into the intergenic regions of BamHI fragment. Pref. the inserted
 CC sequence is ligated between the ATG of the UL55 gene (ORF-6 of AAT39309)
 CC and the junction of UL with the adjacent repeat region. The primers
 CC AAT39332-3 were used to amplify a 163 bp fragment of the upstream region
 CC from the Marek's disease virus (MDV) 1.8 kb RNA gene which contains a
 CC promoter sequence. The template for the amplification was DNA extracted
 CC from chickens infected with MDV strain RB1B. The amplified fragment was
 CC placed in inverse orientation to the cytomegalovirus immediate early (CMV
 CC -IE) promoter in the plasmid pCD002 to generate plasmid pBS002. The
 CC double promoter sequence was then used to generate the plasmid pEL095
 CC which contains the VP2 gene from the infectious bursal disease virus
 CC (IBDV) under control of the CMV-IE promoter and the MDV GB gene under
 CC control of the MDV promoter, all inserted into the herpes virus of
 CC turkeys intergenic region 1 in plasmid pEL079 (see AAT39310-4) to produce
 CC plasmid pEL095. The recombinant vectors can be used to express proteins
 CC for vaccinating poultry against Gumboro disease (caused by IBDV),
 CC Newcastle disease, Marek's disease, infectious bronchitis, infectious
 CC laryngotracheitis and avian anaemia. (Updated on 25-MAR-2003 to correct
 CC PI field.)

SQ Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 15; DB 2; Length 31;
 Best Local Similarity 78.3%; Pred. No. 9.3e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGCGAGCCAGCGGCAC 25

```

Db      6 GAATTCGCGAAGAGAGAGGAAC 28
|||||
RESULT 36
AAT35930
ID      AAT35930 standard; DNA; 31 BP.
XX
AC      AAT35930;
XX
DT      25-MAR-2003 (revised)
DT      03-MAR-1997 (first entry)
XX
DE      Marek disease virus PCR primer MB048.
XX
KW      HVT; turkey herpes virus; THV; UL43; Marek disease virus; MDV RNA1.8;
KW      promoter; live avian vaccine; Gumboro disease; PCR primer;
KW      polymerase chain reaction; infectious bursal disease virus; IBDV; ss.
XX
OS      Synthetic.
XX
PN      FR2728794-A1.
XX
PD      05-JUL-1996.
XX
PF      30-DEC-1994; 94FR-00016015.
XX
PR      30-DEC-1994; 94FR-00016015.
XX
PA      (INNER) RHONE MERIEUX SA.
XX
PI      Audonnet JC, Bublot MJM, Dartell R, Duinat CV, Laplace ELF;
PI      Riviere MEA;
XX
DR      WPI; 1996-335824/34.
XX
PT      Live recombinant avian vaccine based on herpes virus - with sequence
PT      encoding antigenic polypeptide inserted into the UL43 gene, esp. for
PT      protection against Gumboro disease.
XX
PS      Example 11; Page 22; 67pp; French.
XX
PR      Primers MB047 and MB048 (see AAT35929 and AAT35930) were used in a PCR to
CC      amplify a 163 bp fragment from DNA extracted from lymphocytes harvested
CC      from chickens infected by Marek disease virus (MDV) strain R81B. The PCR
CC      product was subsequently used in the construction of a plasmid in which a
CC      VP2/MCMV-IE/RNA 1.8 Kb/MDV GB double cassette was inserted into the UL43
CC      site of herpesvirus of turkeys. The final construct was useful as a viral
CC      vaccine to protect poultry against MDV. (Updated on 25-MAR-2003 to
CC      correct PI field.)
XX
SQ      Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

Query Match      50.0%; Score 15; DB 2; Length 31;
Best Local Similarity 78.3%; Pred. No. 9.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GAATTCGCGAGCCGAGCGGCAC 25
        |||||
DB      6 GAATTCGCGAAGAGAGAGGAAC 28

RESULT 37
ADM41163
ID      ADM41163 standard; DNA; 31 BP.
XX
AC      ADM41163;
XX
DT      17-JUN-2004 (first entry)
XX
DE      PCR primer MB048 used to produce plasmid pBS002.
XX
KW      avian vaccine; avian pathogen; BamHI fragment; vaccine; Gumboro;

```

```

KW      infectious bursal; Marek disease; Newcastle disease;
KW      infectious bronchitis; infectious laryngotracheitis; avian anaemia; ss;
KW      THV; PCR; primer.
XX
OS      Synthetic.
XX
PN      EP1403375-A2.
XX
PD      31-MAR-2004.
XX
PF      28-DEC-1995; 2003EP-00025194.
XX
PR      30-DEC-1994; 94FR-00016017.
PR      28-DEC-1995; 95EP-00402970.
XX
PA      (MERI-) MERIAL.
XX
PI      Audonnet J, Bublot M, Dartell R, Duinat C, Laplace E, Riviere M;
XX
DR      WPI; 2004-271923/26.
XX
PT      Use of a recombinant turkey herpes virus (HVT) with an antigen-coding
PT      sequence inserted into an intergene region, to prepare vaccines for
PT      preventing e.g. Marek or Gumboro disease in poultry.
XX
PS      Example 13; Page 11; 63pp; French.
XX
CC      The specification describes the use of a recombinant turkey herpes virus
CC      (THV) for production of live, recombinant avian vaccines, intended for
CC      vaccination in ovo, of day-old chicks, or of adults to protect against an
CC      avian pathogen. The recombinant THV includes at least one nucleic acid
CC      that encodes and expresses an antigen of the avian pathogen, inserted
CC      into intergene region 1, 2 or 3 of the BamHI fragment of the THV genome.
CC      The nucleic acid especially encodes the VP2, VP3 or a combination of VP2,
CC      3 and 4, from infectious bursal disease (Gumboro disease) virus; GB, GC,
CC      GD or GH plus GL of Marek disease or infectious laryngotracheitis viruses
CC      ; F or NH of Newcastle disease virus; S or M of infectious bronchitis
CC      virus; or VPI (52 kD) or VP2 (24 kD) of avian anaemia virus. The nucleic
CC      acid is inserted under control of the cytomegalovirus immediate-early
CC      (CMV-IE) promoter (human or murine), or the Marek RNA1.8 promoter
CC      (especially used in combination with CMV-IE for increased levels of
CC      expression). The recombinant viruses of the invention are used to
CC      vaccinate chickens against one or more of the viruses that cause Gumboro
CC      (infectious bursal), Marek or Newcastle diseases, infectious bronchitis,
CC      infectious laryngotracheitis or avian anaemia. PCR primers ADM41162-
CC      ADM41163 were used to produce plasmid pBS002, comprising the Marek RNA1.8
CC      promoter.
XX
SQ      Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

Query Match      50.0%; Score 15; DB 12; Length 31;
Best Local Similarity 78.3%; Pred. No. 9.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GAATTCGCGAGCCGAGCGGCAC 25
        |||||
DB      6 GAATTCGCGAAGAGAGAGGAAC 28

RESULT 38
ADR13841
ID      ADR13841 standard; DNA; 45 BP.
XX
AC      ADR13841;
XX
DT      21-OCT-2004 (first entry)
XX
DE      Human hereditary Haemochromatosis (HFE) gene Flanking probe HC63-2.
XX
KW      HFE; hereditary haemochromatosis; human; ss; probe; genetic polymorphism;
KW      single nucleotide polymorphism; SNP.
XX
OS      Homo sapiens.

```

OS Synthetic.

XX Key Location/Qualifiers

FT misc_binding 1. .3

FT /*tag= a

FT /bound_moiety= "Nucleotides 24-22 of SEQ ID 15"

FT /note

FT modified_base 2

FT /*tag= b

FT /mod_base= OTHER

FT /note= "Non-nucleosidic cross-linking moiety"

FT modified_base 14

FT /*tag= c

FT /mod_base= OTHER

FT /note= "Non-nucleosidic cross-linking moiety"

FT misc_binding 43. .45

FT /*tag= d

FT /bound_moiety= "Nucleotides 3-1 of SEQ ID 15"

FT /note

FT modified_base 44

FT /*tag= e

FT /mod_base= OTHER

FT /note= "Non-nucleosidic cross-linking moiety"

XX US2004152118-A1.

XX 05-AUG-2004.

XX 27-JAN-2004; 2004US-00766266.

XX 29-JAN-2003; 2003US-0443820P.

XX (VATT//) VAN ATTA R B.

XX (WOOD//) WOOD M L.

XX Van Atta RB, Wood ML;

XX WPI; 2004-592583/57.

DR Probe set useful for detecting genetic polymorphism in target nucleic

XX acid suspected of containing polymorphism, comprises first flanking

FT probe, capture probe and second flanking probe.

XX Claim 16; SEQ ID NO 17; 31pp; English.

XX The invention relates to a probe set for detecting genetic polymorphisms

CC in target nucleic acids suspected of containing the polymorphisms,

CC comprising a first flanking probe comprising a sequence complementary to

CC a first portion of the nucleic acid sequence, a capture probe comprising

CC a sequence complementary to a second portion of the nucleic acid sequence

CC (the second portion comprising the location of the polymorphism, and

CC being adjacent to the first portion) and a second flanking probe

CC comprising sequence complementary to a third portion of target nucleic

CC acid sequence. The probes further comprise stem regions at the 3' and

CC 5' ends which can form non-covalent bonds with the stem regions of

CC adjacent probes and contain a photoactivatable cross-linking agent. Also

CC included is detecting a genetic polymorphism in a nucleic acid sequence

CC of a target nucleic acid suspected of containing the polymorphism,

CC comprising combining, in a hybridising medium, a nucleic acid sample

CC having the target and several probes, where several probes comprises the

CC probe set above, and comparing the degree of hybridisation of the capture

CC probe to the sequence portion containing the polymorphism to the

CC hybridisation of a capture probe to the target sequence lacking the

CC polymorphism, where the polymorphism is determined. The probe set

CC comprises an additional capture probe which is complementary to the

CC normal nucleic acid sequence of the second portion lacking the

CC polymorphism and a reporter moiety comprising a detectable label. The

CC probe is useful for detecting a genetic polymorphism in a nucleic acid

CC sequence of a target nucleic acid suspected of containing the

CC polymorphism, such as a single nucleotide polymorphism, a point mutation

CC (G1691A) in the Factor V gene, and a point mutation (C187G) or (G845A) in

CC the HFE gene (hereditary haemochromatosis). The probe set diminishes the

CC constraints imposed upon capture probe design, alleviates the need for

CC

CC the cross-linking site near the single nucleotide polymorphism (SNP) site

CC in the target sequence, provides more sites for introducing detectable

CC labels, and permits cross-linking in the stem to include reactions

CC between pairs of unnatural nucleotide analogues, thus expanding the

CC available option from which to select an appropriate choice of reactants.

CC The probe set enables detection of a genetic polymorphism with increased

CC sensitivity and improved data reliability and allows for high-stringency

CC washes of the hybridised probe-target complexes, which significantly

CC lower background contamination levels and result in improvements in the

CC signal-to-noise ratio. The present sequence is a flanking probe for a

CC probe set of the invention.

XX

SQ Sequence 45 BP; 11 A; 12 C; 11 G; 8 T; 0 U; 3 Other;

Query Match 50.0%; Score 15; DB 13; Length 45;

Best Local Similarity 78.3%; Pred. No. 9.6e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGAAATTCGGGAGCCACACGGCA 24

Db 21 GGAGTTCGGGGCTCCACACGGCA 43

RESULT 39

AAT62767

ID AAT62767 standard; DNA; 27 BP.

XX AC AAT62767;

XX 03-JUN-1997 (first entry)

XX Human bax gene forward primer.

DE p53 responsive element; p53-REU; bax gene; apoptosis; cell death; stroke;

XX cancer; tumour suppressor; polymerase chain reaction; PCR; primer; ss.

OS Synthetic.

XX WO9519367-A1.

XX 20-JUL-1995.

XX 12-JAN-1995; 95WO-US0000710.

XX 14-JAN-1994; 94US-00182619.

XX 27-OCT-1994; 94US-00330535.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Reed JC, Miyashita T, Harigai M, Hanada M;

XX WPI; 1995-263824/34.

XX p53 responsive element(s) for down-regulation of bcl-2 gene and up-

FT regulation of bax gene - and identification of agent(s) useful to

XX modulate cell death, e.g. cancer or stroke.

XX Example ID; Page 24; 69pp; English.

XX A forward primer (AAT62767) including an EcoRI linker sequence and a

CC reverse primer (AAT62768) were used to amplify the entire open reading

CC frame of bax cDNA using RT-PCR. The PCR product was used as a bax-

CC specific hybridisation probe to detect Bax mRNA levels in murine myeloid

CC leukaemia M1 cells following transfection with a plasmid encoding a temp.

CC sensitive p53 tumour suppressor. The results indicated that p53 tumour

CC suppressor increases the expression of Bax mRNA. A p53 responsive

CC element, p53-REU, has been identified in the human bax promoter (see also

CC AAT62760)

XX

SQ Sequence 27 BP; 4 A; 5 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 49.3%; Score 14.8; DB 2; Length 27;

Best Local Similarity 73.1%; Pred. No. 1.1e+04;

Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGAATTTCGGCGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTTCGGCGGAGCCAGCGGTCG 26

RESULT 40

AAT03167

ID AAT03167 standard; DNA; 27 BP.

XX

AC AAT03167;

XX 05-JUN-1996 (first entry)

XX

XX Human Bax gene forward PCR primer.

XX

XX Mcl-1; Bax; apoptosis; cell death; regulation; Bcl-2; novel; detection;

KW ss.

XX

XX Synthetic.

XX

XX WO9528497-A1.

XX

XX 26-OCT-1995.

XX

XX 12-APR-1995; 95WO-US004600.

XX

XX 13-APR-1994; 94US-00226876.

XX

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX

XX Reed JC, Sato T;

XX

XX WPI; 1995-373811/48.

XX

XX Detection of novel proteins involved in apoptosis - by interaction with

PT proteins involved in apoptosis.

XX

XX Example 1; Page 23; 62pp; English.

XX

XX AAT03167 and AAT03168 are primers used for the amplification of the human

CC Bax gene. The Bax gene is used in a new method for identifying novel

CC proteins involved in apoptosis. The method involves contacting a suspect

CC protein with a protein known to be involved in apoptosis (excluding the

CC Bax protein). Proteins detected using this method can act as upstream

CC activators or downstream effectors of a cellular protein such as Bax

CC which induces apoptosis. If the protein is a Bcl-2 related protein

CC apoptosis levels are decreased due to the protein binding to and

CC inactivating Bax

XX

SQ Sequence 27 BP; 4 A; 5 C; 13 G; 5 T; 0 U; 0 Other;

XX

Query Match 49.3%; Score 14.8; DB 2; Length 27;

Best Local Similarity 73.1%; Pred. No. 1.1e+04;

Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGAATTTCGGCGGAGCCAGCGGCACTG 27

Db 1 GGAATTTCGGCGGAGCCAGCGGTCG 26

Search completed: November 18, 2005, 11:52:31

Job time : 209.578 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1434.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-7

Perfect score: 30

Sequence: 1 GGGAAATCGCGAGCCAGACGCACTGAAG 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	52.0	36	AZ788496	AZ788496 2M0035E09
2	15.6	52.0	40	AZ597065	AZ597065 1M0410N10
3	15.6	52.0	50	AU104279	AU104279 AU104279
4	14.8	49.3	50	AU108041	AU108041 AU108041
5	14.8	49.3	50	AU108042	AU108042 AU108042
6	14.8	49.3	50	AU108043	AU108043 AU108043
7	14.8	49.3	50	AU108044	AU108044 AU108044
8	14	46.7	40	AZ887629	AZ887629 NG96b05.8
9	14	46.7	48	AZ601433	AZ601433 1M0419N11
10	13.8	46.0	41	H84363	H84363 YH85C09.s1
11	13.6	45.3	26	AZ949204	AZ949204 2M0212M04
12	13.6	45.3	50	AA643428	AA643428 nu31c03.s
13	13.6	45.3	50	CR230947	CR230947 Reverse.s
14	13.4	44.7	48	C01535	C01535 HUMGS000853
15	13.4	44.7	50	AU102737	AU102737 AU102737
16	13.2	44.0	30	AJ668097	AJ668097 AJ668097
17	13.2	44.0	34	BQ594733	BQ594733 E012441-0
18	13.2	44.0	34	BZ764154	BZ764154 SALK 1240
19	13.2	44.0	34	BZ764155	BZ764155 SALK 1240
20	13.2	44.0	40	BQ032379	BQ032379 602301364
21	13.2	44.0	41	CG2426236	CG2426236 01S0576-0
22	13.2	44.0	42	HA275866	HA275866 Homo sapi
23	13.2	44.0	43	AA074398	AA074398 zml6f07.s
24	13.2	44.0	45	BI556158	BI556158 603237933

25	13.2	44.0	50	1	AU107457	AU107457 AU107457
AZ788496	13.2	44.0	50	1	AU108040	AU108040 AU108040
LOCUS	13.2	44.0	50	8	AZ666536	AZ666536 1M0548D16
DEFINITION	13.2	44.0	36	1	AA776443	AA776443 zj50h10.s
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VERSION	13	43.3	46	9	BX230810	BX230810 Danilo rer
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REFERENCE	13	43.3	50	1	AU106592	AU106592 AU106592
AUTHORS	13	43.3	50	1	AU106928	AU106928 AU106928
TITLE	13	43.3	50	9	CG894749	CG894749 O3S4734-0
JOURNAL	12.8	42.7	33	1	AI042471	AI042471 OY14d01.x
COMMENT	12.8	42.7	38	4	BI547045	BI547045 603190269
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	12.8	42.7	41	9	TA90803Q	TA90803Q
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	12.8	42.7	50	4	BG975240	BG975240 602843146
	12.8	42.7	50	8	BH910136	BH910136 SALK 0579
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ALIGNMENTS

AZ788496 36 bp DNA linear GSS 16-FEB-2001
2M0035E09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0035E09 R, genomic survey sequence.

AZ788496 GI:12928357

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 36)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0035 row: E column: 09

Seq primer: CACACAGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 36.

Location/Qualifiers

1. 36

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0035E09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 15.6; DB 8; Length 36;
Best Local Similarity 70.0%; Pred. No. 5.8e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGAATTCGGAGCCAGCGCACTGAAG 30
||||| ||||| ||||| ||||| |||||
Db 5 GAGAATTGGCGGACCAAGGACATGAAG 34

RESULT 2

AZ597065

LOCUS

1M0410N10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0410N10 R, genomic survey sequence.

ACCESSION

AZ597065

VERSION

AZ597065.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 40)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0410 row: N column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 40.

Location/Qualifiers

1..40

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0410N10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 15.6; DB 8; Length 40;
Best Local Similarity 70.0%; Pred. No. 5.8e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGAATTCGGAGCCAGCGCACTGAAG 30
||||| ||||| ||||| ||||| |||||
Db 3 GCGAATTCAGTAACCCACGGCTAGGGAG 32

RESULT 3

AU104279/c

LOCUS

AU104279 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HBP20593, mRNA sequence.

ACCESSION

AU104279

VERSION

AU104279.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

Contact: Yutaka Suzuki

Department of Virology

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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yezuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="HEP20593"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 52.0%; Score 15.6; DB 1; Length 50;
Best Local Similarity 81.8%; Pred. No. 5.9e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 GCGGAGCCAGCGCACTGAAG 30
||||| ||||| ||||| ||||| |||||
Db 43 GCGGAGCCGAGGGCAGCTAAG 22

RESULT 4
 AUI08041
 LOCUS AUI08041 50 bp mRNA linear EST 28-JAN-2004
 DEFINITION AUI08041 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 ZRV61366, mRNA sequence.

ACCESSION AUI08041
 VERSION AUI08041
 KEYWORDS EST.
 SOURCE AUI08041.1 GI:13557563

ORGANISM Homo sapiens (human)
 Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072
 PUBMED 11375929

COMMENT Contact: Yutaka Suzuki
 Department of Virology
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 Email: yuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES Location/Qualifiers

source
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ZRV61366"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 49.3%; Score 14.8; DB 1; Length 50;
 Best Local Similarity 88.9%; Pred. No. 1.3e+05;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCGGAGCCAGCGGCCT 26

DB 9 GCGGAGTCAGACGGCGCT 26

RESULT 5

AUI08042
 LOCUS AUI08042 50 bp mRNA linear EST 28-JAN-2004
 DEFINITION AUI08042 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 ZRV61783, mRNA sequence.

ACCESSION AUI08042
 VERSION AUI08042
 KEYWORDS EST.
 SOURCE AUI08042.1 GI:13557564

ORGANISM Homo sapiens (human)
 Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072
 PUBMED 11375929

COMMENT Contact: Yutaka Suzuki
 Department of Virology
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 Email: yuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES Location/Qualifiers

source
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ZRV61783"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 49.3%; Score 14.8; DB 1; Length 50;
 Best Local Similarity 88.9%; Pred. No. 1.3e+05;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCGGAGCCAGCGGCCT 26

DB 9 GCGGAGTCAGACGGCGCT 26

RESULT 6

AUI08043
 LOCUS AUI08043 50 bp mRNA linear EST 28-JAN-2004
 DEFINITION AUI08043 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 ZRV62110, mRNA sequence.

ACCESSION AUI08043

VERSION AUI08043
 KEYWORDS EST.
 SOURCE AUI08043.1 GI:13557565

ORGANISM Homo sapiens (human)
 Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072
 PUBMED 11375929

COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES Location/Qualifiers

source
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ZRV62110"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 49.3%; Score 14.8; DB 1; Length 50;
 Best Local Similarity 88.9%; Pred. No. 1.3e+05;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCGGAGCCAGCGGCCT 26

DB 11 GCGGAGTCAGACGGCGCT 28

RESULT 7

```

AUI08044
LOCUS       AUI08044               50 bp    mRNA    linear    EST 28-JAN-2004
DEFINITION  AUI08044 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ZRV6CS16, mRNA sequence.
ACCESSION   AUI08044
VERSION     AUI08044.1  GI:13557566
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (bases 1 to 50)
            Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
  JOURNAL   21270072
  MEDLINE   11375929
  PUBMED    11375929
  COMMENT   Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ZRV6CS16"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      49.3%; Score 14.8; DB 1; Length 50;
Best Local Similarity 88.9%; Pred. No. 1.3e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9  GCGGAGCCAGACGGCACT 26
Db      11 GCGGAGTCAGACGGCGCT 28

RESULT 8
AA887629/c
LOCUS       AA887629               40 bp    mRNA    linear    EST 07-APR-1998
DEFINITION  nq36b05.61 NCI CGAP Col10 Homo sapiens cDNA clone IMAGE:1160145 3'
            similar to TR:Q62381 Q62381 TOLLID-LIKE ;, mRNA sequence.
ACCESSION   AA887629
VERSION     AA887629.1  GI:3003304
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (bases 1 to 40)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
  JOURNAL
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
            M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

```

```

www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 797 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..40
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1160145"
                     /tissue_type="colon tumor RER+"
                     /lab_host="DH10B"
                     /clone_lib="NCI CGAP Col10"
                     /notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     RER+ colon tumor, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector. Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo (N-Soares4)."
ORIGIN
Query Match      46.7%; Score 14; DB 1; Length 40;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      1  GCGAATTCGCGGAGCCAGCGCACTGAAG 30
Db      36 GGGTAGTTGAGGGGCCAGCGCGGCTGTAG 7

RESULT 9
AZ601433/c
LOCUS       AZ601433               48 bp    DNA    linear    GSS 13-DEC-2000
DEFINITION  IM0419N1LR Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            Clone UUGC1M0419N11 R, genomic survey sequence.
ACCESSION   AZ601433
VERSION     AZ601433.1  GI:11723623
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE 1 (bases 1 to 48)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
  JOURNAL
  COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0419 row: N column: 11
            Seq primer: CACACAGGAACACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 48.
FEATURES             Location/Qualifiers
     source          1..48
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"

```

```

/clone="UUGC1M0419N11"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi:14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

ORIGIN
Query Match          46.7%; Score 14; DB 8; Length 48;
Best Local Similarity 77.3%; Pred. No. 2.8e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy 1 GCGAATTCGCGAGCCAGCG 22
||||| | | | | | | | | |
Db 40 GCGAGGCACACAGCGCAGCG 19

```

```

RESULT 10
H84363
LOCUS
DEFINITION
Yv95c09.s1 Soares melanocyte 2NbM Homo sapiens cDNA clone
IMAGE:249520 3' similar to gb:L06505 60S RIBOSOMAL PROTEIN L12
(HUMAN); mRNA sequence.

```

```

ACCESSION
H84363
VERSION
H84363.1 GI:1063034
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 41)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: Pronega -21m13
High quality sequence stop: 1.
Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="mRNA"

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FEATURES
source
1..41
/organism="Homo sapiens"
/mol_type="mRNA"

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/db xref="GDB:3867226"
/db_xref="taxon:9606"
/clone="IMAGE:249520"
/sex="Male"
/tissue type="melanocyte"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares melanocyte 2NbM"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCCGAGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

```

ORIGIN

```

Query Match          46.0%; Score 13.8; DB 7; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 9 GCGGAGCGCAGCGCAC 25
||||| | | | | | | | | |
Db 1 GCAGAGGCAGCGCGCAC 17

```

```

RESULT 11
AZ949204/c
LOCUS
DEFINITION
2M0212M04R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0212M04 R, genomic survey sequence.

```

```

ACCESSION
AZ949204
VERSION
AZ949204.1 GI:13820431
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: M column: 04
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1..26
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0212M04"
/sex="Female"
/lab host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson

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FEATURES

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source
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0212M04"
/sex="Female"
/lab host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson

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found there.
FEATURES
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    Location/Qualifiers
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        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /dev_stage="adult"
        /clone_lib="Human adult (K.Okubo)"
        /note="One or more human adult tissue"

ORIGIN
  Query Match      44.7%; Score 13.4; DB 6; Length 48;
  Best Local Similarity 73.9%; Pred. No. 5e+05;
  Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 8 CGCGGAGCCAGCGCAGCTGAAG 30
Db 20 CCGGCGCCCGAGCGCCCGGAAG 42

RESULT 15
LOCUS AU102737 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP13330, mRNA sequence.
ACCESSION AU102737 GI:13552258
VERSION AU102737
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,Y., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
  source
    Location/Qualifiers
      1. 50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone_lib="HEP13330"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
  Query Match      44.7%; Score 13.4; DB 1; Length 50;
  Best Local Similarity 73.9%; Pred. No. 5e+05;
  Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GAATTCGCGGAGCCAGCGGAC 25
Db 27 GTATTTCGCGCCTAGTCGGCTC 49

RESULT 16
LOCUS AJ668097/c 30 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ668097 CSEQRAN09 Sus scrofa cDNA clone C0000044_D15, mRNA
sequence.

found there.
FEATURES
  source
    Location/Qualifiers
      1. 48
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /dev_stage="adult"
        /clone_lib="Human adult (K.Okubo)"
        /note="One or more human adult tissue"

ORIGIN
  Query Match      44.7%; Score 13.4; DB 6; Length 48;
  Best Local Similarity 73.9%; Pred. No. 5e+05;
  Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 8 CGCGGAGCCAGCGCAGCTGAAG 30
Db 20 CCGGCGCCCGAGCGCCCGGAAG 42

RESULT 15
LOCUS AU102737 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP13330, mRNA sequence.
ACCESSION AU102737 GI:13552258
VERSION AU102737
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,Y., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
  source
    Location/Qualifiers
      1. 50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone_lib="HEP13330"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
  Query Match      44.7%; Score 13.4; DB 1; Length 50;
  Best Local Similarity 73.9%; Pred. No. 5e+05;
  Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GAATTCGCGGAGCCAGCGGAC 25
Db 27 GTATTTCGCGCCTAGTCGGCTC 49

RESULT 16
LOCUS AJ668097/c 30 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ668097 CSEQRAN09 Sus scrofa cDNA clone C0000044_D15, mRNA
sequence.

AJ668097
VERSION AJ668097.1 GI:49352548
EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 30)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL Contact: Anderson SI
COMMENT Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES
  source
    Location/Qualifiers
      1. 30
        /organism="Sus scrofa"
        /mol_type="mRNA"
        /db_xref="taxon:9823"
        /clone="C0000044_D15"
        /tissue_type="placenta"
        /clone_lib="CSEQRAN09"
        /note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:
        NotI; Single pass sequencing. Normalised library
        constructed from pooled tissue from day 30 placentas."

ORIGIN
  Query Match      44.0%; Score 13.2; DB 1; Length 30;
  Best Local Similarity 69.2%; Pred. No. 6e+05;
  Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTGCGGAGCCAGCGGACTG 27
Db 26 GGACTTCCTGAGGCGCAGCAGACTG 1

RESULT 17
LOCUS BQ594733/c 34 bp mRNA linear EST 06-DEC-2002
DEFINITION BQ594733 E012441-024-024-O19-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-024-O19 5-PRIME, mRNA sequence.
ACCESSION BQ594733 GI:26124316
VERSION BQ594733
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 34)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radloff,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de

```

Insert Length: 34 Std Error: 0.00
 Plate: 24 row: 0 column: 19
 Seq primer: SP6; CATACGATTAGTGACTATAG.
 Location/Qualifiers
 1. .34
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:192126"
 /db_xref="taxon:161934"
 /clone="024-019"
 /tissue_type="developing root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-developing root"
 /note="Vector: pQWVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-SalI-CCACCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 44.0%; Score 13.2; DB 5; Length 34;
 Best Local Similarity 69.2%; Pred. No. 6e+05; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 8;
 Qy 5 ATTCCGGAGCGACGACCTGAAG 30
 |||||
 Db 28 ATTACGGAGGAGCGCGCATGATG 3

RESULT 18

BZ764154/c
 LOCUS 34 bp DNA linear GSS 13-MAR-2003
 DEFINITION SALK_124025.49.65.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_124025.49.65.x, genomic survey sequence.

ACCESSION

BZ764154

VERSION

BZ764154.1 GI:28936707

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 34)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

COMMENT

Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g04300.
 Class: TDNA tagged.

FEATURES

source

1. .34
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"

/clone="SALK_124025.49.65.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 44.0%; Score 13.2; DB 8; Length 34;
 Best Local Similarity 69.2%; Pred. No. 6e+05; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 8;
 Qy 3 GAATTCGGAGCGACGACCTGA 28
 |||||
 Db 26 GAATTCGGAACCAAGTCGCCGA 1

RESULT 19

BZ764155/c

LOCUS

34 bp DNA linear GSS 13-MAR-2003
 DEFINITION SALK_124027.37.85.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_124027.37.85.x, genomic survey sequence.

ACCESSION

BZ764155

VERSION

BZ764155.1 GI:28936708

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 34)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g04300.
 Class: TDNA tagged.

FEATURES

source

1. .34
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_124027.37.85.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 44.0%; Score 13.2; DB 8; Length 34;
 Best Local Similarity 69.2%; Pred. No. 6e+05; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 8;
 Qy 3 GAATTCGGAGCGACGACCTGA 28
 |||||
 Db 26 GAATTCGGAACCAAGTCGCCGA 1

```

RESULT 20
BG032379
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

        40 bp      mRNA      linear      EST 24-JAN-2001
602301364F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4403174 5',
mRNA sequence.
BG032379
BG032379.1 GI:12423624
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/Drp
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10112 row: o column: 15
High quality sequence stop: 40.
Location/Qualifiers
1..40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4403174"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.383 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 44.0%; Score 13.2; DB 4; Length 40;
Best Local Similarity 69.2%; Pred. No. 6e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 ATTCGCGAGCCAGCGGCACTGAAG 30
|||||
DB 3 ATTCGAGATGACGGCGCTCGGATG 28
|||||

RESULT 21
CG426236/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

        41 bp      DNA      linear      GSS 15-SEP-2003
01S0576-07C1-G08 UniformMu MutTAIL Library Zea mays genomic clone
01S0576-07C1-G08, genomic survey sequence.
CG426236
GSS.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 41)
Latahaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
population
Unpublished (2003)
Contact: Donald R. McCarty

FEATURES
source
1..41
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="01S0576-07C1-G08"
/clone_lib="UniformMu MutTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match 44.0%; Score 13.2; DB 9; Length 41;
Best Local Similarity 83.3%; Pred. No. 6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ATTCGCGAGCCAGCGG 22
|||||
DB 38 AGTCGTGGAGCCAGACAG 21
|||||

RESULT 22
HSA275866
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

        42 bp      DNA      linear      GSS 10-DEC-1999
HSA275866 Homo sapiens DNA for trapped exon, clone j1A63F10, genomic survey
sequence.
AJ275866
GSS; genome survey sequence.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Blouin,J.L., Duriaux Sail,G., Rossier,C. and Antonarakis,S.E.
Isolation of portion of gene that map on chromosome 21q22 by exon
trapping
Unpublished
REFERENCE
2 (bases 1 to 42)
AUTHORS
Blouin,J.L.C.
TITLE
Direct Submission
JOURNAL
Submitted (07-DEC-1999) Blouin J.L.C., Medical Genetics, University
Hospital and School of Medicine of Geneva, 1 rue Michel-Servet,
1211 GENEVA, SWITZERLAND
Location/Qualifiers
1..42
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q22"
/clone="j1A63F10"
/clone_lib="LL21NC02-Q"
1..42
/note="trapped"

exon

ORIGIN
Query Match 44.0%; Score 13.2; DB 9; Length 42;
Best Local Similarity 78.9%; Pred. No. 6e+05;

```

Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmo@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
01S0576-07, Primer set: C
Class: transposon insertion site.

FEATURES

source

1..41

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="01S0576-07C1-G08"
/clone_lib="UniformMu MutTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 44.0%; Score 13.2; DB 9; Length 41;
Best Local Similarity 83.3%; Pred. No. 6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ATTCGCGAGCCAGCGG 22

DB 38 AGTCGTGGAGCCAGACAG 21

RESULT 22

HSA275866

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 10 CGGAGCCGACGCGCACTGA 28
|||||
Db 19 CGGAGACAGAGNTCACTGA 37

RESULT 23

AA074398/c
LOCUS
DEFINITION zml6f07.s1 Stragatene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:525829 3', similar to TR:G1136430 G1136430 KIAA0185 PROTEIN ;,
mRNA sequence.

ACCESSION

AA074398

VERSION

AA074398.1 GI:1614329

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

REFERENCE

1 (bases 1 to 43)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Roifling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.

TITLE

Generation and analysis of 280,000 human expressed sequence tags

JOURNAL

Genome Res. 6 (9), 807-828 (1996)

MEDLINE

97044478

PUBMED

889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1400 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="CDB:3917258"
/db_xref="taxon:9606"
/clone="IMAGE:525829"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene pancreas (#937208)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1:
EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5'
CTCGAGTGTGTTTTTTTTTTT 3'"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 43;
Best Local Similarity 69.2%; Pred. No. 6e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGATTCGCGGACGCGCACTG 27

|||||

Db

RESULT 24

BI556158

LOCUS

DEFINITION

603237933F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5290664 5',

mRNA sequence.

ACCESSION

BI556158

VERSION

BI556158.1 GI:15443472

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 45)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11735 row: b column: 09

High quality sequence stop: 45.

Location/Qualifiers

1. .45

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129.C57BL/6J.FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5290664"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/clone_lib="NCI CGAP Mam3"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI;

Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

ORIGIN

Query Match 44.0%; Score 13.2; DB 4; Length 45;
Best Local Similarity 69.2%; Pred. No. 6e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGATTCGCGGACGCGCACTG 27

|||||

Db 18 GGTCCTCGCGGCGGCGCTCGG 43

RESULT 25

AU107457

LOCUS

DEFINITION

AU107457 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

NBLAN24NF, mRNA sequence.

ACCESSION

AU107457

VERSION

AU107457.1 GI:13556978

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 50)

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NBLAN24NF"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GAATTCGGGAGCCGACGACGACTGA 28
|||||
Db 1 GAAGACGCCGCGCACAGACACAGA 26
|||||

RESULT 26
AUI08040
LOCUS
DEFINITION
AUI08040 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNG09859, mRNA sequence.
ACCESSION
AUI08040
VERSION
AUI08040.1 GI:13557562
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG09859"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Best Local Similarity 83.3%; Pred. No. 6.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 GCGGAGCCGACGCGCACT 26
|||||
Db 11 GCGGAGTGAGACGCGCT 28
|||||

RESULT 27
AZ666536
LOCUS
DEFINITION
AZ666536
ACCESSION
AZ666536.1 GI:11803682
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0548 row: D column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0548D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0548D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 44.0%; Score 13.2; DB 8; Length 50;
Best Local Similarity 83.3%; Pred. No. 6.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Best Local Similarity 69.2%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCGAATTCGCGAGCCAGCGCACTG 26
   ||||| ||||| ||||| |||||
Db 7 GGGTATTCATGAGCGCAGCAACT 32

RESULT 28
LOCUS AA776443 36 bp mRNA linear EST 05-FEB-1998
DEFINITION zj50h10.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA
clone IMAGE:453763 3' similar to gb|U28107|TRRRRH Trichoderma
ressei 25S ribosomal (rRNA); mRNA sequence.
ACCESSION AA776443
VERSION AA776443.1 GI:2835777
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Matra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,X., Wyllie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd ET from Amersham
High quality sequence stop: 1.
FEATURES
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        location/Qualifiers
            1..36
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                /mol_type="mRNA"
                /db_xref="GDB:1390119"
                /db_xref="taxon:9606"
                /clone="IMAGE:453763"
                /sex="male"
                /dev_stage="20 week post conception fetus"
                /lab_host="DH10B (ampicillin resistant)"
                /clone_lib="Soares fetal liver spleen INFLS S1"
                /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                This is a subcloned version of the original Soares fetal
                liver spleen INFLS library. 1st strand cDNA was primed
                with a Pac I - oligo(dT) primer [5'
                AACTGGAGATTAATTAAGACTCTTTTCTTTTCTTTT 3'],
                double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Pac I and cloned into the Pac I
                and Eco RI sites of the modified pT7T3 vector. Library
                went through one round of normalization. Library
                constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
Query Match 43.3%; Score 13; DB 1; Length 36;
Best Local Similarity 65.5%; Pred. No. 7.3e+05;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGAGCCAGCGCACTGAG 30
   ||||| ||||| ||||| |||||
Db 31 GGGCTTCGCGAATCAGCGGGGAAAGAG 3

RESULT 29
LOCUS AA776443 36 bp mRNA linear EST 05-FEB-1998
DEFINITION zj50h10.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA
clone IMAGE:453763 3' similar to gb|U28107|TRRRRH Trichoderma
ressei 25S ribosomal (rRNA); mRNA sequence.
ACCESSION AA776443
VERSION AA776443.1 GI:2835777
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Matra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,X., Wyllie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd ET from Amersham
High quality sequence stop: 1.
FEATURES
    source
        location/Qualifiers
            1..36
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                /mol_type="mRNA"
                /db_xref="GDB:1390119"
                /db_xref="taxon:9606"
                /clone="IMAGE:453763"
                /sex="male"
                /dev_stage="20 week post conception fetus"
                /lab_host="DH10B (ampicillin resistant)"
                /clone_lib="Soares fetal liver spleen INFLS S1"
                /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                This is a subcloned version of the original Soares fetal
                liver spleen INFLS library. 1st strand cDNA was primed
                with a Pac I - oligo(dT) primer [5'
                AACTGGAGATTAATTAAGACTCTTTTCTTTTCTTTT 3'],
                double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Pac I and cloned into the Pac I
                and Eco RI sites of the modified pT7T3 vector. Library
                went through one round of normalization. Library
                constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
Query Match 43.3%; Score 13; DB 1; Length 36;
Best Local Similarity 65.5%; Pred. No. 7.3e+05;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GGAATTCGCGAGCCAGCGCACTGAA 29
   ||||| ||||| ||||| |||||
Db 32 GCGAATTCGCGCGCTAGCGCGCGGAA 4

RESULT 30
LOCUS BX230810 46 bp DNA linear GSS 29-JAN-2003
DEFINITION Danio rerio genomic clone DKEY-54G22, genomic survey sequence.
ACCESSION BX230810
VERSION BX230810.1 GI:28064960
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 46)
AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 54G22. 54G22 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES
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                /organism="Danio rerio"
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ORIGIN
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Best Local Similarity 76.2%; Pred. No. 7.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 10 CGGAGCCAGACGGCACTGAAG 30
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Db 12 CGCCCCAGACTGCACAGAG 32

RESULT 31
AUI03141
LOCUS
DEFINITION
AUI03141 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AUI03141 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
149-156 (1997).
FEATURES
source
1..50
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 65.5%; Pred. No. 7.4e+05;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCAGCGCACTGAAG 30
    |||||
Db 21 GGACTTCGAGTAGGACACAGGACGGAAG 49

RESULT 33
AUI06584/c
LOCUS
DEFINITION
AUI06584 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AUI06584 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
149-156 (1997).
FEATURES
source
1..50
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 8 CGCGAGCCAGACGGCACTGA 28
    |||||
Db 13 CTCGACGAGACTGCACGGA 33

RESULT 32
AUI05783
LOCUS
DEFINITION
AUI05783 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AUI05783 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)

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Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      5 ATTGCGGAGCGACGACGCGC 25
Db      48 AATGCGGAGCGATCAGCTC 28

RESULT 34
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DEFINITION AU106592 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
XAT07173, mRNA sequence.
ACCESSION AU106592
VERSION   AU106592.1 GI:13556113
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE   Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL ENBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             source
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Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.5%; Pred. No. 7.4e+05;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      2 GGAATTCGGGAGCGGCGCTCTGAAG 30
Db      14 GGCAGCCCCGAGCCCGCGCTTAAG 42

RESULT 36
LOCUS   CG894749
DEFINITION CG894734-00A1-C06 UniformMu MUTAIL Library Zea mays genomic clone
0384734-00A1-C06, genomic survey sequence.
ACCESSION CG894749
VERSION   CG894749.1 GI:39550244
KEYWORDS GSS.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 50)
AUTHORS Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
TITLE   Sequence tagged transposon insertions from the UniformMu maize
population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
0384734-00, Primer set: A
Class: transposon insertion site.
FEATURES             source
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        1..50
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        /mol_type="genomic DNA"
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        /cultivar="UniformMu"
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        /clone_lib="0384734-00A1-C06"
        /notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for

```

```

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
ENBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             source
    Location/Qualifiers
        1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 65.5%; Pred. No. 7.4e+05;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      2 GGAATTCGGGAGCGGCGCTCTGAAG 30
Db      14 GGCAGCCCCGAGCCCGCGCTTAAG 42

RESULT 36
LOCUS   CG894749
DEFINITION CG894734-00A1-C06 UniformMu MUTAIL Library Zea mays genomic clone
0384734-00A1-C06, genomic survey sequence.
ACCESSION CG894749
VERSION   CG894749.1 GI:39550244
KEYWORDS GSS.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 50)
AUTHORS Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
TITLE   Sequence tagged transposon insertions from the UniformMu maize
population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
0384734-00, Primer set: A
Class: transposon insertion site.
FEATURES             source
    Location/Qualifiers
        1..50
        /organism="Zea mays"
        /mol_type="genomic DNA"
        /strain="W22 (ACR, bz1-m9)"
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        /clone_lib="0384734-00A1-C06"
        /notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for

```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 58.289 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: us-10-788-779-7

Perfect score: 30

Sequence: 1 GGGGAATTCGGGAGCCAGCGCACTGAAG 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1	US-07-989-160-7
2	17.2	57.3	31	3	US-09-113-750A-46
3	16.2	54.0	23	2	US-08-479-614-20
4	16.2	54.0	23	2	US-09-159-385-5
5	16.2	54.0	23	3	US-09-186-277-5
6	16.2	54.0	38	2	US-08-403-852D-42
7	16.2	54.0	38	3	US-08-510-646B-44
8	16.2	54.0	38	3	US-09-231-818-42
9	16.2	54.0	38	4	US-09-635-359B-42
10	15.2	50.7	33	3	US-08-984-277-3
11	15.2	50.7	33	4	US-09-759-112A-3
12	15	50.0	31	1	US-08-368-803-26
13	15	50.0	31	2	US-08-578-096A-27
14	15	50.0	31	3	US-09-240-426-27
15	14.8	49.3	26	4	US-08-997-685A-26
16	14.8	49.3	27	1	US-08-182-619-8
17	14.8	49.3	27	1	US-08-330-535A-8
18	14.8	49.3	27	1	US-08-607-289-4
19	14.8	49.3	27	1	US-08-607-289-12
20	14.8	49.3	27	1	US-08-688-145-4
21	14.8	49.3	27	1	US-08-616-732A-1
22	14.8	49.3	27	2	US-08-838-844-8
23	14.8	49.3	27	3	US-09-037-742B-1
24	14.8	49.3	27	5	PCT-US95-04600-4
25	14.8	49.3	27	5	PCT-US95-04600-12
26	14.8	49.3	30	1	US-07-642-734C-25
27	14.8	49.3	30	3	US-08-439-009A-25

28	14.6	48.7	25	4	US-09-396-196G-68463	Sequence 68463, A
29	14.6	48.7	50	4	US-09-443-199C-940	Sequence 940, Appl
30	14.4	48.0	25	4	US-09-396-196G-68465	Sequence 68465, A
c 31	14.4	48.0	44	4	US-09-410-935B-15	Sequence 15, Appl
c 32	14.4	48.0	44	4	US-09-784-403A-15	Sequence 15, Appl
c 33	14.4	48.0	50	3	US-08-951-200A-3	Sequence 3, Appl
34	14.2	47.3	39	1	US-08-253-155A-88	Sequence 88, Appl
35	14.2	47.3	39	1	US-08-625-209A-17	Sequence 17, Appl
36	14.2	47.3	39	3	US-08-853-733B-17	Sequence 17, Appl
c 37	14.2	47.3	47	4	US-09-422-978-3058	Sequence 3058, Ap
38	14	46.7	30	2	US-08-821-782-8	Sequence 8, Appli
39	14	46.7	30	2	US-08-821-782-24	Sequence 24, Appl
40	14	46.7	30	3	US-09-292-435A-8	Sequence 8, Appli
41	14	46.7	30	3	US-09-292-435A-24	Sequence 24, Appl
c 42	14	46.7	33	1	US-08-170-290A-52	Sequence 52, Appl
c 43	14	46.7	33	3	US-09-198-723A-73	Sequence 73, Appl
44	14	46.7	33	3	US-09-198-723A-74	Sequence 74, Appl
c 45	14	46.7	33	4	US-09-684-881-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-07-989-160-7
; Sequence 7, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-07-989-160-7

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGAATTCGGGAGCCAGCGCACTGAAG 30
|||||

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Db      1 GGGAAATTCGGGAGCCAGCGCACTGAAG 30

RESULT 2
US-09-113-750A-46
; Sequence 46, Application US/09113750A
; Patent No. 6294176
; GENERAL INFORMATION:
; APPLICANT: David E. Junker and Mark D. Cochran
; TITLE OF INVENTION: Recombinant Raccoonpox virus
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,750A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 55744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)262-0400
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Synthetic
; ORIGINAL SOURCE:
; US-09-113-750A-46

Query Match      57.3%; Score 17.2; DB 3; Length 31;
Best Local Similarity 73.3%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGGGAGCCAGCGCACTGAAG 30
        |||||
Db      2 GGGAAATTCATCGCGTACGCGCACTGAGG 31

RESULT 3
US-08-479-614-20
; Sequence 20, Application US/08479614
; Patent No. 5861294
; GENERAL INFORMATION:
; APPLICANT: Cowart, Marlon Daniel, Halbert, Donald N.,
; APPLICANT: Kerwin, Jr., James F., McNally, Teresa
; TITLE OF INVENTION: Adenosine Kinase Polypeptides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: D-377 AP6D, 100 Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System 7.1
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,614
; FILING DATE: June 7, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5749.US.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 937-4884
; TELEFAX: (708) 938-2623
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-479-614-20

Query Match      54.0%; Score 16.2; DB 2; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GAATTCGGGAGCCAGCGGC 23
        |||||
Db      1 GAATTCGTGGAGCCAAACGC 21

RESULT 4
US-09-159-385-5
; Sequence 5, Application US/09159385
; Patent No. 5958748
; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: KAWAI, TARO
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
; FILE REFERENCE: PH-569
; CURRENT APPLICATION NUMBER: US/09/159,385
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: JP97/261589
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotides
US-09-159-385-5

Query Match      54.0%; Score 16.2; DB 2; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGGGAGCCAGCAGC 21
        |||||
Db      1 GGGAAATTCGGGAGCCAGCAGG 21

RESULT 5
US-09-186-277-5
; Sequence 5, Application US/09186277
```

; Patent No. 6171841
; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: KAWAI, TARO
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
; FILE REFERENCE: 081356/0128
; CURRENT APPLICATION NUMBER: US/09/186,277
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: JP97/261589
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-186-277-5

Query Match 54.0%; Score 16.2; DB 3; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGCAGC 21
Db 1 GGGAAATTCGGGAGCCAGGAGG 21

RESULT 6

US-08-403-852D-42
; Sequence 42, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,852D
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-852D-42

Query Match 54.0%; Score 16.2; DB 2; Length 38;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGCAGCAGCTG 27
Db 11 GSGAGTTTCGCGCGCTGGGACGCGCACCG 37

RESULT 7

US-08-510-646B-44
; Sequence 44, Application US/08510646B
; Patent No. 6077699
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,646B
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-510-646B-44

Query Match 54.0%; Score 16.2; DB 3; Length 38;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGCGGCACTG 27
|:|||||:|:|
Db 11 GSGAGTTCCGCGCGTGGGACGCGCACCG 37

RESULT 8

US-09-231-818-42
; Sequence 42, Application US/09231818
; Patent No. 6171846

GENERAL INFORMATION:

; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie

; TITLE OF INVENTION: Polypeptides Involved In The

; Biosynthesis Of Streptogramins, Nucleotide Sequences
; Coding For These Polypeptides And Their Use

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/231.818

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/403.852

; FILING DATE: 10-MAY-1995

; APPLICATION NUMBER: PC7/FR 93/00923

; FILING DATE: 25-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 92/11441

; FILING DATE: 25-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 03806.0054-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 42:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-231-818-42

Query Match 54.0%; Score 16.2; DB 3; Length 38;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGCGGCACTG 27
|:|||||:|:|
Db 11 GSGAGTTCCGCGCGTGGGACGCGCACCG 37

RESULT 9

US-09-635-359B-42

; Sequence 42, Application US/09635359B

; Patent No. 6670157

; GENERAL INFORMATION:

; APPLICANT: Blanc, Veronique

; APPLICANT: Blanche, Francis

; APPLICANT: Crouzet, Joel

; APPLICANT: Jacques, Nathalie

; APPLICANT: Lacroix, Patricia

; APPLICANT: Thibaut, Denis

; APPLICANT: Zagorec, Monique

; APPLICANT: Debussche, Laurent

; APPLICANT: De Crecy-Lagard, Valerie

; TITLE OF INVENTION: Polypeptides Involved In The
; Biosynthesis Of Streptogramins, Nucleotide Sequences
; Coding For These Polypeptides And Their Use

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/635.359B

; FILING DATE: 09-Aug-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/231.818

; FILING DATE: 15-JAN-1999

; APPLICATION NUMBER: US 08/403.852

; FILING DATE: 10-MAY-1995

; APPLICATION NUMBER: PC7/FR 93/00923

; FILING DATE: 25-SEP-1993

; APPLICATION NUMBER: FR 92/11441

; FILING DATE: 25-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 03806.0054-03000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 42:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-09-635-359B-42

Query Match 54.0%; Score 16.2; DB 4; Length 38;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGCGGCACTG 27
|:|||||:|:|
Db 11 GSGAGTTCCGCGCGTGGGACGCGCACCG 37

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RESULT 10
US-08-984-277-3
; Sequence 3, Application US/08984277
; Patent No. 6057421
; GENERAL INFORMATION:
; APPLICANT: Muller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1F7
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/984,277
; FILING DATE: 3-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca, Daniel
; REGISTRATION NUMBER: 42,368
; REFERENCE/DOCKET NUMBER: 50200-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-756-8600
; TELEFAX: 202-756-8699
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-984-277-3

Query Match 50.7%; Score 15.2; DB 3; Length 33;
Best Local Similarity 85.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGAC 20
Db 1 GGGAAATTCATGGAGACAGAC 20

RESULT 11
US-09-759-112A-3
; Sequence 3, Application US/09759112A
; Patent No. 6768004
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 200-013
; STREET:
; CITY:
; STATE:
; COUNTRY:
; ZIP:
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 33
; TYPE: DNA
; ORGANISM: mouse
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; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)..(33)
; OTHER INFORMATION: 1F7 light chain 5' primer
US-09-759-112A-3

Query Match 50.7%; Score 15.2; DB 4; Length 33;
Best Local Similarity 85.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGAC 20
Db 1 GGGAAATTCATGGAGACAGAC 20

RESULT 12
US-08-368-803-26
; Sequence 26, Application US/08368803
; Patent No. 5733554
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, Jean-Christophe F
; APPLICANT: BUBLOT, Michel J
; APPLICANT: DARTEIL, Raphael J
; APPLICANT: DUINAT, Carole V
; APPLICANT: LAPLACE, Eliane L
; APPLICANT: RIVIERE, Michel A
; TITLE OF INVENTION: Avian Herpesvirus-based live recombinant avian
; TITLE OF INVENTION: vaccine, in particular against Gumboro disease
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LARSON AND TAYLOR
; STREET: 727 SOUTH 23RD STREET
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,803
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SARRO, Thomas
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 920-7200
; TELEFAX: (703) 892-8428
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-368-803-26

Query Match 50.0%; Score 15; DB 1; Length 31;
Best Local Similarity 78.3%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGGAGCCAGCCAGAC 25
Db 6 GAATTCGGAAGAGAGAGGAAC 28

RESULT 13
US-08-578-096A-27
; Sequence 27, Application US/08578096A
```

; Patent No. 5980906
; GENERAL INFORMATION:
; APPLICANT: Avian herpesvirus-based live recombinant
; TITLE OF INVENTION: avian vaccine
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578.096A
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-578-096A-27

Query Match 50.0%; Score 15; DB 2; Length 31;
Best Local Similarity 78.3%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 3 GAATTCGGGAGCCAGCGGCAC 25
|||
Db 6 GAATTCGGGAGGAGGAGGAC 28

RESULT 14
US-09-240-426-27
; Sequence 27, Application US/09240426
; Patent No. 6045803
; GENERAL INFORMATION:
; APPLICANT: Avian herpesvirus-based live recombinant
; TITLE OF INVENTION: avian vaccine
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240.426
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578.096
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-240-426-27

Query Match 50.0%; Score 15; DB 3; Length 31;
Best Local Similarity 78.3%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 3 GAATTCGGGAGCCAGCGGCAC 25
|||
Db 6 GAATTCGGGAGGAGGAGGAC 28

RESULT 15
US-08-997-685A-26
; Sequence 26, Application US/08997685A

; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997.685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 26
; TYPE: DNA
; ORGANISM: mouse;
; US-08-997-685A-26

Query Match 49.3%; Score 14.8; DB 4; Length 26;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 5 ATTGCGGAGCCAGCGGCACCTGAAG 30
|||
Db 1 ATGTTCCGAGCCAGAGGCGGTGGAG 26

RESULT 16
US-08-182-619-8
; Sequence 8, Application US/08182619
; Patent No. 5484710
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Miyashita, Toshiyuki
; APPLICANT: Harigai, Masayoshi
; APPLICANT: Hanada, Motoi
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN
; TITLE OF INVENTION: CELL DEATH
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
; US-08-182-619-8
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182.619
; FILING DATE: 14-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9867
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26

RESULT 17

US-08-330-535A-8
; Sequence 8, Application US/08330535A
; Patent No. 5659024
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Miyashita, Toshiyuki
; APPLICANT: Harigai, Masayoshi
; APPLICANT: Hanada, Motoi
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
; TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
; TITLE OF INVENTION: DEATH
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; STREET: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330.535A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182.619
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-330-535A-8

Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26

RESULT 18

US-08-607-269-4
; Sequence 4, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607.269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226.876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-607-269-4

Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26

RESULT 19

US-08-607-269-12
; Sequence 12, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607.269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226.876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-607-269-12
Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 20
US-08-688-145-4
; Sequence 4, Application US/08688145
; Patent No. 5744310
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Promoter Sequence and Screening
; Patent No. 5744310
; TITLE OF INVENTION: Assays for Identifying Agents that Regulate BAX Gene
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4170 La Jolla Village Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,145
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-688-145-4
Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-607-269-12
Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 21
US-08-616-732A-1
; Sequence 1, Application US/08616732A
; Patent No. 5770690
; GENERAL INFORMATION:
; APPLICANT: Bitler, Catherine Mastroni
; APPLICANT: Bowersox, Stephen Scott
; APPLICANT: Crea, Roberto
; APPLICANT: Demo, Susan Dunham
; APPLICANT: Horne, William A.
; APPLICANT: Zhou, Mei
; TITLE OF INVENTION: Bax Omega Protein and Methods
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/616,732A
; FILING DATE: 15-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/495,042
; FILING DATE: 27-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 5865-0017.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: PCR primer Bax F
;
US-08-616-732A-1
Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 22
US-08-838-844-8
; Sequence 8, Application US/08838844
; Patent No. 5908750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Miyashita, Toshiyuki
; APPLICANT: Harigai, Masayoshi
; APPLICANT: Hanada, Motoi
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
```

;; TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
;; TITLE OF INVENTION: DEATH
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell & Flores LLP
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92122

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/838,844

;; FILING DATE: 11-APR-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/182,619
;; FILING DATE: 14-JAN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/330,535

;; FILING DATE: 27-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LJ 2520
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)

US-08-838-844-8
Query Match 49.3%; Score 14.8; DB 2; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGAATTCGGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTCGGGATGGACGGGTCCG 26

RESULT 23
US-09-037-742B-1
;; Sequence 1, Application US/09037742B
;; Patent No. 6140484
;; GENERAL INFORMATION:
;; APPLICANT: Bitler, Catherine Mastroni
;; APPLICANT: Bowersox, Stephen Scott
;; APPLICANT: Crea, Roberto
;; APPLICANT: Demo, Susan Dunham
;; APPLICANT: Horne, William A.
;; APPLICANT: Zhou, Mei

;; TITLE OF INVENTION: Bax Omega Protein and Methods
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dehlinger & Associates
;; STREET: 350 Cambridge Avenue, Suite 250
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94306

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/037,742B
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/616,732

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sholtz, Charles K.
;; REGISTRATION NUMBER: 38,615
;; REFERENCE/DOCKET NUMBER: 5865-0017.30
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 324-0880
;; TELEFAX: (415) 324-0960

;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: PCR primer Bax F

US-09-037-742B-1
Query Match 49.3%; Score 14.8; DB 3; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGAATTCGGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTCGGGATGGACGGGTCCG 26

RESULT 24
PCT-US95-04600-4
;; Sequence 4, Application PC/TUS9504600
;; GENERAL INFORMATION:
;; APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
;; TITLE OF INVENTION: Interaction of Proteins Involved in
;; TITLE OF INVENTION: a Cell Death Pathway
;; NUMBER OF SEQUENCES: 29
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell and Flores
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92122

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/04600
;; FILING DATE: 12-APR-1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Imbra, Richard J.
;; REGISTRATION NUMBER: 37,643
;; REFERENCE/DOCKET NUMBER: FP-LJ 1361
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-04600-4

Query Match          49.3%; Score 14.8; DB 5; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGCGGCACTG 27
    |||||
Db 1 GGAATTCGCGTGATGACGCGGTCG 26

RESULT 25
PCT-US95-04600-12
; Sequence 12, Application PC/TUS9504600
; GENERAL INFORMATION:
; APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
; TITLE OF INVENTION: Interaction of Proteins Involved in
; TITLE OF INVENTION: a Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04600
; FILING DATE: 12-APR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Imbra, Richard J.
; REGISTRATION NUMBER: 37,643
; REFERENCE/DOCKET NUMBER: FP-LJ 1361
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-04600-12

Query Match          49.3%; Score 14.8; DB 5; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGCGGCACTG 27
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Db 1 GGAATTCGCGTGATGACGCGGTCG 26

RESULT 26
US-07-642-734C-25
; Sequence 25, Application US/07642734C
; Patent No. 5824513
; GENERAL INFORMATION:
; APPLICANT: Katz, L
; APPLICANT: Donadio, S
; APPLICANT: Mcalpine, J B
; TITLE OF INVENTION: Recombinant DNA Method for Producing
; TITLE OF INVENTION: Erythromycin Analogs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstock
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
```

```
; ADDRESSEE: Edward H. Gorman
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,734C
; FILING DATE: 17-JAN-91
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckers, Andreas M
; REGISTRATION NUMBER: 32652
; REFERENCE/DOCKET NUMBER: 4952.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-9396
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: PCR primer 10b
; US-07-642-734C-25

Query Match          49.3%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGCGGCACTG 27
    |||||
Db 2 GGAATTCGCGTGATGACGCGGCACTG 27

RESULT 27
US-08-439-009A-25
; Sequence 25, Application US/08439009A
; Patent No. 6004787
; GENERAL INFORMATION:
; APPLICANT: Donadio, S
; APPLICANT: Katz, L
; APPLICANT: Mcalpine, J B
; TITLE OF INVENTION: Method of Directing Biosynthesis of
; TITLE OF INVENTION: Specific Polyketides
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstock
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
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RESULT 31
US-09-410-935B-15/c
/ Sequence 15, Application US/09410935B
/ Patent No. 6504083
/ GENERAL INFORMATION:
/ APPLICANT: Barbour, Eric
/ APPLICANT: SuChaire Meyer, Terry
/ APPLICANT: Eid Saad, Mohammed
/ TITLE OF INVENTION: No. 6504083el Maize Promoters
/ FILE REFERENCE: 5718-72
/ CURRENT APPLICATION NUMBER: US/09/410.935B
/ CURRENT FILING DATE: 1999-10-04
/ PRIOR APPLICATION NUMBER: US 60/107,201
/ PRIOR FILING DATE: 1998-11-05
/ PRIOR APPLICATION NUMBER: US 60/103,294
/ PRIOR FILING DATE: 1998-10-06
/ NUMBER OF SEQ ID NOS: 19

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gene specific primer 3 for Gos-2
US-09-410-935B-15

Query Match      48.0%; Score 14.4; DB 4; Length 44;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2  GGAATTCGCGAGCGACGACGAC 25
Db      31  GGAAGCGAGGATCCACGAC 8

RESULT 32
US-09-784-403A-15/c
; Sequence 15, Application US/09784403A
; Patent No. 6670467
; GENERAL INFORMATION:
; APPLICANT: Barbour, Eric
; APPLICANT: Euclaire Meyer, Terry
; APPLICANT: Eid Saad, Mohammed
; TITLE OF INVENTION: No. 6670467el Maize Promoters
; FILE REFERENCE: 35718/208067
; CURRENT APPLICATION NUMBER: US/09/784,403A
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/107,201
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 60/103,294
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 09/410,935
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gene specific primer 3 for Gos-2
US-09-784-403A-15

Query Match      48.0%; Score 14.4; DB 4; Length 44;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2  GGAATTCGCGAGCGACGACGAC 25
Db      31  GGAAGCGAGGATCCACGAC 8

RESULT 33
US-08-951-200A-3/c
; Sequence 3, Application US/08951200A
; Patent No. 6013495
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Martin A.
; APPLICANT: Meredith Jr., Jere E.
; APPLICANT: Takada, Yoshikazu
; APPLICANT: Languino, Lucia
; TITLE OF INVENTION: METHODS OF USE FOR INTEGRIN B1c CELL
; TITLE OF INVENTION: GROWTH INHIBITOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA

; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,200A
; FILING DATE: 14-OCT-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,118
; FILING DATE: 21-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07300/026002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-951-200A-3

Query Match      48.0%; Score 14.4; DB 3; Length 50;
Best Local Similarity 75.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      3  GAATTCGCGAGCGACGACGCACT 26
Db      26  GAATTCGCGCGCGAGGCACT 3

RESULT 34
US-08-253-155A-88
; Sequence 88, Application US/08253155A
; Patent No. 5691147
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: CDK4 Binding Proteins
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,155A
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
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RECORDED 36
US-08-853-733B-17
; Sequence 17, Application US/08853733B
; Patent No. 6015692
; GENERAL INFORMATION:
; APPLICANT: Gvuris, Jeno

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; SEQ ID NO 3038
;
; LENGTH: 47
;
; TYPE: DNA
;
; ORGANISM: Homo Sapiens
;
; FEATURE:
;
; NAME/KEY: allele
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; LOCATION: 24
; OTHER INFORMATION: 99-21916-359 : polymorphic base A or G
US-09-422-978-3058

Query Match      47.3%; Score 14.2; DB 4; Length 47;
Best Local Similarity 84.2%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGAGCCAGCGCACTGAA 29
    ||||| | ||||| |
Db 43 GGAGCCATAGGCACTGCA 25

RESULT 38
US-08-821-782-8
; Sequence 8, Application US/08821782
; Patent No. 5981183
; GENERAL INFORMATION:
; APPLICANT: Yutaka, Takarada
; APPLICANT: Hiroaki, Inoue
; APPLICANT: Shuji, Shibata
; APPLICANT: Yoshihisa, Kawamura
; TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
; TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING THERMOSTABLE ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 61601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: Dos 5.0
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821.782
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ahern, Paul L.
; REGISTRATION NUMBER: 17020
; REFERENCE/DOCKET NUMBER: 66425
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: (25)3533
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
US-08-821-782-8

Query Match      45.7%; Score 14; DB 2; Length 30;
Best Local Similarity 77.3%; Pred. No. 6.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TTCCGGAGCGCAGCGCACTG 27
    || ||||| | ||||| |
Db 2 TTGACGGAGCGGACGGCGCTG 23

RESULT 39
US-08-821-782-24
; Sequence 8, Application US/09292435A
; Patent No. 6303306
; GENERAL INFORMATION:
; APPLICANT: Yutaka, Takarada
; APPLICANT: Hiroaki, Inoue
; APPLICANT: Shuji, Shibata
; APPLICANT: Yoshihisa, Kawamura
; TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
; TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING THERMOSTABLE ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
```

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; Sequence 24, Application US/08821782
; Patent No. 5981183
; GENERAL INFORMATION:
; APPLICANT: Yutaka, Takarada
; APPLICANT: Hiroaki, Inoue
; APPLICANT: Shuji, Shibata
; APPLICANT: Yoshihisa, Kawamura
; TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
; TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING THERMOSTABLE ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 61601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: Dos 5.0
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821.782
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ahern, Paul L.
; REGISTRATION NUMBER: 17020
; REFERENCE/DOCKET NUMBER: 66425
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: (25)3533
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
US-08-821-782-24

Query Match      46.7%; Score 14; DB 2; Length 30;
Best Local Similarity 77.3%; Pred. No. 6.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TTCCGGAGCGCAGCGCACTG 27
    || ||||| | ||||| |
Db 2 TTGACGGAGCGGACGGCGCTG 23

RESULT 40
US-09-292-435A-8
; Sequence 8, Application US/09292435A
; Patent No. 6303306
; GENERAL INFORMATION:
; APPLICANT: Yutaka, Takarada
; APPLICANT: Hiroaki, Inoue
; APPLICANT: Shuji, Shibata
; APPLICANT: Yoshihisa, Kawamura
; TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
; TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING THERMOSTABLE ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
```


STATE: Illinois
COUNTRY: USA
ZIP: 61601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM PC
OPERATING SYSTEM: Dos 5.0
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/292,435A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ahern, Paul L.
REGISTRATION NUMBER: 17020
REFERENCE/DOCKET NUMBER: 66425
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: (25)3533
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: Genomic DNA
US-09-292-435A-8

Query Match 46.7%; Score 14; DB 3; Length 30;
Best Local Similarity 77.3%; Pred. No. 6.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 TTCGCGGAGCCAGCGGCACTG 27
||| ||||| ||||| |||||
Db 2 TTGACGGAGGCGGCGGCTG 23

Search completed: November 18, 2005, 11:22:01
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OM nucleic - nucleic search, using sw model

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(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-7

Perfect score: 30

Sequence: 1 GGGAAATCGCGAGCCAGCGCACTGAAG 30

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Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	30	100.0	30	US-10-788-779-7	Sequence 7, Appli
3	18.8	62.7	50	US-10-349-780A-28	Sequence 28, Appl
4	17	56.7	25	US-11-036-317-804897	Sequence 804897,
5	16.4	54.7	25	US-10-956-157-203038	Sequence 203038,

c	6	16.2	54.0	38	21	US-10-716-803-42	Sequence 42, Appl
	7	16.2	54.0	39	15	US-10-123-036-15	Sequence 15, Appl
	8	16.2	54.0	39	22	US-10-483-289A-3	Sequence 3, Appli
	9	15.8	52.7	25	22	US-10-719-900-439430	Sequence 439430,
	10	15.6	52.0	25	16	US-10-098-263B-97474	Sequence 97474, A
c	11	15.6	52.0	25	16	US-10-098-263B-128306	Sequence 128306,
	12	15.6	52.0	25	24	US-10-719-956-258512	Sequence 258512,
	13	15.6	52.0	25	24	US-10-719-956-258513	Sequence 258513,
c	14	15.6	52.0	25	26	US-11-036-317-21919	Sequence 21919, A
	15	15.6	52.0	25	26	US-11-036-317-875174	Sequence 875174,
c	16	15.4	51.3	25	22	US-10-719-900-805772	Sequence 805772,
	17	15.4	51.3	25	22	US-10-719-900-844398	Sequence 844398,
c	18	15.4	51.3	25	26	US-11-036-317-804896	Sequence 804896,
	19	15.4	51.3	25	26	US-11-060-756-299133	Sequence 299133,
c	20	15.4	51.3	34	9	US-09-858-349-14	Sequence 14, Appl
	21	15.4	51.3	41	19	US-10-035-833A-1888	Sequence 1888, Ap
c	22	15.4	51.3	41	19	US-10-035-833A-4483	Sequence 4483, Ap
	23	15.2	50.7	24	20	US-10-667-891-24	Sequence 24, Appl
	24	15.2	50.7	24	21	US-10-807-466-35	Sequence 35, Appl
c	25	15.2	50.7	25	22	US-10-719-900-784963	Sequence 784963,
	26	15.2	50.7	25	24	US-10-719-956-25613	Sequence 25613, A
	27	15.2	50.7	25	26	US-11-036-317-503091	Sequence 503091,
	28	15.2	50.7	25	26	US-11-036-317-61467	Sequence 61467,
	29	15.2	50.7	25	26	US-11-060-756-148502	Sequence 148502,
	30	15.2	50.7	25	26	US-11-060-756-255015	Sequence 255015,
c	31	15.2	50.7	33	10	US-09-759-112A-3	Sequence 3, Appli
	32	15	50.0	25	22	US-10-719-900-169041	Sequence 169041,
c	33	15	50.0	25	22	US-10-956-157-231991	Sequence 231991,
	34	15	50.0	25	22	US-10-956-157-285782	Sequence 285782,
	35	15	50.0	25	26	US-11-036-317-142021	Sequence 142021,
	36	15	50.0	25	26	US-11-036-317-561534	Sequence 561534,
	37	15	50.0	25	26	US-11-036-317-674828	Sequence 674828,
c	38	15	50.0	25	26	US-11-036-317-708626	Sequence 708626,
	39	15	50.0	25	26	US-11-036-317-794581	Sequence 794581,
	40	15	50.0	25	26	US-11-036-317-830452	Sequence 830452,
	41	15	50.0	25	26	US-11-036-317-965123	Sequence 965123,
	42	15	50.0	28	20	US-10-802-441-10	Sequence 10, Appl
	43	15	50.0	29	10	US-09-841-994-12	Sequence 12, Appl
	44	14.8	49.3	25	22	US-10-956-157-161705	Sequence 161705,
	45	14.8	49.3	25	22	US-10-956-157-177245	Sequence 177245,

ALIGNMENTS

RESULT 1
US-08-469-172-7
; Sequence 7, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

✓

```

;
; REGISTRATION NUMBER: 46,063
; REFERENCE/DOCKET NUMBER: 03806.0054-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-716-803-42
;
Query Match 54.0%; Score 16.2; DB 21; Length 38;
Best Local Similarity 66.7%; Pred. No. 3.2e+03;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
;
Qy 1 GGGAAATTCGGGAGCCAGACGGCACTG 27
Db 11 GSGAGTTCGCGCGCTGGGACGGCACCG 37
;
;
RESULT 7
US-10-123-036-15/c
; Sequence 15, Application US/10123036
; Publication No. US20030073656A1
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital Research Foundation
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF HEPATIC DISORDERS
; FILE REFERENCE: 0010872/0483963
; CURRENT APPLICATION NUMBER: US/10/123,036
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/283,788
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-123-036-15
;
Query Match 54.0%; Score 16.2; DB 15; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
Qy 8 CGCGGAGCCAGACGGCACTGA 28
Db 26 CGCGGAACCAAGACGCGCGCTGA 6
;
;
RESULT 8
US-10-483-289A-3
; Sequence 3, Application US/10483289A
; Publication No. US20050048466A1
; GENERAL INFORMATION:
; APPLICANT: Qian, Qijun
; TITLE OF INVENTION: A specific proliferation in tumour cell which can express
; FILE REFERENCE: antioncogene with high efficiency and the use of it.
; FILE REFERENCE: IEC020038PUS
; CURRENT APPLICATION NUMBER: US/10/483,289A
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-10-483-289A-3

```

Query Match 54.0%; Score 16.2; DB 22; Length 39;
Best Local Similarity 72.4%; Pred. No. 3.2e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGCACTGAAG 30
|||||
Db 1 GGAATTCGCGGCGCCGAGATCTCACAGACG 29

RESULT 9

US-10-719-900-439430
; Sequence 439430, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 439430
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-10-719-900-439430

Query Match 52.7%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGAGCCAGACGGCACTGAA 29
|||||
Db 5 GGAGCCAGAGGTACTGAA 23

RESULT 10

US-10-098-263B-97474
; Sequence 97474, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 97474
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-10-098-263B-97474

Query Match 52.0%; Score 15.6; DB 16; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGC 23
|||||
Db 2 GGAATTCGCGAAGCAAGAGGGC 23

RESULT 11

US-10-098-263B-128306/c
; Sequence 128306, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael

; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 128306
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-10-098-263B-128306

Query Match 52.0%; Score 15.6; DB 16; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGC 23
|||||
Db 24 GGAATTCGCGAAGCAAGAGGGC 3

RESULT 12

US-10-719-956-258512
; Sequence 258512, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 258512
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-10-719-956-258512

Query Match 52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 CGCGGAGCCAGCGCACTGAA 29
|||||
Db 1 CGCGGAGCCACAAAGGCCCGAA 22

RESULT 13

US-10-719-956-258513
; Sequence 258513, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 258513
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-10-719-956-258513

Query Match 52.0%; Score 15.6; DB 24; Length 25;

Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 CGCGAGCCAGACGGCACTGAA 29
Db 1 CGCGAGCCACATGGCCCGGAA 22

RESULT 14

US-11-036-317-21919/c
; Sequence 21919, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-21919

Query Match 52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 CGCGAGCCAGACGGCACTGAAG 30
Db 23 GCAGAGCAAAAGGCACTGAAG 2

RESULT 15

US-11-036-317-875174
; Sequence 875174, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 875174
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-875174

Query Match 52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGAATTCGGCGGACGAGCGGC 23
Db 2 GGAATTCGGCGGACGAGCTGC 23

RESULT 16

US-10-719-900-805772/c
; Sequence 805772, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 805772
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-805772

Query Match 51.3%; Score 15.4; DB 22; Length 25;
Best Local Similarity 76.0%; Pred. No. 7.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 AATTGGCGGACCGACGGCACTGA 28
Db 25 AAGACCCGGATACCGACGGCACTGA 1

RESULT 17

US-10-719-900-844398/c
; Sequence 844398, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 844398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-844398

Query Match 51.3%; Score 15.4; DB 22; Length 25;
Best Local Similarity 94.1%; Pred. No. 7.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 AGCCGAGCGGCACTGAA 29
Db 24 AGCCGAGCGGCACTGAA 8

RESULT 18

US-11-036-317-804896
; Sequence 804896, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 804896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-804896

```
Query Match      51.3%; Score 15.4; DB 26; Length 25;
Best Local Similarity 76.0%; Pred. No. 7.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 TTTCGGGAGCCAGCGGCACTGAAG 30
Db 1 TGCAGTGAGCCAGCGCCCTGAAG 25

RESULT 19
US-11-060-756-299133/c
; Sequence 299133, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031895-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 299133
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-299133

Query Match      51.3%; Score 15.4; DB 26; Length 25;
Best Local Similarity 76.0%; Pred. No. 7.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ATTCGGGAGCCAGCGCACTGAA 29
Db 25 ATTCAGAACCAATGTCACTGAA 1

RESULT 20
US-09-858-349-14
; Sequence 14, Application US/09858349
; Patent No. US20020012909A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, Daniel
; TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
; FILE REFERENCE: 87534-2800
; CURRENT APPLICATION NUMBER: US/09/858,349
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 34
; TYPE: DNA
; ORGANISM: pET-21aVH3, XhoI
US-09-858-349-14

Query Match      51.3%; Score 15.4; DB 9; Length 34;
Best Local Similarity 76.0%; Pred. No. 7.2e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGCGGCAC 25
Db 1 GGGAAATTCCTCGAGCTATGCGGCAC 25

RESULT 21
US-10-035-833A-1888/c
; Sequence 1888, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
```

```
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1888
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-1888

Query Match      51.3%; Score 15.4; DB 19; Length 41;
Best Local Similarity 70.4%; Pred. No. 7.1e+03;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 4 AATTCGGGAGCCAGCGGCACTGAAG 30
Db 41 AACTACAGAGCCAGCGCAGCRCTGCAG 15

RESULT 22
US-10-035-833A-4483/c
; Sequence 4483, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4483
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-4483

Query Match      51.3%; Score 15.4; DB 19; Length 41;
Best Local Similarity 70.4%; Pred. No. 7.1e+03;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 4 AATTCGGGAGCCAGCGGCACTGAAG 30
Db 41 AACTACAGAGCCAGCGCAGCRCTGCAG 15

RESULT 23
US-10-667-891-24
; Sequence 24, Application US/10667891
; Publication No. US20040171024A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, CHARLES W.
; APPLICANT: BREY, PAUL T.
; APPLICANT: HOLM, INGE
; APPLICANT: GRAILLES, MARINE
; APPLICANT: RZHETSKY, ANDREY
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND
; FILE REFERENCE: 03495.0294-00000
; CURRENT APPLICATION NUMBER: US/10/667,891
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/413,469
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
```



```
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer
US-10-667-891-24

Query Match          50.7%; Score 15.2; DB 20; Length 24;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGGGAGCCAGAC 20
Db      1 GGGAAATTCGGTGGACAGAC 20

RESULT 24
US-10-807-466-35
; Sequence 35, Application US/10807466
; Publication No. US20040244066A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, CHARLES W.
; APPLICANT: BREY, PAUL T.
; APPLICANT: HOLM, INGE
; APPLICANT: GRAILLES, MARINE
; APPLICANT: RZHETSKY, ANDREY
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND
; FILE REFERENCE: 03495-0294-01000
; CURRENT APPLICATION NUMBER: US/10/807,466
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 10/667,891
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/413,469
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 35
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer
US-10-807-466-35

Query Match          50.7%; Score 15.2; DB 21; Length 24;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGGGAGCCAGAC 20
Db      1 GGGAAATTCGGTGGACAGAC 20

RESULT 25
US-10-719-900-784963/c
; Sequence 784963, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 784963
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: Mus musculus
US-10-719-900-784963

Query Match          50.7%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      7 TCGCGAGCCAGACGGCACT 26
Db      25 TTGCAGAGTCAGACGGCACT 6

RESULT 26
US-10-719-956-25613
; Sequence 25613, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 25613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-25613

Query Match          50.7%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      10 CGGAGCCAGACGGCACTGAA 29
Db      4 CGGAGCGTGACGGCGCTGAA 23

RESULT 27
US-11-036-317-503091
; Sequence 503091, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 503091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-503091

Query Match          50.7%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      8 CGCGAGCCAGACGGCACTG 27
Db      3 CGTGAGCCAGATGGCACAG 22

RESULT 28
US-11-036-317-611467
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```
; Sequence 611467, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 611467
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-611467

Query Match      50.7%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      7 TCGCGGAGCCAGCGGCACT 26
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Db      6 TCACGGAGCCAGACGGTAGT 25

RESULT 29
US-11-060-756-148502
; Sequence 148502, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148502
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-148502

Query Match      50.7%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GGAATTTCGGGAGCCAGACG 21
        ||| ||||| ||||| |||
Db      4 GGAGTTTCGGGAGCCAGAGG 23

RESULT 30
US-11-060-756-255015
; Sequence 255015, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 255015
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: probe
US-11-060-756-255015

Query Match      50.7%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GGAATTTCGGGAGCCAGACG 21
        ||| ||||| ||||| |||
Db      1 GGAGTTTCGGGAGCCAGAGG 20

RESULT 31
US-09-759-112A-3
; Sequence 3, Application US/09759112A
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 33
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)-(33)
; OTHER INFORMATION: 1F7 light chain 5' primer
US-09-759-112A-3

Query Match      50.7%; Score 15.2; DB 10; Length 33;
Best Local Similarity 85.0%; Pred. No. 8.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGGGAGCCAGAC 20
        ||||| ||||| ||||| |||
Db      1 GGGAAATTCATGGAGACAGAC 20

RESULT 32
US-10-719-900-169041/c
; Sequence 169041, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169041
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-169041

Query Match      50.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGGGAGCCAGACGC 23
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Db      24  GGTACTTTGTGGAGCCGACTGC 2
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; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 142021
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-142021

Query Match      50.0%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  GAAATTCGGGAGCCAGCGGCAC 25
      |||||
Db      2  GAATCTCAGAGGAGGAGGCAC 24

RESULT 36
US-11-036-317-561534
; Sequence 561534, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 561534
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-561534

Query Match      50.0%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      8  CGCGGAGCCAGCGGCACTGAAG 30
      |||||
Db      1  CACTGAGCGACGCGCCCTGAAG 23

RESULT 37
US-11-036-317-674828
; Sequence 674828, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 674828
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-674828

Query Match      50.0%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db      23  TCACTGAGCCAGCGGCATTGCA 1

RESULT 35
US-11-036-317-142021
; Sequence 142021, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 231991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-956-157-231991

Query Match      50.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  GGAATTCGGGAGCCAGCGGC 23
      |||||
Db      1  GAGAATTCGGGAGCCAGCTGTC 23

RESULT 34
US-10-956-157-285782/c
; Sequence 285782, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 285782
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-956-157-285782

Query Match      50.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      7  TCGCGGAGCCAGCGGCACTGNA 29
      |||||
Db      23  TCACTGAGCCAGCGGCATTGCA 1

RESULT 33
US-10-956-157-231991
; Sequence 231991, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 231991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-956-157-231991

Query Match      50.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      7  TCGCGGAGCCAGCGGCACTGNA 29
      |||||
Db      23  TCACTGAGCCAGCGGCATTGCA 1
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US-11-036-317-674828
; Sequence 674828, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 674828
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-674828

Query Match      50.0%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 721.376 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCTCTCTTGTGTACTCTCTCTGCTC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_phi.*

8: gb_pl.*

9: gb_pr.*

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11: gb_sbs.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	100.0	26	6	112901	112901 Sequence 8
2	17.2	66.2	24	6	BD172395	BD172395 Secreted
3	17.2	66.2	24	6	BD172714	BD172714 Secreted
4	17.2	66.2	24	6	BD173033	BD173033 Secreted
5	17.2	66.2	24	6	BD173352	BD173352 Secreted
6	17.2	66.2	24	6	BD175386	BD175386 Secreted
7	17.2	66.2	24	6	AR410764	AR410764 Sequence
8	17.2	66.2	24	6	AR439128	AR439128 Sequence
9	17.2	66.2	24	6	AR473148	AR473148 Sequence
10	17.2	66.2	24	6	AR527134	AR527134 Sequence
11	17.2	66.2	24	6	AR566167	AR566167 Sequence
12	17.2	66.2	24	6	AX697613	AX697613 Sequence
13	17.2	66.2	24	6	BD075535	BD075535 Secretory
14	17	65.4	30	6	IB4403	IB4403 Sequence 4
15	17	65.4	30	6	AR202764	AR202764 Sequence
16	17	65.4	36	6	A91851	A91851 Sequence 10
17	17	65.4	39	6	IB4408	IB4408 Sequence 9
18	17	65.4	48	4	AB022055	AB022055 Canis fam
19	17	65.4	48	4	AB022058	AB022058 Canis fam

C 20	17	65.4	48	6	AR178317	AR178317 Sequence
C 21	17	65.4	48	6	AX323399	AX323399 Sequence
C 22	17	65.4	50	6	AS1711	AS1711 Sequence 17
C 23	17	65.4	50	6	AR167590	AR167590 Sequence
C 24	17	65.4	50	6	AR178300	AR178300 Sequence
C 25	17	65.4	50	6	BD223995	BD223995 Near infr
C 26	17	65.4	50	6	AR200395	AR200395 Sequence
C 27	17	65.4	50	6	AX323382	AX323382 Sequence
C 28	17	65.4	50	6	AX686852	AX686852 Sequence
C 29	16.6	63.8	25	6	CQ628816	CQ628816 Sequence
C 30	16.6	63.8	25	6	CQ628817	CQ628817 Sequence
C 31	16.6	63.8	25	6	CQ628818	CQ628818 Sequence
C 32	16.6	63.8	25	6	AR469879	AR469879 Sequence
C 33	16.6	63.8	25	6	AR469880	AR469880 Sequence
C 34	16.6	63.8	25	6	AR469881	AR469881 Sequence
C 35	16.6	63.8	42	6	AR031676	AR031676 Sequence
C 36	16.6	63.8	42	6	I90294	I90294 Sequence 36
C 37	16.6	63.8	48	6	AR111808	AR111808 Sequence
C 38	16.6	63.8	48	6	AR236256	AR236256 Sequence
C 39	16.6	63.8	48	6	AR275530	AR275530 Sequence
C 40	16.4	63.1	28	6	AR120088	AR120088 Sequence
C 41	16.4	63.1	28	6	AR120089	AR120089 Sequence
C 42	16.4	63.1	28	6	BD183077	BD183077 Novel ins
C 43	16.4	63.1	28	6	BD103248	BD103248 Novel ins
C 44	16.4	63.1	40	6	A35229	A35229 Synthetic p
C 45	16.4	63.1	40	6	AR012257	AR012257 Sequence

ALIGNMENTS

RESULT 1
LOCUS 112901 26 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 8 from patent US 5429923.
ACCESSION 112901
VERSION 112901.1 GI:910878
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 8 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTCTTGTGTACTCTCTCTGCTC 26

Db 1 CCTCTCTTGTGTACTCTCTCTGCTC 26

RESULT 2

LOCUS BD172395/c 24 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.
ACCESSION BD172395
KEYWORDS JP 200223786-A/168.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)

AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002223786-A 168 13-AUG-2002;

COMMENT GENENTECH INC

OS Artificial Sequence

PN JP 2002223786-A/168

PD 13-AUG-2002

PF 18-DEC-2001 JP 2001385135

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062285 PR

18-SEP-1997 US 60/062287, 17-OCT-1997 US 60/062286 PR

21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR

21-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR

24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR

27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR

29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR

31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064103 PR

17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065186 PR

21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/065693 PR

24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10,

PC C12P21/02, C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC (C12P21/02, C12R1:645), C12N15/00, C12N5/00

CC Description of Artificial Sequence: Synthetic FH Key

FT Location/Qualifiers

FT source 1. .24

FEATURES Location/Qualifiers

source 1. .24

ORIGIN /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"

Query Match 66.2%; Score 17.2; DB 6; Length 24;

Best Local Similarity 86.4%; Pred. No. 2.4e+04;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAAGTCTCTCTGCTC 26

Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 3

BD172714/c

LOCUS BD172714

DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD172714

VERSION BD172714.1 GI:28414018

KEYWORDS JP 2002238586-A/168.

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

1 (bases 1 to 24)

Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002238586-A 168 27-AUG-2002;

COMMENT GENENTECH INC

OS Artificial Sequence

PN JP 2002238586-A/168

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385205

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR

21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR

24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR

24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR

27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063735 PR

29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR

31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064103 PR

07-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR

17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10,

PC C12P21/02, C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC (C12N5/10, C12R1:91), (C12P21/02, C12R1:91), (C12P21/02, C12R1:645), PC (C12P21/02, C12R1:19), (C12P21/08, C12R1:91), C12N15/00, C12N5/00, PC (C12N5/00, C12R1:91)

CC Description of Artificial Sequence: Synthetic FH Key

FT Location/Qualifiers

FT source 1. .24

FEATURES Location/Qualifiers

source 1. .24

ORIGIN /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"

Query Match 66.2%; Score 17.2; DB 6; Length 24;

Best Local Similarity 86.4%; Pred. No. 2.4e+04;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAAGTCTCTCTGCTC 26

Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 4

BD173033/c

LOCUS BD173033

DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD173033

BD173033.1 GI:28414339
JP 2002238587-A/168.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 24)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: JP 2002238587-A 168 27-AUG-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002238587-A/168
PD 27-AUG-2002
PR 18-DEC-2001 JP 2001385248
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
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17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
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29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR
29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063735 PR
29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/064103 PR
31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR
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21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/065693 PR
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24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
C12P21/02, C12P21/08, C12P21/02, C12R1:91, (C12P21/02, C12R1:19), PC
(C12P21/02, C12R1:645), C12N15/00, C12N5/00, C12N15/00 CC
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Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CTTCTTGTTACTCTCTCTGCTC 26
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Db 24 CCTACTACTACTCTCTCTGCTC 3
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RESULT 5
BD173352/c
LOCUS
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding

the same.
BD173352
BD173352.1 GI:28414663
JP 2002238588-A/168.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 24)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: JP 2002238588-A 168 27-AUG-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002238588-A/168
PD 27-AUG-2002
PR 18-DEC-2001 JP 2001385315
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
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18-SEP-1997 US 60/059287, 17-OCT-1997 US 60/062285 PR
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27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063341 PR
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17-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR
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24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066364 PR
24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
C12P21/02, C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),
PC (C12N5/10, C12R1:91), C12N15/00, C12N5/00, C12N5/00, C12R1:91) CC
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Location/Qualifiers 1. .24
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FEATURES
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
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Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CTTCTTGTTACTCTCTCTGCTC 26
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RESULT 6
BD175386/c
LOCUS
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding

LOCUS AR473148 24 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 204 from patent US 6686451.
ACCESSION AR473148
VERSION AR473148.1 GI:42708523
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Desnovers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Mather, J.P., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6686451-A 204 03-FEB-2004;
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Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTGTACTCTCTCGTCTC 26
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Db 24 CCTACTACTCTCTCTCGTCTC 3
RESULT 10
AR527134/c
LOCUS AR527134 24 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 204 from patent US 6723535.
ACCESSION AR527134
VERSION AR527134.1 GI:53914051
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6723535-A 204 20-APR-2004;
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Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTGTACTCTCTCGTCTC 26
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Db 24 CCTACTACTCTCTCTCGTCTC 3
RESULT 11
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LOCUS AR566167 24 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 204 from patent US 6767995.
ACCESSION AR566167
VERSION AR566167.1 GI:53983077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Desnovers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Mather, J.P., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6767995-A 204 27-JUL-2004;
FEATURES Location/Qualifiers
source 1..24
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/mol_type="genomic DNA"
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Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
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Qy 5 CCTTCTGTACTCTCTCGTCTC 26
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Db 24 CCTACTACTCTCTCTCGTCTC 3
RESULT 12
AX697613/c
LOCUS AX697613 24 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 204 from Patent WO0104311.
ACCESSION AX697613
VERSION AX697613.1 GI:29498708
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Ashkenazi, A.J., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0104311-A 204 18-JAN-2001;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Probe"
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Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
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Qy 5 CCTTCTGTACTCTCTCGTCTC 26
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Db 24 CCTACTACTCTCTCTCGTCTC 3
RESULT 13
BD075535/c
LOCUS BD075535 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding the same.
ACCESSION BD075535
VERSION BD075535.1 GI:22621138
KEYWORDS JP 2001516580-A/168.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.
TITLE Secretory and transmembrane polypeptide and nucleic acid encoding the same
JOURNAL Patent: JP 2001516580-A 168 02-OCT-2001;

REFERENCE 1 (bases 1 to 24)
AUTHORS Desnovers, L., Goddard, A., Godowski, P.J., Gurney, A.L. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: US 6767995-A 204 27-JUL-2004;
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Qy 5 CCTTCTGTACTCTCTCGTCTC 26
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Db 24 CCTACTACTCTCTCTCGTCTC 3
RESULT 12
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LOCUS AX697613 24 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 204 from Patent WO0104311.
ACCESSION AX697613
VERSION AX697613.1 GI:29498708
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Ashkenazi, A.J., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0104311-A 204 18-JAN-2001;
FEATURES Location/Qualifiers
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/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Probe"
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Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTGTACTCTCTCGTCTC 26
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Db 24 CCTACTACTCTCTCTCGTCTC 3
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DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding the same.
ACCESSION BD075535
VERSION BD075535.1 GI:22621138
KEYWORDS JP 2001516580-A/168.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.
TITLE Secretory and transmembrane polypeptide and nucleic acid encoding the same
JOURNAL Patent: JP 2001516580-A 168 02-OCT-2001;

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GENENTECH, INC
OS Artificial Sequence
PN JP 2001516580-A/168
PD 02-OCT-2001
PF 16-SEP-1998 JP 2000511867
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
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24-NOV-1997 US 60/066466, 24-NOV-1997 US 60/066770 PR
25-NOV-1997 US 60/066511, 24-NOV-1997 US 60/066453 PR
PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDLEY GODDARD, DIANE PENICA, PI
JEAN CHEN,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K14/705, C07K16/18, C07K16/28, C07K19/00,
PC C12N1/19,
PC C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/02, C12P21/08, PC
C12R1/31,
PC C12N15/00, C12N5/00
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Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CCTCTCTGTACTCCTCCTCGTC 26
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RESULT 14
184403/c
LOCUS
DEFINITION Sequence 4 from patent US 5695933.
ACCESSION 184403
VERSION 184403.1 GI:3021923
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Schalling, M., Hudson, T.J. and Housman, D.E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 4 09-DEC-1997;
FEATURES
Location/Qualifiers
Query Match 65.4%; Score 17; DB 6; Length 36;
Best Local Similarity 80.0%; Pred. No. 2.8e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 CCTCTCTCTGTACTCCTCCTCGTC 26
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Db 1 CCTCTCTCTCCTCCTCCTCCTCCTC 25
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RESULT 15
AR202764
LOCUS
DEFINITION Sequence 12 from patent US 6365344.
ACCESSION AR202764
VERSION AR202764.1 GI:21498978
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Nolan, G.P. and Rothenberg, S. Michael.
TITLE Methods for screening for transdominant effector peptides and RNA molecules
JOURNAL Patent: US 6365344-A 12 02-APR-2002;
FEATURES
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/mol_type="unassigned DNA"
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Best Local Similarity 80.0%; Pred. No. 2.8e+04;
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Db 1 CCTCTCTCTCCTCCTCCTCCTCCTC 25
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RESULT 16
A91851/c
LOCUS
DEFINITION Sequence 10 from Patent WO9823743.
ACCESSION A91851
VERSION A91851.1 GI:6740735
KEYWORDS
SOURCE
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS DAVIES, K.E. and Theodosiou, A.
TITLE MURINE GUANINE NUCLEOTIDE EXCHANGE FACTOR - (MNGEF) AND HUMAN
HOMOLOGUES THEREOF
JOURNAL Patent: WO 9823743-A 10 04-JUN-1998;
MEDICAL RES COUNCIL (GB); DAVIES KAY ELIZABETH (GB)
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Best Local Similarity 80.0%; Pred. No. 2.6e+04;
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Db  47 CCTCCTCTCTCTCTCTCTCTCTCTCTCTC 23

RESULT 21
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ACCESSION  AX323399
VERSION     AX323399.1 GI:18094161
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
TITLE       Purification of a triple helix formation with an immobilized
            oligonucleotide
JOURNAL     Patent: WO 0192511-A 34 06-DEC-2001;
            Aventis Pharma (FR)
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Db  47 CCTCCTCTCTCTCTCTCTCTCTCTCTCTC 23

RESULT 22
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LOCUS      A51711
DEFINITION Sequence 17 from Patent WO9618744.
ACCESSION  A51711
VERSION     A51711.1 GI:2304515
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Crouzet,J., Scherman,D. and Wils,P.
TITLE       PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN IMMOBILIZED
            OLIGONUCLEOTIDE
JOURNAL     Patent: WO 9618744-A 17 20-JUN-1996;
            RHONE POULENC RORER SA (FR)
COMMENT     Other publication AU 4178996 960703
            Other publication FR 2728264 960621.
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Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db  49 CCTCCTCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 23
AR167590/c
LOCUS      AR167590
DEFINITION Sequence 17 from patent US 6287762.
ACCESSION  AR167590
VERSION     AR167590.1 GI:17903379
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Crouzet,J., Scherman,D. and Wils,P.
TITLE       Purification of a triple helix formation with an immobilized
            oligonucleotide
JOURNAL     Patent: US 6287762-A 17 11-SEP-2001;
            Location/Qualifiers
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Db  49 CCTCCTCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 24
AR178300/c
LOCUS      AR178300
DEFINITION Sequence 17 from patent US 6319672.
ACCESSION  AR178300
VERSION     AR178300.1 GI:20219438
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
TITLE       Purification of a triple helix formation with an immobilized
            oligonucleotide
JOURNAL     Patent: US 6319672-A 17 20-NOV-2001;
            Location/Qualifiers
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Best Local Similarity 80.0%; Pred. No. 2.6e+04;
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LOCUS      BD223995
DEFINITION Near infrared chemiluminescent acridinium compounds and uses
            thereof.
ACCESSION  BD223995
VERSION     BD223995.1 GI:33033765
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
TITLE       Purification of a triple helix formation with an immobilized
            oligonucleotide
JOURNAL     Patent: US 6319672-A 17 20-NOV-2001;
            Location/Qualifiers
FEATURES    source
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            /mol_type="unassigned DNA"

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Best Local Similarity 80.0%; Pred. No. 2.6e+04;
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KEYWORDS JP 2002522530-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 50)
JOURNAL Natrajan,A., Jiang,Q., Sharpe,D. and Law,S.-J.
COMMENT Near infrared chemiluminescent acridinium compounds and uses
thereof
PATENT: JP 2002522530-A 4 23-JUL-2002;
BAYER CORP
OS Homo sapiens (human)
PN JP 2002522530-A/4
PD 23-JUL-2002
PF 10-AUG-1999 JP 2000564941
PI 11-AUG-1998 US 60/096073
PR ANAND NATRAJAN,QINGPING JIANG,DAVID SHARPE,SAY JONG LAW PC
C07D219/04,C07D401/12,C09K3/00,C09K11/07,C12N15/09,C12Q1/68, PC
G01N21/76,
PC G01N33/58//C07K14/765,C07K16/26,G01N33/532,C12N15/00 CC
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Db 26 CCTCTCTCTCTCTCTCTCTCTC 2
RESULT 26
AR200395/c
LOCUS AR200395 50 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6355803.
ACCESSION AR200395
VERSION AR200395.1 GI:20250469
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Natrajan,A., Jiang,Q., Sharpe,D. and Law,S.-J.
TITLE Near infrared chemiluminescent acridinium compounds and uses
thereof
JOURNAL Patent: US 6355803-A 4 12-MAR-2002;
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Db 26 CCTCTCTCTCTCTCTCTCTCTC 2
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LOCUS AX323382 50 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 17 from Patent WO0192511.

AX323382
VERSION AX323382.1 GI:18094144
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Crouzet,J., Scherman,D., Wils,P., Blanche,P. and Cameron,B.
TITLE Purification of a triple helix formation with an immobilized
oligonucleotide
JOURNAL Patent: WO 0192511-A 17 06-DEC-2001;
FEATURES Aventis Pharma (FR)
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RESULT 28
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LOCUS AX686852 50 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 17 from Patent EP1281774.
ACCESSION AX686852
VERSION AX686852.1 GI:29372393
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Couzet,J., Scherman,D. and Wils,P.
TITLE Purification of a triple helix formation with an immobilized
oligonucleotide
JOURNAL Patent: EP 1281774-A 17 05-FEB-2003;
FEATURES Aventis Pharma S.A. (FR)
source Location/Qualifiers
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RESULT 29
CQ628816/c
LOCUS CQ628816 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13556 from Patent WO0192524.
ACCESSION CQ628816
VERSION CQ628816.1 GI:41679034
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13556 06-DEC-2001;
Aeomica, Inc. (US)
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LOCUS CQ628817 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13557 from Patent WO0192524.
ACCESSION CQ628817
VERSION CQ628817.1 GI:41679035
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13557 06-DEC-2001;
Aeomica, Inc. (US)
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Db 24 CTCCTTCTTGGAAGTCTCTCTGCT 2
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CQ628818/c
LOCUS CQ628818 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13558 from Patent WO0192524.
ACCESSION CQ628818
VERSION CQ628818.1 GI:41679036
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13558 06-DEC-2001;
Aeomica, Inc. (US)
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Best Local Similarity 82.6%; Pred. No. 4.1e+04;
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Db 23 CTCCTTCTTGGAAGTCTCTCTGCT 1
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RESULT 32
AR469879/c
LOCUS AR469879 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13556 from patent US 6686188.
ACCESSION AR469879
VERSION AR469879.1 GI:42704936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13556 03-FEB-2004;
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Qy 3 CTCCTTCTTGTAAGTCTCTCTGCT 25
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Db 25 CTCCTTCTTGGAAGTCTCTCTGCT 3
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RESULT 33
AR469880/c
LOCUS AR469880 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13557 from patent US 6686188.
ACCESSION AR469880
VERSION AR469880.1 GI:42704937
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13557 03-FEB-2004;
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Db 24 CTCCTTCTTGCTTCTCCAGCT 2
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DEFINITION Sequence 13558 from patent US 6686188.
ACCESSION AR469881
VERSION AR469881.1 GI:42704938
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13558 03-FEB-2004;
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LOCUS AR031676/c 42 bp DNA
DEFINITION Sequence 36 from patent US 5866394.
ACCESSION AR031676
VERSION AR031676.1 GI:5945965
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 42)
AUTHORS Houtz,R.L.
TITLE Cloning and developmental expression of pea
ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
epsilon N-methyltransferase
JOURNAL Patent: US 5866394-A 36 02-FEB-1999;
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RESULT 36
LOCUS I90294 42 bp DNA
DEFINITION Sequence 36 from patent US 5723752.
ACCESSION I90294
VERSION I90294.1 GI:3410234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 42)
AUTHORS Houtz,R.L.
TITLE Cloning and developmental expression of pea
ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
epsilon N-methyltransferase
JOURNAL Patent: US 5723752-A 36 03-MAR-1998;
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Qy 4 TCCTTCTTGCTTCTCTCTGCTC 26
Db 33 TCCTTCTTGCTTCTCTCTCTC 11
RESULT 37
LOCUS AR111808/c 48 bp DNA
DEFINITION Sequence 7 from patent US 6127521.
ACCESSION AR111808
VERSION AR111808.1 GI:12828656
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Berlin,V., Chiu,M.Isabel., Cottarel,G. and Damagnez,V.
TITLE Immunosuppressant target proteins
JOURNAL Patent: US 6127521-A 7 03-OCT-2000;
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Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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LOCUS AR236256/c 48 bp DNA
DEFINITION Sequence 7 from patent US 6464974.
ACCESSION AR236256
VERSION AR236256.1 GI:27280077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Berlin,V., Chiu,M.I., Cottarel,G. and Damagnez,V.
TITLE Immunosuppressant target proteins
JOURNAL Patent: US 6464974-A 7 15-OCT-2002;
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Db 42 TTCTACTTGTACTCTCTCCACCTC 20

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LOCUS AR275530 48 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 7 from patent US 6509152.
ACCESSION AR275530
VERSION AR275530.1 GI:29708948
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 48)
Unclassified.
AUTHORS Berlin,V., Chiu,M.I., Cottarel,G. and Damagnez,V.
TITLE Immunosuppressant target proteins
JOURNAL Patent: US 6509152-A 7 21-JAN-2003;
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LOCUS AR120088 28 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6153596.
ACCESSION AR120088
VERSION AR120088.1 GI:14102787
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 28)
Unclassified.
AUTHORS Liotta,D.C., Petros,J.A., Wey,S.-J., Karr,J.F. and Pohl,J.
TITLE Polycationic oligomers
JOURNAL Patent: US 6153596-A 2 28-NOV-2000;
FEATURES
Location/Qualifiers
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Qy 1 CCTCTCTTGTGTTACTCTCTCTGCTC 26
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Job time : 723.476 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 179.034 Seconds
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Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCTCTCTTGTACTCTCTCTGCTC 26

Scoring table: IDENTITY NUC

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Total number of hits satisfying chosen parameters: 4167236

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: geneseqn2001as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	26	100.0	26	9	ACA63118 Human bet
3	26	100.0	26	13	ADR05304 Human bet
4	18.6	71.5	50	10	ABZ22093 Polyanion
5	18.6	71.5	50	10	ABZ22129 Polyanion
6	18.4	70.8	32	3	AAA30793 Human Bip
7	17.2	66.2	24	2	AAx52400 Reverse P
8	17.2	66.2	24	3	ADC78524 Human PRO
9	17.2	66.2	24	4	AAf72558 Human PRO
10	17.2	66.2	24	8	ACA60167 Human sec
11	17.2	66.2	24	8	ACD07567 Novel hum
12	17.2	66.2	24	8	ABx71615 Human sec
13	17.2	66.2	24	8	ACH06947 Human sec
14	17.2	66.2	24	8	ABx96184 Human sec
15	17.2	66.2	24	8	ACA05505 Human sec
16	17.2	66.2	24	8	ACD20172 Human sec
17	17.2	66.2	24	8	ACA54975 Novel sec
18	17.2	66.2	24	9	ACD19810 Human sec
19	17.2	66.2	24	9	ADB29409 Human sec
20	17.2	66.2	24	9	ADA18265 Human sec

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C 24	17.2	66.2	24	9	ADA42385	Ada42385 Human sec
C 25	17.2	66.2	24	9	ACD23296	AcD23296 Human PRO
C 26	17.2	66.2	24	9	ADA16664	Ada16664 Human sec
C 27	17.2	66.2	24	9	ADA13093	Ada13093 Human sec
C 28	17.2	66.2	24	9	ADA11961	Ada11961 Human sec
C 29	17.2	66.2	24	9	ADA17308	Ada17308 Human sec
C 30	17.2	66.2	24	9	ADA42811	Ada42811 Human sec
C 31	17.2	66.2	24	9	ACD23658	AcD23658 Human PRO
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C 34	17.2	66.2	24	10	ADC28512	AdC28512 Human sec
C 35	17.2	66.2	24	10	ADC39712	AdC39712 Human sec
C 36	17.2	66.2	24	10	ADC40226	AdC40226 Human sec
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C 40	17.2	66.2	24	10	ADC28936	AdC28936 Human sec
C 41	17.2	66.2	24	10	ADC40821	AdC40821 Human sec
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ALIGNMENTS

RESULT 1

AAQ91128
ID AAQ91128 standard; cDNA; 26 BP.

XX AC AAQ91128;

XX DT 19-FEB-1996 (first entry)

XX DE Beta-cardiac myosin heavy chain PCR primer D'.

XX KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
diagnosis; primer; mutation; detection; ss.

XX OS Synthetic.

XX PN US5429923-A.

XX PD 04-JUL-1995.

XX PF 11-DEC-1992; 92US-00989160.

XX PR 11-DEC-1992; 92US-00989160.

XX PA (HARD) HARVARD COLLEGE.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
(GHEO-) GEN HOSPITAL SHENYANG MILITARY AREA.

XX PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX WPI; 1995-245715/32.

XX DR Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
useful for testing asymptomatic individual(s).

XX PT Example 1; Col 10; 22pp; English.

XX PS AAQ91121-091130 are nested PCR primers used for the amplification and
identification of beta-cardiac myosin heavy-chain RNA. They are used in a
new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
the method involves detecting the presence or absence of specific HC-
associated mutations in the beta-cardiac myosin heavy-chain obtained from
a blood sample. The method may be used to diagnose familial or sporadic
HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 26 BP; 1 A; 13 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTCTTGTACTCTCTCTGCTC 26

Db 1 CCTCTCTTGTACTCTCTCTGCTC 26

RESULT 2

ACA63118

ID ACA63118 standard; DNA; 26 BP.

XX AC ACA63118;

XX DT 28-AUG-2003 (first entry)

XX DE Human beta cardiac myosin heavy chain PCR primer D'.

XX Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
 KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
 KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
 KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

XX US2003054343-A1.

XX PD 20-MAR-2003.

XX PF 06-JUN-1995; 95US-00469172.

XX PR 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with
 PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
 PT hemophilia, by detecting a mutation in an amplified product of a beta
 PT cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (sporadic or familial SHC
 CC and FHC) comprises detecting a mutation associated with hypertrophic
 CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy
 CC chain DNA. The mutations associated with SHC/FHC are detected in the
 CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-
 CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
 CC sample). FHC associated point mutation can be classified and used to
 CC determine life expectancy in affected individuals e.g. using a Kaplan-
 CC Meier curve for the classified type of FHC causing point mutation. Also
 CC included are an RNA probe comprising ribonucleotides arranged in a
 CC sequence which is complementary to at least a portion of beta-cardiac
 CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
 CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a nested PCR primer used to amplify a region of the beta cardiac
 CC myosin heavy chain cDNA containing an FHC-associated mutation

XX Sequence 26 BP; 1 A; 13 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTCTTGTACTCTCTCTGCTC 26

Db 1 CCTCTCTTGTACTCTCTCTGCTC 26

RESULT 3

ADR05304

ID ADR05304 standard; DNA; 26 BP.

XX AC ADR05304;

XX DT 21-OCT-2004 (first entry)

XX DE Human beta cardiac myosin heavy chain mutation detection primer D'A.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;

KW familial hypertrophic cardiomyopathy;

KW sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

XX US2004152121-A1.

XX PD 05-AUG-2004.

XX PF 27-FEB-2004; 2004US-00788779.

XX PR 11-DEC-1992; 92US-00989160.

XX PR 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to
 PT diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
 PT myosin heavy-chain DNA and detecting the mutation in the amplified
 PT product.

XX Claim 18; SEQ ID NO 8; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
 CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
 CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
 CC amplified product, and detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy in the amplified product,
 CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
 CC included are a set of DNA oligonucleotide primers for amplifying beta-
 CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

CC Sequence 26 BP; 1 A; 13 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTCTTGTACTCTCTCGTC 26
Db 1 CCTCTCTTGTACTCTCTCGTC 26

RESULT 4

ABZ22093
ID ABZ22093 standard; DNA; 50 BP.

XX AC ABZ22093;

XX 11-MAR-2003 (first entry)

XX Polyanionic polymer related oligonucleotide #47.

XX Polyanionic polymer; bioactivity; water solubility; ss.

XX Synthetic.

XX WO200277036-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US008614.

XX 21-MAR-2001; 2001US-0277705P.

XX (LEUNG/) LEUNG D W.

XX Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;
XX Waggoner DW;

XX WPI; 2003-058367/05.

XX Producing monodispersed preparation of polyanionic polymer for therapy,
XX by expressing vector comprising ligation product of oligonucleotides
XX encoding glutamate/aspartate residues in host cell and isolating the
XX product.

XX Disclosure; Fig 5; 74pp; English.

CC The present invention describes a method (M) for producing a
CC monodispersed preparation of a polyanionic polymer (PP) larger than 10
CC kD. (M) involves inserting into an expression vector (EV) a ligation
CC product formed by ligating together oligonucleotides that encode
CC glutamate/aspartate residues, expressing EV in a host cell, and isolating
CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is
CC approximately of the same molecular weight. Also described: (1) a
CC recombinant fusion protein (I) comprising a polyanionic polypeptide and
CC another polypeptide at either one end or at both ends of it; (2) a
CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and
CC leucine, where the polyanionic polymer is polyglutamic acid or
CC polyaspartic acid; (3) a vector (III) comprising a cassette which
CC comprises a nucleotide sequence encoding a polyanionic polymer and at
CC least one other nucleotide sequence, where the polyanionic polymer is
CC polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell
CC (IV) comprising (II) or a vector that comprises a nucleotide sequence
CC that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a
CC recombinantly-produced polyanionic polymer (V) that is of any molecular
CC weight or is larger than 10 kD, and is conjugated to another protein. (I)
CC is useful for treating a disease or ailment in an individual by
CC administering (I) to the individual. (I) is also useful for delivering an
CC effective amount of a pharmaceutically active agent, a therapeutic
CC protein or a drug to a patient in need of it, or for diagnostic and
CC testing or research purposes. ABZ22045 to ABZ22131 and ABP56374 to
CC ABP56400 represent sequences used in the exemplification of the present
CC invention

CC Sequence 50 BP; 1 A; 24 C; 1 G; 24 T; 0 U; 0 Other;

Query Match 71.5%; Score 18.6; DB 10; Length 50;
Best Local Similarity 84.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CCTCTCTTGTACTCTCTCGTC 26
Db 21 CCTCTCTTGTACTCTCTCGTC 45

RESULT 5

ABZ22129
ID ABZ22129 standard; DNA; 50 BP.

XX AC ABZ22129;

XX 11-MAR-2003 (first entry)

XX Polyanionic polymer related oligonucleotide #83.

XX Polyanionic polymer; bioactivity; water solubility; ss.

XX Synthetic.

XX WO200277036-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US008614.

XX 21-MAR-2001; 2001US-0277705P.

XX (LEUNG/) LEUNG D W.

XX Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;
XX Waggoner DW;

XX WPI; 2003-058367/05.

XX Producing monodispersed preparation of polyanionic polymer for therapy,
XX by expressing vector comprising ligation product of oligonucleotides
XX encoding glutamate/aspartate residues in host cell and isolating the
XX product.

XX Example 7; Fig 8; 74pp; English.

XX The present invention describes a method (M) for producing a
 CC monodispersed preparation of a polyanionic polymer (PP) larger than 10
 CC kD. (M) involves inserting into an expression vector (EV) a ligation
 CC product formed by ligating together oligonucleotides that encode
 CC glutamate/aspartate residues, expressing EV in a host cell, and isolating
 CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is
 CC approximately of the same molecular weight. Also described: (1) a
 CC recombinant fusion protein (I) comprising a polyanionic polypeptide and
 CC another polypeptide at either one end or at both ends of it; (2) a
 CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and
 CC leukine, where the polyanionic polymer is polyglutamic acid or
 CC polyaspartic acid; (3) a vector (III) comprising a cassette which
 CC comprises a nucleotide sequence encoding a polyanionic polymer and at
 CC least one other nucleotide sequence, where the polyanionic polymer is
 CC polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell
 CC (IV) comprising (III) or a vector that comprises a nucleotide sequence
 CC that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a
 CC recombinantly-produced polyanionic polymer (V) that is of any molecular
 CC weight or is larger than 10 kD, and is conjugated to another protein. (I)
 CC is useful for treating a disease or ailment in an individual by
 CC administering (I) to the individual. (I) is also useful for delivering an
 CC effective amount of a pharmaceutically active agent, a therapeutic
 CC protein or a drug to a patient in need of it, or for diagnostic and
 CC testing or research purposes. AB222045 to AB222131 and ABP56374 to
 CC ABP56400 represent sequences used in the exemplification of the present
 CC invention

SQ Sequence 50 BP; 1 A; 24 C; 1 G; 24 T; 0 U; 0 Other;

Query Match 71.5%; Score 18.6; DB 10; Length 50;
 Best Local Similarity 84.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 CCTCCTCTTGTACTCCCTGCTC 26
 |||||
 Db 21 CCTCCTCTTGTACTCCCTGCTC 45

RESULT 6

AAA30793/c
 ID AAA30793 standard; cDNA; 32 BP.

XX AAA30793;

XX 29-AUG-2000 (first entry)

XX Human BiP(78KD) forward PCR primer, derived from GenBank X87949.

XX Immunoglobulin heavy chain binding protein; BiP(78KD); chondrocyte;
 KW autoantigen; rheumatoid arthritis; antiarthritic; antirheumatic; p78;
 KW PCR primer; ss.

XX Homo sapiens.

XX WO200021995-A1.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-GB003316.

XX 09-OCT-1998; 98GB-00022115.

XX (UNLO) KINGS COLLEGE LONDON.

XX Panayi GS, Corrigan VM, Bodman-Smith MD, Fife MS, Lanchbury JS;

XX WPI; 2000-317942/27.

XX New human immunoglobulin heavy chain binding protein and encoding
 PT polynucleotide, useful for diagnosis and treatment of rheumatoid
 PT arthritis.

PS Example 2; Page 8; 53pp; English.

XX The invention relates to a human immunoglobulin heavy chain binding
 CC protein, BiP(78KD) (Y90693), having a 639 amino acid sequence, and to the
 CC cDNA encoding it (A30792). The invention also encompasses a BiP(78KD)
 CC protein of 633 amino acids (Y90694). The cDNA encoding BiP(78KD), also
 CC referred to as p78 in the specification, was isolated from human
 CC chondrocytes (the specialised cells of articular cartilage) and human
 CC chondrosarcoma cell lines. The BiP(78KD) cDNA of this invention contains
 CC a number of differences compared with the published sequence (GenBank
 CC accession number X87949), and has therefore been deposited with
 CC GenBank with the accession number AF188611). These differences comprise 6
 CC single nucleotide substitutions and a codon insertion, and result in
 CC three amino acid substitutions and an arginine insertion at position 834-
 CC 836 of the protein. The BiP(78KD) proteins react with antibodies present
 CC in the serum of rheumatoid arthritis patients, and is therefore a
 CC putative autoantigen for this autoimmune disease. BiP(78KD) is also able
 CC to selectively proliferate synovial T-cells from patients with rheumatoid
 CC arthritis. BiP(78KD) or peptides derived from the protein are useful as
 CC reagents to indicate the presence of rheumatoid arthritis, and can be
 CC used in prognostic or diagnostic tests of body fluids for rheumatoid
 CC arthritis by ELISA (enzyme linked immunosorbent assay) or Western
 CC blotting. The protein or the cDNA encoding it can also be used to test
 CC for rheumatoid arthritis by detecting antibodies to the protein.
 CC BiP(78KD), its peptides and polynucleotides are also useful
 CC therapeutically. Sequences A30743-A30794 represent human BiP(78KD) PCR
 CC primers used in an exemplification of the invention for subcloning into a
 CC bacterial expression vector. The sequence of the primers are based on the
 CC previously published BiP(78KD) sequence (GenBank X87949)

SQ Sequence 32 BP; 13 A; 3 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 70.8%; Score 18.4; DB 3; Length 32;
 Best Local Similarity 95.0%; Pred. No. 1.7e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CCTCCTCTTGTACTCCCTCC 21
 |||||
 Db 29 CCTCCTCTTGTACTCCCTCC 10

RESULT 7

AA52400/c

ID AA52400 standard; DNA; 24 BP.

XX AA52400;

XX 25-JUN-1999 (first entry)

XX Reverse PCR primer used to amplify cDNA encoding PRO263.

XX Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
 KW wound healing; tissue repair; PCR primer; ss.

XX Synthetic.

XX WO9914328-A2.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059115P.

XX 17-SEP-1997; 97US-0059117P.

XX 17-SEP-1997; 97US-0059119P.

XX 17-SEP-1997; 97US-0059121P.

XX 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064213P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 PR (GETH) GENENTECH INC.
 PA Wood WI, Gurney AL, Pennica D, Chen J, Yuan J;
 PI WPI; 1999-229533/19.
 XX New isolated human genes and polypeptides used in, e.g. treatment of
 XX gastrointestinal ulceration.
 XX Example 33; Page 140; 320pp; English.
 XX Oligonucleotides AAX52276-532 represent PCR primers and probes used to
 CC isolate and amplify cDNA encoding secreted and transmembrane human
 CC proteins (see AAX52213-74 and AAX1344-403). The cDNA sequences are
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides have
 CC specific uses based on their homology to known polypeptides, e.g. PRO211
 CC and PRO217 can be used for disorders associated with the preservation and
 CC maintenance of gastrointestinal mucosa and the repair of acute and
 CC chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome,
 CC gastrointestinal ulceration and congenital microvillus atrophy), skin
 CC diseases associated with abnormal keratinocyte differentiation (e.g.
 CC psoriasis, epithelial cancers such as lung squamous cell carcinoma of the
 CC vulva and gliomas), potent effects on cell growth and development,
 CC diseases related to growth or survival of nerve cells including
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer.
 CC PRO265 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may

CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 66.2%; Score 17.2; DB 2; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5 CCTTCTGTACTCTCTCGTCTC 26
 ||| || ||||| |||||
 DB 24 CCTACTACTCTCTCGTCTC 3
 RESULT 8
 ADC78524/c
 ID ADC78524 standard; DNA; 24 BP.
 XX
 AC ADC78524;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human PRO protein-related reverse PCR primer SEQ ID 204.
 XX
 KW antiinflammatory; antiulcer; cytostatic; antipsoiatic; antiparkinsonian;
 KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;
 KW neurotrophic; osteopathic; antiasthatic; antirheumatic; antirheumatic;
 KW antiarteriosclerotic; cardiac; antidiabetic; cerebroprotective;
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; primer; PCR.
 OS Homo sapiens.
 XX WO200015796-A2.
 PN
 XX 23-MAR-2000.
 PD
 XX 15-SEP-1999; 99WO-US021090.
 XX
 PR 16-SEP-1998; 98WO-US019330.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 PI Yuan J;
 XX
 DR WPI; 2000-271434/23.
 XX
 PT Novel nucleic acids encoding secreted and transmembrane polypeptides with
 PT homology, e.g. to growth and cancer-associated antigens.
 XX
 PS Example 33; SEQ ID NO 204; 355pp; English.
 XX
 CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
 CC The polypeptides and polynucleotides of the invention may be useful as
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-
 CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
 CC scarring and wound healing, nerve repair, thrombosis, bone and/or
 CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
 CC infertility, premature aging, AIDS, diabetes complications and stroke.
 CC The molecules may also be utilised during gene therapy procedures and
 CC transgenic animal production. The current sequence is that of the PCR
 CC primer of the invention which was used to analyse the human PRO DNA of

CC the invention.

XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

SQ Query Match 66.2%; Score 17.2; DB 3; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAATCTCTCTGCTC 26
 ||| || ||||| ||||| |||||
 Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 9
 AAF72558/c
 ID AAF72558 standard; DNA; 24 BP.
 XX AC AAF72558;
 XX 24-APR-2001 (first entry)
 DT Human PRO polypeptide gene PCR primer SEQ ID NO: 204.
 XX Human; PRO: dermatologic; antipsoriatic; cytostatic; antiinflammatory;
 XX antiparkinsonian nootropic; neuroprotective; vulnerary; cardiac;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation; PCR primer; ss.
 XX Homo sapiens.
 OS
 XX WO200104311-A1.
 PN 18-JAN-2001.
 XX 22-FEB-2000; 2000WO-US004414.
 PF 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145639P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI; 2001-081051/09.
 DR Sixty one nucleic acids encoding PRO polypeptides which are useful in the
 XX treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
 XX cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 XX disease).
 PS Example 33; Page 178; 393pp; English.
 XX The present sequence is a primer which was used in the isolation of one

CC of sixty one nucleic acids encoding novel secreted and transmembrane PRO
 polypeptides. The PRO polypeptides are useful for treating skin diseases
 (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
 ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
 disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
 CC infertility, AIDS and diabetes and retinal disorders such as retinitis
 CC pigmentosum. The PRO nucleic acids have applications in molecular
 CC biology, including use as hybridization probes, and in chromosome and
 CC gene mapping
 XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 SQ Query Match 66.2%; Score 17.2; DB 4; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAATCTCTCTGCTC 26
 ||| || ||||| ||||| |||||
 Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 10
 ACA60167/c
 ID ACA60167 standard; DNA; 24 BP.
 XX AC ACA60167;
 XX 12-JUN-2003 (first entry)
 DT Human secreted/transmembrane protein PRO263 PCR primer #3.
 DE Human; ss; PCR; secreted protein; transmembrane protein; PRO;
 KW gene therapy; chromosome identification; chromosome marker; primer.
 XX Homo sapiens.
 OS
 XX US2003003530-A1.
 PN 02-JAN-2003.
 PD 11-JUL-2001; 2001US-00904011.
 PF 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 27-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-00634335P.
 PR 29-OCT-1997; 97US-00637049P.
 PR 29-OCT-1997; 97US-00637329P.
 PR 29-OCT-1997; 97US-00637339P.
 PR 29-OCT-1997; 97US-00637349P.
 PR 29-OCT-1997; 97US-00637359P.
 PR 29-OCT-1997; 97US-00637369P.
 PR 31-OCT-1997; 97US-00642115P.
 PR 31-OCT-1997; 97US-00638709P.
 PR 31-OCT-1997; 97US-00641039P.
 PR 03-NOV-1997; 97US-00642489P.
 PR 07-NOV-1997; 97US-00648099P.
 PR 12-NOV-1997; 97US-00651869P.
 PR 17-NOV-1997; 97US-00655846P.
 PR 18-NOV-1997; 97US-00656939P.
 PR 21-NOV-1997; 97US-00661209P.
 PR 21-NOV-1997; 97US-00663649P.
 PR 24-NOV-1997; 97US-00664539P.
 PR 24-NOV-1997; 97US-00664669P.
 PR 24-NOV-1997; 97US-00665119P.
 PR 24-NOV-1997; 97US-00667709P.
 PR 24-NOV-1997; 97US-00667729P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028331.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003585.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI; 2003-329602/31.
 DR
 XX New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, in generating probes and in tissue typing.
 XX
 XX Example 33; Page 109; 484pp; English.
 PS
 CC The invention relates to an isolated nucleic acid with at least 80%
 CC nucleic acid sequence identity to a nucleotide sequence encoding one of
 CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
 CC PRO protein extracellular domain. Also included are a vector comprising
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO

CC polypeptide (by culturing the host cell for the expression of the PRO
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),
 CC an isolated PRO polypeptide (having at least 80% sequence identity to:
 CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
 CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC
 CC number (detailed in the specification); or (c) an extracellular domain of
 CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal
 CC peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a
 CC heterologous amino acid sequence, an anti-PRO antibody, detecting a
 CC PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
 CC linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
 CC modulating at least one biological activity of a cell expressing a PRO245
 CC or PRO1868. Nucleic acids which encode PRO can be used to generate either
 CC transgenic animals or knock-out animals which may be used in the
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy, in chromosome identification, as
 CC chromosome markers, or in generating probes. The PRO polypeptides are
 CC useful as molecular markers for protein electrophoresis, and the isolated
 CC nucleic acids may be used for recombinantly expressing those markers. The
 CC PRO polypeptides and nucleic acids may also be used in tissue typing.
 CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. The present sequence is a PCR primer used to isolate a cDNA
 CC encoding a PRO protein
 XX
 SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 Query Match 66.2%; Score 17.2; DB 8; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5 CCTTCTGTACTCTCTCTGCTC 26
 Db 24 CCTACTACTACTCTCTCTGCTC 3
 RESULT 11
 ACDC07567/c
 ID ACDC07567 standard; DNA; 24 BP.
 XX
 AC ACDC07567;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PCR primer #77.
 XX
 KW Human; secreted and transmembrane protein; PRO; pharmaceutical;
 KW diagnostic; biosensor; bioreactor; Parkinson's disease;
 KW Alzheimer's disease; inflammation; nephritis; wound healing;
 KW nerve repair; collateral blood vessel formation; cancer;
 KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
 KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
 KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
 KW infertility; gene therapy; PCR; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX US2002197671-A1.
 PN
 XX 26-DEC-2002.
 PD
 XX 17-JUL-2001; 2001US-00907824.
 PP
 XX 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.

PR	17-OCT-1997;	97US-0062285P.	PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PR	17-OCT-1997;	97US-0062287P.	PI	Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PR	21-OCT-1997;	97US-0063486P.	PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PR	24-OCT-1997;	97US-0062814P.	PI	Williams PM, Wood WI;
PR	24-OCT-1997;	97US-0063045P.	XX	WPI; 2003-370793/35.
PR	24-OCT-1997;	97US-0063120P.	XX	
PR	24-OCT-1997;	97US-0063121P.	XX	
PR	24-OCT-1997;	97US-0063127P.	PT	New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PR	24-OCT-1997;	97US-0063128P.	PT	PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
PR	27-OCT-1997;	97US-0063327P.	PT	cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
PR	27-OCT-1997;	97US-0063329P.	PT	or strokes.
PR	28-OCT-1997;	97US-0063351P.	XX	
PR	28-OCT-1997;	97US-0063542P.	PS	Example 33; Page 100; 482pp; English.
PR	28-OCT-1997;	97US-0063544P.	XX	
PR	28-OCT-1997;	97US-0063549P.	XX	
PR	28-OCT-1997;	97US-0063550P.	CC	The invention describes a new isolated nucleic acid molecule comprising
PR	28-OCT-1997;	97US-0063550P.	CC	the full length coding sequence of the DNA deposited with the American
PR	28-OCT-1997;	97US-0063564P.	CC	Type Culture Collection (e.g. ATCC Deposit No. 209258) or a sequence
PR	29-OCT-1997;	97US-0063435P.	CC	with at least 80% identity to a DNA encoding a PRO polypeptide comprising
PR	29-OCT-1997;	97US-0063704P.	CC	any of 61 sequences having 164-1119 amino acids fully defined in the
PR	29-OCT-1997;	97US-0063732P.	CC	specification. The PRO polypeptides or polynucleotides are useful as
PR	29-OCT-1997;	97US-0063732P.	CC	pharmaceuticals, diagnostics, biosensors or bioreactors. These are
PR	29-OCT-1997;	97US-0063734P.	CC	particularly useful for detecting or treating e.g. Parkinson's disease,
PR	29-OCT-1997;	97US-0063735P.	CC	Alzheimer's disease, inflammations, nephritis, wound healing, nerve
PR	29-OCT-1997;	97US-0064215P.	CC	repair, collateral blood vessel formation, cancers (e.g. colorectal
PR	29-OCT-1997;	97US-0064215P.	CC	cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
PR	31-OCT-1997;	97US-0063870P.	CC	arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
PR	31-OCT-1997;	97US-0064103P.	CC	ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
PR	03-NOV-1997;	97US-0064248P.	CC	infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
PR	07-NOV-1997;	97US-0064809P.	CC	pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
PR	12-NOV-1997;	97US-0065186P.	CC	therapeutic intervention in these diseases, and diagnostic determination
PR	17-NOV-1997;	97US-0065846P.	CC	of the presence of these diseases. The PRO polypeptides are also useful
PR	18-NOV-1997;	97US-0065693P.	CC	as molecular weight markers, or for chromosome identification. The PRO
PR	21-NOV-1997;	97US-0066120P.	CC	genes are useful as hybridisation probes, or for screening libraries of
PR	21-NOV-1997;	97US-0066364P.	CC	human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
PR	24-NOV-1997;	97US-0066433P.	CC	therapy, particularly for replacing a defective gene. This sequence
PR	24-NOV-1997;	97US-0066466P.	CC	represents a novel human secreted and transmembrane PRO polypeptide
PR	24-NOV-1997;	97US-0066770P.	CC	associated primer
PR	24-NOV-1997;	97US-0066772P.	XX	
PR	10-SEP-1998;	98WO-US01882A.	SQ	Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
PR	14-SEP-1998;	98WO-US019177.		
PR	16-SEP-1998;	98WO-US019330.		
PR	17-SEP-1998;	98WO-US019437.		
PR	01-DEC-1998;	98WO-US025108.		
PR	08-SEP-1999;	99WO-US020594.		
PR	13-SEP-1999;	99WO-US020944.		
PR	15-SEP-1999;	99WO-US021090.		
PR	15-SEP-1999;	99WO-US021547.		
PR	05-OCT-1999;	99WO-US023089.		
PR	30-NOV-1999;	99WO-US028214.		
PR	01-DEC-1999;	99WO-US028313.		
PR	02-DEC-1999;	99WO-US028301.		
PR	02-DEC-1999;	99WO-US028564.		
PR	16-DEC-1999;	99WO-US028565.		
PR	20-DEC-1999;	99WO-US030095.		
PR	20-DEC-1999;	99WO-US030911.		
PR	05-JAN-2000;	2000WO-US000219.		
PR	11-FEB-2000;	2000WO-US003565.		
PR	24-FEB-2000;	2000WO-US004414.		
PR	02-MAR-2000;	2000WO-US005004.		
PR	20-MAR-2000;	2000WO-US005841.		
PR	30-MAR-2000;	2000WO-US007377.		
PR	22-MAY-2000;	2000WO-US008439.		
PR	02-JUN-2000;	2000WO-US014042.		
PR	28-JUL-2000;	2000WO-US015264.		
PR	24-AUG-2000;	2000WO-US020710.		
PR	18-SEP-2000;	2000WO-US023328.		
PR		2000WO-US0665350.		
PA	(GETH) GENENTECH INC.			
XX				
XX	Ashkenazi A, Botstein D, Deanoyers L, Eaton DL, Ferrara N;			
PI				

XX	19-SEP-2002.		PR	11-FEB-2000; 2000WO-US003565.	
PD			PR	22-FEB-2000; 2000WO-US004414.	
XX			PR	24-FEB-2000; 2000WO-US005004.	
PF	18-JUL-2001; 2001US-00909320.		PR	02-MAR-2000; 2000WO-US005841.	
XX			PR	20-MAR-2000; 2000WO-US007377.	
PR	17-SEP-1997; 97US-0059113P.		PR	30-MAR-2000; 2000WO-US008439.	
PR	17-SEP-1997; 97US-0059115P.		PR	02-MAY-2000; 2000WO-US014042.	
PR	17-SEP-1997; 97US-0059117P.		PR	22-JUN-2000; 2000WO-US015264.	
PR	17-SEP-1997; 97US-0059119P.		PR	28-JUL-2000; 2000WO-US020710.	
PR	17-SEP-1997; 97US-0059121P.		PR	24-AUG-2000; 2000WO-US023328.	
PR	17-SEP-1997; 97US-0059122P.		PR	18-SEP-2000; 2000US-00665350.	
PR	17-SEP-1997; 97US-0059184P.		XX		
PR	18-SEP-1997; 97US-0059263P.		PA	(GETH) GENENTECH INC.	
PR	18-SEP-1997; 97US-0059266P.		XX		
PR	15-OCT-1997; 97US-0062125P.		XX	Askenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N;	
PR	17-OCT-1997; 97US-0062285P.		PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;	
PR	17-OCT-1997; 97US-0062287P.		PI	Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;	
PR	21-OCT-1997; 97US-0063486P.		PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;	
PR	24-OCT-1997; 97US-0062814P.		PI	Williams PM, Wood WI;	
PR	24-OCT-1997; 97US-0062816P.		XX		
PR	24-OCT-1997; 97US-0063045P.		XX	WPI; 2003-147434/14.	
PR	24-OCT-1997; 97US-0063120P.		DR		
PR	24-OCT-1997; 97US-0063121P.		XX		
PR	24-OCT-1997; 97US-0063127P.		PT	New PRO polypeptides and nucleic acid molecules, useful in diagnosing or	
PR	24-OCT-1997; 97US-0063128P.		PT	treating inflammatory diseases, organ failure, atherosclerosis, cardiac	
PR	27-OCT-1997; 97US-0063327P.		PT	injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's	
PR	27-OCT-1997; 97US-0063329P.		PT	disease.	
PR	27-OCT-1997; 97US-0063329P.		XX		
PR	28-OCT-1997; 97US-0063541P.		XX	Example 33; Page 99; 473pp; English.	
PR	28-OCT-1997; 97US-0063542P.		PS		
PR	28-OCT-1997; 97US-0063544P.		XX		
PR	28-OCT-1997; 97US-0063549P.		CC	The invention relates to an isolated PRO polypeptide having at least 80%	
PR	28-OCT-1997; 97US-0063550P.		CC	amino acid sequence identity to: (a) any one of 61 fully defined amino	
PR	28-OCT-1997; 97US-0063556P.		CC	acid sequences given in the specification (appearing as ABUS4347-	
PR	28-OCT-1997; 97US-0063564P.		CC	ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence	
PR	29-OCT-1997; 97US-0063435P.		CC	deposited under American Type Culture Collection (accession numbers	
PR	29-OCT-1997; 97US-0063704P.		CC	listed in the specification); (c) any one of the PRO sequences which	
PR	29-OCT-1997; 97US-0063732P.		CC	lacks its associated signal peptide; (d) an extracellular domain of the	
PR	29-OCT-1997; 97US-0063734P.		CC	PRO polypeptide with its associated signal peptide; or (e) an	
PR	29-OCT-1997; 97US-0063735P.		CC	extracellular domain of the PRO polypeptide which lacks its associated	
PR	29-OCT-1997; 97US-0063738P.		CC	signal peptide. Also include are the nucleic acids encoding the PRO	
PR	29-OCT-1997; 97US-0064215P.		CC	polypeptides, vectors, host cells and anti-PRO antibodies. The PRO	
PR	31-OCT-1997; 97US-0063870P.		CC	polypeptides and nucleic acids are useful in diagnosing or treating	
PR	31-OCT-1997; 97US-0064103P.		CC	enterocolitis, gastrointestinal ulceration, skin diseases associated with	
PR	03-NOV-1997; 97US-0064248P.		CC	abnormal keratinocyte differentiation, e.g. psoriasis or epithelial	
PR	07-NOV-1997; 97US-0064809P.		CC	cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's	
PR	12-NOV-1997; 97US-0065186P.		CC	disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.	
PR	17-NOV-1997; 97US-0065846P.		CC	rheumatoid arthritis, asthma or multiple sclerosis, organ failure,	
PR	18-NOV-1997; 97US-0065693P.		CC	atherosclerosis, cardiac injury, infertility, birth defects, premature	
PR	21-NOV-1997; 97US-0066120P.		CC	aging, AIDS, cancer, diabetic complications, or mutations in general. The	
PR	21-NOV-1997; 97US-0066364P.		CC	polypeptides are also useful for wound repair and associated therapies	
PR	24-NOV-1997; 97US-0066453P.		CC	concerned with re-growth of tissue. The nucleotide sequences may be used	
PR	24-NOV-1997; 97US-0066511P.		CC	as hybridisation probes in chromosome and gene mapping, or in generating	
PR	24-NOV-1997; 97US-0066770P.		CC	antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO	
PR	24-NOV-1997; 97US-0066772P.		CC	polypeptides, in assays to identify other proteins or molecules involved	
PR	10-SEP-1998; 98WO-US018824.		CC	in binding reaction, to generate transgenic animals or knockout animals,	
PR	14-SEP-1998; 98WO-US019177.		CC	which in turn are useful in the development and screening of	
PR	16-SEP-1998; 98WO-US019330.		CC	therapeutically useful reagents, for chromosome identification, and	
PR	17-SEP-1998; 98WO-US019437.		CC	tissue typing. The PRO polypeptides and nucleic acid molecules are also	
PR	01-DEC-1998; 98WO-US025108.		CC	useful in gene therapy, and as molecular weight markers for protein	
PR	08-SEP-1999; 99WO-US020594.		CC	electrophoresis purposes. The anti-PRO antibodies may be used in	
PR	13-SEP-1999; 99WO-US020944.		CC	diagnostic assays for PRO, or for the affinity purification of PRO from	
PR	15-SEP-1999; 99WO-US021090.		CC	recombinant cell culture or natural sources. The present sequence is a	
PR	15-SEP-1999; 99WO-US021547.		CC	PCR primer used to isolate a cDNA encoding a PRO polypeptide	
PR	05-OCT-1999; 99WO-US023089.		XX		
PR	29-NOV-1999; 99WO-US028214.		SQ	Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;	
PR	30-NOV-1999; 99WO-US028313.				
PR	01-DEC-1999; 99WO-US028301.		Query Match	66.2%; Score 17.2; DB 8; Length 24;	
PR	02-DEC-1999; 99WO-US028564.		Best Local Similarity	86.4%; Pred. No. 4.7e+03;	
PR	02-DEC-1999; 99WO-US028565.		Matches	19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
PR	16-DEC-1999; 99WO-US030095.				
PR	20-DEC-1999; 99WO-US030911.		Qy	5 CCTTCTTGTTACTCTCTCTGCTC 26	
PR	20-DEC-1999; 99WO-US030999.		Db	24 CCTACTACTACTCTCTCTGCTC 3	
PR	06-JAN-2000; 2000WO-US000219.				

CC PRO187 polypeptide is useful for treating Parkinson's disease,
 CC Alzheimer's disease, amyotrophic lateral sclerosis (ALS), neuropathies
 CC and disease related to uncontrolled cell growth, e.g. cancer. PRO219
 CC polypeptide plays a regulatory role in the blood coagulation cascade.
 CC PRO246 polypeptides which serves as tumour specific antigens may be
 CC exploited as therapeutic targets for anti-tumour drugs. PRO269
 CC polypeptide is useful as an antithrombotic agent with reduced risk for
 CC haemorrhage as compared with heparin. PRO317 polypeptide is useful in
 CC treating endometrial bleeding angiogenesis. PRO287 polypeptides and
 CC portion have therapeutic applications in wound healing and tissue repair.
 CC PRO234 polypeptides are useful for treating asthma, rheumatoid arthritis,
 CC psoriasis and multiple sclerosis. The polypeptide and its nucleic acid
 CC are useful for tissue typing. PRO antibodies are useful for
 CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO
 CC antibodies are useful in diagnostic assays for PRO e.g. detecting its
 CC expression in specific cells, tissues or serum and for affinity
 CC purification of PRO from recombinant cell culture or natural sources. The
 CC present sequence represents a human secreted/transmembrane PRO
 CC polypeptide PCR primer

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 8; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTCTGCTACTCCCTCGCTC 26
 ||||| ||||| ||||| |||||
 Db 24 CCTACTACTCTCTCTCGCTC 3

RESULT 14

ABX96184/c
 ID ABX96184 standard; DNA; 24 BP.

AC ABX96184;

XX 13-MAY-2003 (first entry)

XX Human secreted/transmembrane protein, #38, PCR primer #3.

XX Human; PCR; primer; ss; PRO; secreted; transmembrane; pharmaceutical;
 KW diagnostic; biosensor; bioreactor; therapeutic; hyperplasia;
 KW endometriosis; cancer; tumour; ischaemia; coronary arterial disease;
 KW polycystic kidney disease; renal failure; inflammatory response; asthma;
 KW rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy;
 KW cytostatic; gynecological; cardiant; nephrotropic; hepatotropic;
 KW antiinflammatory.

XX Homo sapiens.

XX US2002160374-A1.

PN 31-OCT-2002.

PD 12-JUL-2001; 2001US-00905291.

PF 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 31-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 03-NOV-1997; 97US-0064103P.
 PR 07-NOV-1997; 97US-0064248P.
 PR 12-NOV-1997; 97US-0064809P.
 PR 17-NOV-1997; 97US-0065186P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 10-SEP-1998; 97US-0066772P.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019177.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 01-DEC-1999; 98WO-US028301.
 PR 02-DEC-1999; 98WO-US028564.
 PR 02-DEC-1999; 98WO-US028565.
 PR 16-DEC-1999; 98WO-US030095.
 PR 20-DEC-1999; 98WO-US030911.
 PR 20-DEC-1999; 98WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 XX Mather JP, Pan J, Paoni NF, Roy NA, Stewart TA, Tumas D;
 XX Williams PM, Wood WI;
 XX WPI; 2003-288105/28.

XX New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245)
PT and genes encoding them, useful for detecting or treating e.g.
PT hyperplasia, endometriosis, cancers, ischemia, coronary arterial disease
PT or inflammations.
XX
PS Example 33; Page 105; 477pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors, for detecting or treating e.g. hyperplasia,
CC endometriosis, cancers (e.g. those involving solid tumours), ischaemia,
CC coronary arterial disease, polycystic kidney disease, chronic or acute
CC renal failure, or inflammatory responses (e.g. asthma, rheumatoid
CC arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The sequences presented in ABX96017-ABX96378 are the genes
CC encoding, the primers amplifying and the probes detecting the PRO
CC polynucleotides of the invention
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 8; Length 24;
Best Local Similarity 86.4%; Pred No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0
Qy 5 CCTTCTTGTA~~CTCTCTCTG~~CTC 26
||| ||| ||||| |||||
Db 24 CCTACTACTACT~~CTCTCTG~~CTC 3
RESULT 15
ACA05505/c
ID ACA05505 standard; DNA; 24 BP.
XX ACA05505;
XX
DT 29-MAY-2003 (first entry)
XX
DE Human secreted protein PRO263 reverse primer.
XX
KW Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease;
KW psoriasis; cancer; lung cancer; colon cancer; nerve cell disease;
KW Alzheimer's disease; Parkinson's disease; Usher syndrome; angiogenesis;
KW atrophila areata; inflammatory disease; asthma; rheumatoid arthritis;
KW ischaemia; ss; primer; PCR.
XX
OS Homo sapiens.
XX
XX US2003023054-A1.
XX
XX 30-JAN-2003.
XX
PF 16-JUL-2001; 2001US-00906742.
XX
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063814P.

PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-417923/39.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
XX Example 33; Page 103; 469pp; English.
XX
XX The invention relates to an isolated, secreted and transmembrane
CC polypeptide, termed PRO polypeptide. The polypeptide is useful for
CC identifying agonists or antagonists of the polypeptide, for preparing
CC variants of the polypeptide, as molecular weight markers for protein
CC electrophoresis purpose and the nucleic acid is useful for recombinantly
CC expressing those markers. The polypeptide is also useful as therapeutic
CC agent. PRO is useful in assays to identify other proteins or molecules
CC involved in binding interaction. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, in generation of
CC antisense RNA and DNA, in the preparation of PRO polypeptide, for
CC generating transgenic animals or knockout animals which in turn are
CC useful in the development and screening of therapeutically useful
CC reagents, to construct hybridisation probes for mapping the gene which
CC encodes the PRO and for the genetic analysis of individuals with genetic
CC disorders, in gene therapy, for chromosome identification, as chromosome
CC marker, and for generating probes for polymerase chain reaction (PCR),
CC Northern analysis, Southern analysis and Western analysis. PRO antibody
CC is useful in diagnostic assays for PRO, e.g. detecting its expression in
CC specific cells, tissues or serum and for affinity purification of PRO
CC from recombinant cell culture or natural sources. The polypeptide or its
CC antibody is useful for the preparation of medicament for treating
CC conditions which is responsive to the PRO polypeptide or anti-PRO
CC antibody e.g. tumour. The polypeptide and the nucleic acid is useful for
CC tissue typing. The polypeptide is useful for treating obesity, diabetes
CC or hypo- or hyper-insulinaemia and cardiac insufficiency disorders, for
CC inhibiting tumour growth, enhances vascular permeability and immune
CC response, for inducing regeneration of auditory hair cells and for
CC treating hearing loss in mammals and for treating bone and/or cartilage
CC disorders such as sports injuries and arthritis. The present sequence
CC represents a human secreted and transmembrane PRO polypeptide PCR primer
XX
XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
SQ

Query Match 66.2%; Score 17.2; DB 8; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTTCTGTACTCTCTCTGCTC 26
||| || ||||| |||||
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 17
ACA54975/c
ID ACA54975 standard; DNA; 24 BP.
XX
AC ACA54975;
XX
DT 05-JUN-2003 (first entry)
XX
DE Novel secreted and transmembrane protein associated primer #89.
XX
XX Human; secreted and transmembrane protein; gene therapy; psoriasis;
KW enterocolitis; gastrointestinal ulceration; skin disease;
KW keratinocyte differentiation; epithelial cancer; Alzheimer's disease;
KW squamous cell carcinoma; Parkinson's disease; inflammatory disease;
KW amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;
KW multiple sclerosis; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; wound repair; tissue re-growth; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX US2003017463-A1.
XX
XX 23-JAN-2003.
XX
XX 11-JUL-2001; 2001US-00903640.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.

18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066468P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0068425P.
PR 04-JUN-1998; 98US-008028P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113298P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030919.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003555.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PW, Wood WI;
XX WPI; 2003-341586/32.
XX
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
PT disease.
XX
XX Example 33; Page 99; 473pp; English.
XX
XX The invention describes sixty one nucleic acids encoding PRO polypeptides
CC (secreted and transmembrane). The PRO polypeptides and nucleic acids are
CC useful in diagnosing or treating enterocolitis, gastrointestinal
CC ulceration, skin diseases associated with abnormal keratinocyte
CC differentiation, e.g. psoriasis or epithelial cancers such as squamous

cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic
CC lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,
CC asthma or multiple sclerosis, organ failure, atherosclerosis, cancer,
CC injury, infertility, birth defects, premature aging, AIDS, cancer,
CC diabetic complications, or mutations in general. The polypeptides are
CC also useful for wound repair and associated therapies concerned with re-
CC growth of tissue. The PRO polypeptides and nucleic acid molecules are
CC also useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The anti-PRO antibodies may be used in
CC diagnostic assays for PRO, or for the affinity purification of PRO from
CC recombinant cell culture or natural sources. This sequence represents a
CC novel human PRO polypeptide associated primer
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 8; Length 24;
Best Local Similarity 86.4%; Pred. NO. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 5 CCTTCTTCTACTCCTCCTGCTC 26
Db 24 CCTACTACTACTCCTCCTGCTC 3
RESULT 18
ACD19810/C
ID ACD19810 standard; DNA; 24 BP.
XX
XX ACD19810;
AC
AC 22-AUG-2003 (first entry)
DT
DE Human secreted / transmembrane polypeptide PRO263 reverse primer.
XX
XX Human; ss; PCR; primer; gene therapy; apoptosis; bleeding; tumour; ALS;
KW gynaecological disease; hysterectomy; angiogenesis; skin disease; cancer;
KW coronary ischaemic condition; gastrointestinal mucosa disorder; asthma;
KW mucosal lesion repair; keratinocyte differentiation; psoriasis;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
KW neuropathy; blood coagulation cascade disorder; thrombosis; haemorrhage;
KW neurodegenerative disease; endometrial bleeding; wound healing;
KW tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
XX
XX Homo sapiens.
XX
XX US2003027143-A1.
XX
XX 06-FEB-2003.
XX
XX 16-JUL-2001; 2001US-00906838.
XX
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.

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PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063556P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0098003P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100859P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 02-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX (GETH ) GENENTECH INC.
FA
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI
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PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KU, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
XX WPI; 2003-417249/39.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them useful for treating abnormal bleeding involved in
XX gynecological diseases, skin diseases and neurodegenerative diseases.
XX
XX Example 33; Page 98; 467pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane PRO
XX polypeptide. The PRO polypeptides are useful for modulating biological
XX activity of a cell, in diagnosing or treating abnormal bleeding involved
XX in gynaecological diseases e.g. to avoid or lessen the need for
XX hysterectomy, for treating angiogenesis, tumour, coronary ischaemic
XX condition, disorders associated with the preservation and maintenance of
XX gastrointestinal mucosa and the repair of acute and chronic mucosal
XX lesions, skin diseases associated with abnormal keratinocyte
XX differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
XX disease, amyotrophic lateral sclerosis (ALS), neuropathies, disease
XX related to uncontrolled cell growth (e.g. cancer), blood coagulation
XX cascade disorders, neurodegenerative disease, thrombosis, haemorrhage,
XX endometrial bleeding, wound healing, tissue repair, asthma, rheumatoid
XX arthritis, multiple sclerosis. Nucleic acid encoding PRO polypeptides are
XX useful in molecular biology including uses as hybridisation probes and in
XX the generation of antisense RNA and DNA, for preparing PRO polypeptides,
XX for generating transgenic animals or knockout animals. The PRO
XX polypeptides and their nucleic acids are useful for tissue typing. PRO
XX antibodies are useful for immunohistochemical staining and/or assay of
XX sample fluids. Anti-PRO antibodies are useful in diagnostic assays for
XX PRO e.g. detecting its expression in specific cells, tissues or serum and
XX for affinity purification of PRO from recombinant cell culture or natural
XX sources. The present sequence represents a human secreted and
XX transmembrane PRO polypeptide PCR primer
XX
XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 66.2%; Score 17.2; DB 9; Length 24;
XX Best Local Similarity 86.4%; Pred. No. 4.7e+03;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 5 CCTTCTTGTTACTCTCTCTGCTC 26
XX ||| || ||||| |||||
XX Db 24 CCTACTACTACTCTCTCTGCTC 3
XX
XX RESULT 19
XX ADB29409/c
XX ID ADB29409 standard; DNA; 24 BP.
XX
XX AC ADB29409;
XX
XX XX 20-NOV-2003 (first entry)
XX
XX XX Human secreted/transmembrane protein, #40, PCR primer #3.
XX
XX Human; PCR; primer; ss; PRO; secreted; transmembrane;
XX gastrointestinal mucosa; mucosal lesion; skin disease;
XX keratinocyte differentiation; psoriasis; Parkinson's disease;
XX Alzheimer's disease; amyotrophic lateral sclerosis; ALS; neuropathy;
XX cell growth; cancer; tumour; viral infection; neurodegenerative disease;
XX antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;
XX kidney tissue; apoptosis; therapeutic; tissue typing;
XX immunohistochemical staining; gene therapy; nontropic; neuroprotective;
XX cytosstatic; virucide; anticoagulant.
XX
XX OS Homo sapiens.
XX
XX XX US2003092002-A1.
XX
XX XX
```


CC are useful as molecular marker for protein electrophoresis purposes, as
 CC therapeutic agents, for screening compounds to identify those that mimic
 CC the PRO polypeptide (agonists) or prevent the effect of the PRO
 CC polypeptide (antagonists). The polynucleotides and proteins are useful
 CC for tissue typing. PRO antibodies are useful for immunohistochemical
 CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
 CC diagnostic assays for PRO e.g. detecting its expression in specific
 CC cells, tissues or serum and for affinity purification of PRO from
 CC recombinant cell culture or natural sources. The PRO genes may also be
 CC used in gene therapy, particularly for replacing a defective gene. The
 CC sequence presented is a PCR primer which was used to amplify a PRO
 CC polynucleotide of the invention.

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 9; Length 24;

Best Local Similarity 86.4%; Pred. No. 4.7e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTCTGTACTCTCTCTGCTC 26
 ||| || ||||| |||||
 DB 24 CCTACTACTACTCTCTGCTC 3

RESULT 20

ADA18265/C

ID ADA18265 standard; DNA; 24 BP.

XX AC ADA18265;

XX DT 20-NOV-2003 (first entry)

DE Human secreted/transmembrane protein, #40, PCR primer #3.

XX Human; PCR; primer; ss; PRO; secreted; transmembrane;

KW gastrointestinal mucosa; mucosal lesion; skin disease;

KW keratinocyte differentiation; psoriasis; Parkinson's disease;

KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;

KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;

KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;

KW kidney tissue; apoptosis; therapeutic; tissue typing;

KW immunohistochemical staining; gene therapy; neurotropic; neuroprotective;

KW cytosstatic; virucide; anticoagulant.

XX OS Homo sapiens.

XX PN US2003039971-A1.

XX PD 27-FEB-2003.

XX PF 16-JUL-2001; 2001US-00906646.

XX PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 18-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0082125P.

PR 17-OCT-1997; 97US-0082285P.

PR 17-OCT-1997; 97US-0082287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-0066453P.

PR 24-NOV-1997; 97US-0066456P.

PR 24-NOV-1997; 97US-0066511P.

PR 24-NOV-1997; 97US-0066770P.

PR 24-NOV-1997; 97US-0066772P.

PR 25-NOV-1997; 97US-0066840P.

PR 12-DEC-1997; 97US-0069425P.

PR 04-JUN-1998; 98US-0088026P.

PR 10-SEP-1998; 98US-0099803P.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98US-0100262P.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98US-0100858P.

PR 17-SEP-1998; 98WO-US019437.

PR 13-OCT-1998; 98US-0104080P.

PR 20-NOV-1998; 98US-0109304P.

PR 01-DEC-1998; 98WO-US025108.

PR 22-DEC-1998; 98US-0113296P.

PR 07-JUL-1999; 99US-0143048P.

PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 05-JAN-2000; 2000WO-US000219.

PR 11-FEB-2000; 2000WO-US003565.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 20-MAR-2000; 2000WO-US007377.

PR 30-MAR-2000; 2000WO-US008439.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 24-AUG-2000; 2000WO-US023328.

PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

XX PA

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PU, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-503392/47.
DR
XX
XX
PT New secreted and transmembrane polypeptides useful for treating skin,
PT neurodegenerative diseases, asthma, rheumatoid arthritis, psoriasis and
PT multiple sclerosis.
XX
XX Example 33; SEQ ID NO 204; 471pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
CC for treating disorders associated with the preservation and maintenance
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
CC PRO polypeptides also serve as tumour specific antigens which may be
CC exploited as therapeutic targets for anti-tumour drugs, and are also
CC employed therapeutically in vivo for lessening the effects of viral
CC infection. The PRO polypeptides can be also used in assays to determine
CC if it has a role in neurodegenerative diseases or their reversal, as an
CC antithrombotic agent with reduced risk for haemorrhage as compared with
CC heparin, in treating other PRO-associated disorders, in modulating
CC endometrial bleeding angiogenesis, and may also have an effect on kidney
CC tissue. PRO polypeptides and their portions affect the expression of
CC genes which have a role in apoptosis. The polynucleotides are useful in
CC molecular biology including uses as hybridisation probes for cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC for preparing PRO polypeptides, for generating transgenic animals or
CC knockout animals which are useful in the development and screening of
CC therapeutically useful reagents, as probes and for the genetic analysis
CC of individuals with genetic disorders as well as for recombinantly
CC expressing the protein and for chromosome identification. The proteins
CC are useful as molecular marker for protein electrophoresis purposes, as
CC therapeutic agents, for screening compounds to identify those that mimic
CC the PRO polypeptide (agonists) or prevent the effect of the PRO
CC polypeptide (antagonists). The polynucleotides and proteins are useful
CC for tissue typing. PRO antibodies are useful for immunohistochemical
CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
CC diagnostic assays for PRO e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO from
CC recombinant cell culture or natural sources. The PRO genes may also be
CC used in gene therapy, particularly for replacing a defective gene. The
CC sequence presented is a PCR primer which was used to amplify a PRO
CC polynucleotide of the invention.
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. NO. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTTCTACTCTCTCTGCTC 26
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 21
ACD66957/c

ID ACD66957 standard; DNA; 24 BP.
XX
AC ACD66957;
XX
DT 17-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO263 PCR primer #3.
XX
KW Human; ss; PRO; secreted and transmembrane protein; inflammation;
KW rheumatoid arthritis; psoriasis; multiple sclerosis; atherosclerosis;
KW infertility; birth defect; premature aging; malignancy; cancer; stroke;
KW heart attack; hypertension; gastrointestinal ulceration;
KW Parkinson's disease; Alzheimer's disease; AIDS; cholesterol uptake;
KW wound healing; tissue repair; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003045693-A1.
XX
PD 06-MAR-2003.
XX
PF 11-JUL-2001; 2001US-00903749.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063552P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 31-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 03-NOV-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065933P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 25-NOV-1997; 97US-0066842P.

PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088028P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 98US-0143048P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

PA (GETH) GENENTECH INC.

XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;

XX WPI; 2003-512316/48.

DR New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
XX PRO1868), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, AIDS or multiple sclerosis in
PT mammals.

XX Example 33; Page 100; 476pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 61 PRO (secreted and transmembrane protein) polypeptides appearing as
CC ABO32Y56-ABO32816, or (b) any of 61 nucleotide sequences having 50-4053bp
CC fully defined in the specification; or the full length coding sequence of
CC any these 61 nucleotide sequences. Also included are the isolated PRO
CC polypeptide (lacking its associated signal peptide or an extracellular
CC domain of the PRO polypeptide, with or lacking its associated signal
CC peptide), a vector comprising the nucleic acid molecule, a host cell
CC comprising the vector fused to produce the PRO polypeptide, a chimaeric
CC molecule comprising the PRO polypeptide fused to a heterologous amino
CC acid sequence, an anti-PRO antibody, detecting PRO245 or PRO1868
CC polypeptide in a sample suspected of containing any of these PRO
CC polypeptides, linking a bioactive molecule to a cell expressing a PRO245

CC or PRO1868 polypeptide and modulating at least one biological activity of
CC a cell expressing the PRO245 or PRO1868 polypeptide. The PRO polypeptides
CC or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors
CC or bioreactors. These are particularly useful for diagnosing or treating
CC e.g. inflammations, rheumatoid arthritis, psoriasis, multiple sclerosis,
CC atherosclerosis, infertility, birth defects, premature aging, malignancy
CC (e.g. cancers), strokes, heart attacks, hypertension, gastrointestinal
CC ulcerations, Parkinson's diseases, Alzheimer's disease, or AIDS in
CC mammals. These are also useful for modulating cholesterol uptake in the
CC body, and in wound healing or tissue repair. The PRO polypeptides are
CC useful in drug screening. The PRO polypeptides are also useful as
CC molecular weight markers, or for chromosome identification. The PRO genes
CC are useful as hybridisation probes, or for screening libraries of human
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. The present
CC sequence is an oligonucleotide (PCR primer or probe) used in the
CC isolation of a PRO cDNA

XX SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTCTGTACTCTCTCTGCTC 26
||| || ||||| |||||
Db 24 CCTACTACTACTCTCTGCTC 3

RESULT 22
ACD83118/c
ID ACD83118 standard; DNA; 24 BP.
XX AC ACD83118;
XX 22-SEP-2003 (first entry)
XX Human PRO PCR primer #91.
DE Human; PRO; primer; ss; secreted polypeptide; transmembrane polypeptide;
XX abnormal bleeding; gynaecological disease; hysterectomy; mucosal lesion;
KW coronary ischaemic condition; gastrointestinal mucosa; skin disease; ALS;
KW keratinocyte differentiation; psoriasis; Parkinson's disease; asthma;
KW Alzheimer's disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW amyotrophic lateral sclerosis; neuropathy; uncontrolled cell growth; PCR.
OS Homo sapiens.
XX US2003044793-A1.
PN 06-MAR-2003.
XX 11-JUL-2001; 2001US-00903786.
PF 17-SEP-1997; 97US-0059113P.
PF 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059283P.
PR 18-SEP-1997; 97US-0059286P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.

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PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100859P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030939.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX

PA (GETH ) GENENTECH INC.
XX Ashkenazi A, Botstein D, Deanovsers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy WA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-492256/46.
XX
XX Novel secreted and transmembrane PRO polypeptides and polynucleotides
PT encoding them, useful for treating abnormal bleeding involved in
PT synecological diseases, skin diseases and neurodegenerative diseases.
XX
XX Example 33; Page 100; 475pp; English.
XX
XX The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The PRO polypeptides and polynucleotides can be used in diagnosing or
CC treating abnormal bleeding involved in gynaecological diseases e.g. to
CC avoid or lessen the need for hysterectomy. They can also be used in
CC treating coronary ischaemic conditions, disorders associated with the
CC preservation and maintenance of gastrointestinal mucosa and the repair of
CC acute and chronic mucosal lesions, skin diseases associated with abnormal
CC keratinocyte differentiation (e.g. psoriasis), Parkinson's disease,
CC Alzheimer's disease, asthma, rheumatoid arthritis, multiple sclerosis,
CC amyotrophic lateral sclerosis (ALS), neuropathies and diseases related to
CC uncontrolled cell growth, such as cancer. This sequence represents a PCR
CC primer used to isolate a human PRO polynucleotide of the invention
XX
XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Ov 5 CCTTCTTGTACTCCTCCTGCTC 26
Dn 24 CCTACTACTACTCCTCCTGCTC 3
RESULT 23
ADAL6240/C
ID ADAL6240 standard; DNA; 24 BP.
XX
XX ADAL6240;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human secreted/transmembrane protein, #40, PCR primer #3.
XX
XX Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
XX tissue typing; immunohistochemical staining; gene therapy;
XX neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
XX endothelial cell; stimulated T-lymphocyte; retinal neuron;
XX rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
XX cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
XX retinitis pigmentosa; obesity; diabete; hyperinsulinaemia;
XX hypoinsulinaemia; bone disorder; cartilage disorder; sport injury;
XX arthritis; cardiac; vulnery; cytostatic; ophthalmological;
XX osteopathic; antiarthritic; anorectic.
XX
XX Homo sapiens.
XX
XX US2003049621-A1.
XX
XX 13-MAR-2003.
XX
XX 11-JUL-2001; 2001US-00904119.
XX
XX 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
XX 17-SEP-1997; 97US-0059117P.
```


PT Alzheimer's disease, enterocolitis, Zollinger-Ellison syndrome.
 PT psoriasis, epidermoid carcinoma of the vulva and gliomas, gynecological
 XX diseases.
 XX
 PS Example 33; SEQ ID NO 204; 479pp; English.
 XX
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides
 CC and the nucleic acid encoding them. The polypeptides can be used to raise
 CC antibodies that specifically bind to the PRO polypeptide, for linking a
 CC bioactive molecule to a cell expressing a PRO protein and for modulating
 CC at least one biological activity of a cell. PRO polypeptides are useful
 CC for detecting other PRO polypeptides in a sample and for linking a
 CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
 CC polypeptide antibodies are useful for modulating the biological activity
 CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
 CC for treating disorders associated with the preservation and maintenance
 CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
 CC lesions, skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
 CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
 CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
 CC PRO polypeptides also serves as tumour specific antigens which may be
 CC exploited as therapeutic targets for anti-tumour drugs, and are also
 CC employed therapeutically in vivo for lessening the effects of viral
 CC infection. The PRO polypeptides can be also used in assays to determine
 CC if it has a role in neurodegenerative diseases or their reversal, as an
 CC antithrombotic agent with reduced risk for haemorrhage as compared with
 CC heparin, in treating other PRO-associated disorders, in modulating
 CC endometrial bleeding angiogenesis, and may also have an effect on kidney
 CC tissue. PRO polypeptides and their portions affect the expression of
 CC genes which have a role in apoptosis. The polynucleotides are useful in
 CC molecular biology including uses as hybridisation probes for cDNA library
 CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC for preparing PRO polypeptides, for generating transgenic animals or
 CC knockout animals which are useful in the development and screening of
 CC therapeutically useful reagents, as probes and for the genetic analysis
 CC of individuals with genetic disorders as well as for recombinantly
 CC expressing the protein and for chromosome identification. The proteins
 CC are useful as molecular marker for protein electrophoresis purposes, as
 CC therapeutic agents, for screening compounds to identify those that mimic
 CC the PRO polypeptide (agonists) or prevent the effect of the PRO
 CC polypeptide (antagonists). The polynucleotides and proteins are useful
 CC for tissue typing. PRO antibodies are useful for immunohistochemical
 CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
 CC diagnostic assays for PRO e.g. detecting its expression in specific
 CC cells, tissues or serum and for affinity purification of PRO from
 CC recombinant cell culture or natural sources. The PRO genes may also be
 CC used in gene therapy, particularly for replacing a defective gene. The
 CC sequence presented is a PCR primer which was used to amplify a PRO
 CC polynucleotide of the invention.
 XX
 SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 Query Match 66.2%; Score 17.2; dB 9; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 CCTTCTGTACTCTCTCGTC 26
 Db 24 CCTACTACTCTCTCGTC 3
 RESULT 25
 ACD23296/C
 ID ACD23296 standard; DNA; 24 BP.
 XX
 AC ACD23296;
 XX
 DT 26-AUG-2003 (first entry)
 XX
 DE Human PRO PCR primer #83.
 XX

KW Human; PRO; primer; ss; Parkinson's disease; Alzheimer's disease; ALS;
 KW amyotrophic lateral sclerosis; neuropathy; cancer; viral infection; AIDS;
 KW Usher's syndrome; haemorrhage; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; congenital microvillus atrophy; psoriasis;
 KW skin disease; endometrial bleeding; angiogenesis; ischaemic condition;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disease;
 KW atherosclerosis; infertility; birth defect; premature aging; stroke; PCR;
 KW diabetic complication.
 XX Homo sapiens.
 OS
 XX US2003064367-A1.
 PN
 XX 03-APR-2003.
 PD
 XX 13-JUL-2001; 2001US-00904485.
 PF
 XX 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066354P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 25-NOV-1997; 97US-0069425P.
 PR 04-JUN-1998; 98US-0088026P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98US-0100262P.
 PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 13-OCT-1998; 98US-0104080P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-DEC-1998; 98US-0113296P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski FJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WT;
 XX WPI; 2003-567176/53.
 XX
 DR Novel isolated PRO polypeptides e.g. PRO245 and PRO1868, useful for
 PT treating e.g. Parkinson's disease, Alzheimer's disease, amyotrophic
 PT lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
 XX
 PS Example 33; Page 101; 477pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are used for treating
 CC diseases related to growth or survival of nerve cells such as Parkinson's
 CC disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS) and
 CC neuropathies, diseases related to uncontrolled cell growth such as
 CC cancer, viral infections, Usher's syndrome, haemorrhage, enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration, congenital
 CC microvillus atrophy, skin diseases such as psoriasis and epithelial
 CC cancers, endometrial bleeding, angiogenesis, ischaemic conditions,
 CC asthma, rheumatoid arthritis, multiple sclerosis, inflammatory diseases,
 CC atherosclerosis, cardiac injury, infertility, birth defects, premature
 CC aging, AIDS, stroke and diabetic complications. The polynucleotides are
 CC also useful in chromosome and gene mapping. This sequence represents a
 CC PCR primer used in isolation of a human PRO polynucleotide of the
 CC invention
 XX
 SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 Query Match 66.2%; Score 17.2; DB 9; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTCTGTAAGTCTCTCTGCTC 26
 |||||
 Db 24 CCTACTACTACTCTCTCTGCTC 3
 RESULT 26
 ADA16664/c
 ID ADA16664 standard; DNA; 24 BP.
 XX ADA16664;
 AC
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein, #40, PCR primer #3.
 XX
 KW Human; PCR; primer; ss; PRO; secreted; transmembrane;
 KW gastrointestinal mucosa; mucosal lesion; skin disease;
 KW keratinocyte differentiation; psoriasis; Parkinson's disease;
 KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;
 KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;
 KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;
 KW kidney tissue; apoptosis; therapeutic; tissue typing;
 KW immunohistochemical staining; gene therapy; nootropic; neuroprotective;
 KW cytostatic; viricide; anticoagulant.
 XX
 OS Homo sapiens.
 XX
 PN US2003039969-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 12-JUL-2001; 2001US-00904786.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059124P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063556P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.

OS Homo sapiens.
XX US2003049622-A1.
XX 13-MAR-2003.
XX PF 14-JUL-2001; 2001US-00904956.
XX 17-SEP-1997; 97US-00591113P.
PR 17-SEP-1997; 97US-00591115P.
PR 17-SEP-1997; 97US-00591117P.
PR 17-SEP-1997; 97US-00591119P.
PR 17-SEP-1997; 97US-00591212P.
PR 17-SEP-1997; 97US-00591222P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062123P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063129P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066849P.
PR 12-DEC-1997; 97US-0069423P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US0211547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
PA Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AJ, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-521802/49.
XX New secreted and transmembrane PRO polypeptides, useful for treating the
PT cancer, skin disorders, neurodegenerative diseases, and for lessening the
PT effects of viral infection.
XX Example 33; SEQ ID NO 204; 473pp; English.
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC biactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC biactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
CC for treating disorders associated with the preservation and maintenance
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
CC PRO polypeptides also serves as tumour specific antigens which may be
CC exploited as therapeutic targets for anti-tumour drugs, and are also
CC employed therapeutically in vivo for lessening the effects of viral
CC infection. The PRO polypeptides can be also used in assays to determine
CC if it has a role in neurodegenerative diseases or their reversal, as an
CC antithrombotic agent with reduced risk for haemorrhage as compared with
CC heparin, in treating other PRO-associated disorders, in modulating
CC endometrial bleeding angiogenesis, and may also have an effect on kidney
CC tissue. PRO polypeptides and their portions affect the expression of
CC genes which have a role in apoptosis. The polynucleotides are useful in
CC molecular biology including uses as hybridisation probes for cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC for preparing PRO polypeptides, for generating transgenic animals or
CC knockout animals which are useful in the development and screening of

therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polynucleotides and proteins are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO polynucleotide of the invention.

Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTTCTTCTACTCTCTCGTC 26

Db 24 CCTACTACTCTCTCGTC 3

RESULT 28

ADA41961/c

ID ADA41961 standard; DNA; 24 BP.

XX ADA41961;

XX 20-NOV-2003 (first entry)

XX Human secreted/transmembrane protein, #40, PCR primer #3.

XX Human; PCR; primer; ss; PRO; secreted; transmembrane;

KW gastrointestinal mucosa; mucosal lesion; skin disease;

KW keratinocyte differentiation; psoriasis; Parkinson's disease;

KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;

KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;

KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;

KW kidney tissue; apoptosis; therapeutic; tissue typing;

KW immunohistochemical staining; gene therapy; nontropic; neuroprotective;

KW cytostatic; virucide; anticoagulant.

XX Homo sapiens.

XX US2003082540-A1.

XX 01-MAY-2003.

XX 10-JUL-2001; 2001US-00902634.

XX 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059117P.

XX 17-SEP-1997; 97US-0059119P.

XX 17-SEP-1997; 97US-0059121P.

XX 17-SEP-1997; 97US-0059122P.

XX 17-SEP-1997; 97US-0059184P.

XX 18-SEP-1997; 97US-0059263P.

XX 18-SEP-1997; 97US-0059266P.

XX 15-OCT-1997; 97US-0062125P.

XX 17-OCT-1997; 97US-0062285P.

XX 17-OCT-1997; 97US-0062287P.

XX 21-OCT-1997; 97US-0063486P.

XX 24-OCT-1997; 97US-0062814P.

XX 24-OCT-1997; 97US-0062816P.

XX 24-OCT-1997; 97US-0063045P.

XX 24-OCT-1997; 97US-0063120P.

XX 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-00633541P.
PR 28-OCT-1997; 97US-00633542P.
PR 28-OCT-1997; 97US-00633544P.
PR 28-OCT-1997; 97US-00633549P.
PR 28-OCT-1997; 97US-00633550P.
PR 28-OCT-1997; 97US-00633564P.
PR 29-OCT-1997; 97US-00633704P.
PR 29-OCT-1997; 97US-00633704P.
PR 29-OCT-1997; 97US-00633732P.
PR 29-OCT-1997; 97US-00633734P.
PR 29-OCT-1997; 97US-00633735P.
PR 29-OCT-1997; 97US-00633738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 04-MAR-2000; 2000WO-US005004.
PR 24-FEB-2000; 2000WO-US005841.
PR 02-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

XX (GETH) GENENTECH INC.

XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski FJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavlin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams EM, Wood WT;

XX WPI; 2003-755103/71.

XX New PRO polypeptides useful for treating Parkinson's disease,

PT enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration,

PT Alzheimer's disease, amyotrophic lateral sclerosis and Usher syndrome.

XX Example 33; SEQ ID NO 204; 469pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides

CC and the nucleic acid encoding them. The polypeptides can be used to raise

CC antibodies that specifically bind to the PRO polypeptide, for linking a

CC bioactive molecule to a cell expressing a PRO protein and for modulating

CC at least one biological activity of a cell. PRO polypeptides are useful

CC for detecting other PRO polypeptides in a sample and for linking a

CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO

CC polypeptide antibodies are useful for modulating the biological activity

CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful

CC for treating disorders associated with the preservation and maintenance

CC of gastrointestinal mucosa and the repair of acute and chronic mucosal

CC lesions, skin diseases associated with abnormal keratinocyte

CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's

CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and

CC additionally, disease related to uncontrolled cell growth, e.g. cancer.

CC PRO polypeptides also serves as tumour specific antigens which may be

CC exploited as therapeutic targets for anti-tumour drugs, and are also

CC employed therapeutically in vivo for lessening the effects of viral

CC infection. The PRO polypeptides can be also used in assays to determine

CC if it has a role in neurodegenerative diseases or their reversal, as an

CC antithrombotic agent with reduced risk for haemorrhage as compared with

CC heparin, in treating other PRO-associated disorders, in modulating

CC endometrial bleeding angiogenesis, and may also have an effect on kidney

CC tissue. PRO polypeptides and their portions affect the expression of

CC genes which have a role in apoptosis. The polynucleotides are useful in

CC molecular biology including uses as hybridisation probes for cDNA library

CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in

CC chromosome and gene mapping, in the generation of antisense RNA and DNA,

CC for preparing PRO polypeptides, for generating transgenic animals or

CC knockout animals which are useful in the development and screening of

CC therapeutically useful reagents, as probes and for the genetic analysis

CC of individuals with genetic disorders as well as for recombinantly

CC expressing the protein and for chromosome identification. The proteins

CC are useful as molecular marker for protein electrophoresis purposes, as

CC therapeutic agents, for screening compounds to identify those that mimic

CC the PRO polypeptide (agonists) or prevent the effect of the PRO

CC polypeptide (antagonists). The polynucleotides and proteins are useful

CC for tissue typing. PRO antibodies are useful for immunohistochemical

CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in

CC diagnostic assays for PRO e.g. detecting its expression in specific

CC cells, tissues or serum and for affinity purification of PRO from

CC recombinant cell culture or natural sources. The PRO genes may also be

CC used in gene therapy, particularly for replacing a defective gene. The

CC sequence presented is a PCR primer which was used to amplify a PRO

CC polynucleotide of the invention.

XX

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 9; Length 24;

Best Local Similarity 86.4%; Pred. No. 4.7e-03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTGATCTCTCTGTC 26

Db 24 CCTACTACTACTCTCTGTC 3

RESULT 29

ADA17308/c

ID ADA17308 standard; DNA; 24 BP.

XX

AC ADA17308;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human secreted/transmembrane protein, #40, PCR primer #3.

XX

KW Human; PCR; primer; ss; PRO; secreted; transmembrane;

KW Gastrointestinal mucosa; mucosal lesion; skin disease;

KW keratinocyte differentiation; psoriasis; Parkinson's disease;

KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;

KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;

KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;

KW kidney tissue; apoptosis; therapeutic; tissue typing;

KW immunohistochemical staining; gene therapy; nontropic; neuroprotective;

KW cytostatic; virucide; anticoagulant.

XX

OS Homo sapiens.

XX

PN US2003017498-A1.

XX

PD 23-JAN-2003.

XX

PF 17-JUL-2001; 2001US-00908093.

XX

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 18-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

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PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 25-NOV-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088036P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 22-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
XX Flivaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
XX
XX WPI; 2003-531434/50.
XX
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
XX PRO1868, useful in molecular biology, chromosome and gene mapping, in
XX generating antisense RNA and DNA, and in gene therapy.
XX
XX Example 33; SEQ ID NO 204; 475pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX and the nucleic acid encoding them. The polypeptides can be used to raise
XX antibodies that specifically bind to the PRO polypeptide, for linking a
XX bioactive molecule to a cell expressing a PRO protein and for modulating
XX at least one biological activity of a cell. PRO polypeptides are useful
XX for detecting other PRO polypeptides in a sample and for linking a
XX bioactive molecule to a cell expressing a PRO polypeptide. The PRO
XX polypeptide antibodies are useful for modulating the biological activity
XX of a cell expressing PRO polypeptides. PRO polypeptides are also useful
XX for treating disorders associated with the preservation and maintenance
XX of gastrointestinal mucosa and the repair of acute and chronic mucosal
XX lesions, skin diseases associated with abnormal keratinocyte
XX differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
XX diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
XX additionally, disease related to uncontrolled cell growth, e.g. cancer.
XX PRO polypeptides also serves as tumour specific antigens which may be
XX exploited as therapeutic targets for anti-tumour drugs, and are also
XX employed therapeutically in vivo for lessening the effects of viral
XX infection. The PRO polypeptides can be also used in assays to determine
XX if it has a role in neurodegenerative diseases or their reversal, as an
XX antithrombotic agent with reduced risk for haemorrhage as compared with
XX heparin, in treating other PRO-associated disorders, in modulating
XX endometrial bleeding angiogenesis, and may also have an effect on kidney
XX tissue. PRO polypeptides and their portions affect the expression of
XX genes which have a role in apoptosis. The polynucleotides are useful in
XX molecular biology including uses as hybridisation probes for cDNA library
XX to isolate the full-length PRO cDNA or to isolate other cDNAs, in
XX chromosome and gene mapping, in the generation of antisense RNA and DNA,
XX for preparing PRO polypeptides, for generating transgenic animals or
XX knockout animals which are useful in the development and screening of
XX therapeutically useful reagents, as probes and for the genetic analysis
XX of individuals with genetic disorders as well as for recombinantly
XX expressing the protein and for chromosome identification. The proteins
XX are useful as molecular marker for protein electrophoresis purposes, as
XX therapeutic agents, for screening compounds to identify those that mimic
XX the PRO polypeptide (agonists) or prevent the effect of the PRO
XX polypeptide (antagonists). The polynucleotides and proteins are useful
XX for tissue typing. PRO antibodies are useful for immunohistochemical
XX staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
XX diagnostic assays for PRO e.g. detecting its expression in specific
XX cells, tissues or serum and for affinity purification of PRO from
XX recombinant cell culture or natural sources. The PRO genes may also be
XX used in gene therapy, particularly for replacing a defective gene. The
XX sequence presented is a PCR primer which was used to amplify a PRO
XX polynucleotide of the invention.
XX
XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 66.2%; Score 17.2; DB 9; Length 24;
XX Best Local Similarity 86.4%; Pred. No. 4.7e+03;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 5 CCTCTGTGTACTCTCTCTGCTC 26
XX ||| || ||||| |||||
XX Db 24 CCTACTACTACTCTCTGCTC 3
XX
XX RESULT 30
XX ADA42811/C
XX ID ADA42811 standard; DNA; 24 BP.
XX
XX AC ADA42811;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Human secreted/transmembrane protein, #40, PCR primer #3.
XX
XX KW Human; PCR; primer; ss; PRO; secreted; transmembrane;
XX gastrointestinal mucosa; mucosal lesion; skin disease;
XX keratinocyte differentiation; psoriasis; Parkinson's disease;
XX Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;
XX cell growth; cancer; tumour; viral infection; neurodegenerative disease;
XX antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;
XX kidney tissue; apoptosis; therapeutic; tissue typing;
XX immunohistochemical staining; gene therapy; nontropic; neuroprotective;
XX cytosstatic; virucide; anticoagulant.
XX
XX OS Homo sapiens.
XX
XX PN US2003054351-A1.
XX
XX PD 20-MAR-2003.
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XX 13-JUL-2001; 2001US-00904462.
PF 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062123P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063043P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 31-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0100859P.
PR 13-OCT-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146223P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 02-JUN-2000; 2000WO-US014042.
PR 22-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
PA Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-755052/71.
XX Novel isolated secreted and transmembrane PRO polypeptide, useful for
XX tissue typing, treating Parkinson's disease, Alzheimer's disease, birth
XX defects, cancer.
XX Example 33; SEQ ID NO 204; 464pp; English.
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX and the nucleic acid encoding them. The polypeptides can be used to raise
XX antibodies that specifically bind to the PRO polypeptide, for linking a
XX bioactive molecule to a cell expressing a PRO protein and for modulating
XX at least one biological activity of a cell. PRO polypeptides are useful
XX for detecting other PRO polypeptides in a sample and for linking a
XX bioactive molecule to a cell expressing a PRO polypeptide. The PRO
XX polypeptide antibodies are useful for modulating the biological activity
XX of a cell expressing PRO polypeptides. PRO polypeptides are also useful
XX for treating disorders associated with the preservation and maintenance
XX of gastrointestinal mucosa and the repair of acute and chronic mucosal
XX lesions, skin diseases associated with abnormal keratinocyte
XX differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
XX diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
XX additionally, disease related to uncontrolled cell growth, e.g. cancer.
XX PRO polypeptides also serves as tumour specific antigens which may be
XX exploited as therapeutic targets for anti-tumour drugs, and are also
XX employed therapeutically in vivo for lessening the effects of viral
XX infection. The PRO polypeptides can be also used in assays to determine
XX if it has a role in neurodegenerative diseases or their reversal, as an
XX antithrombotic agent with reduced risk for haemorrhage as compared with
XX heparin, in treating other PRO-associated disorders, in modulating
XX endometrial bleeding angiogenesis, and may also have an effect on kidney
XX tissue. PRO polypeptides and their portions affect the expression of
XX genes which have a role in apoptosis. The polynucleotides are useful in
XX molecular biology including uses as hybridisation probes for cDNA library
XX to isolate the full-length PRO cDNA or to isolate other cDNAs, in
XX chromosome and gene mapping, in the generation of antisense RNA and DNA,
XX for preparing PRO polypeptides, for generating transgenic animals or
XX knockout animals which are useful in the development and screening of
XX therapeutically useful reagents, as probes and for the genetic analysis
XX of individuals with genetic disorders as well as for recombinantly
XX expressing the protein and for chromosome identification. The proteins
XX are useful as molecular marker for protein electrophoresis purposes, as
XX therapeutic agents, for screening compounds to identify those that mimic

CC the PRO polypeptide (agonists) or prevent the effect of the PRO
CC polypeptide (antagonists). The polynucleotides and proteins are useful
CC for tissue typing. PRO antibodies are useful for immunohistochemical
CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
CC diagnostic assays for PRO e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO from
CC recombinant cell culture or natural sources. The PRO genes may also be
CC used in gene therapy, particularly for replacing a defective gene. The
CC sequence presented is a PCR primer which was used to amplify a PRO
CC polynucleotide of the invention.

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTTGTACTCTCTCGGTC 26
|||||
Db 24 CCTACTACTCTCTCTGCTC 3

RESULT 31

ACD23658/c

ID ACD23658 standard; DNA; 24 BP.

XX ACD23658;

XX 26-AUG-2003 (first entry)

XX Human PRO PCR primer #83.

KW Human; PRO; primer; ss; secreted polypeptide; transmembrane polypeptide;
KW leukocyte homing; rheumatoid arthritis; psoriasis; multiple sclerosis;
KW mucosal lesion; enterocolitis Zollinger Ellison syndrome; asthma; PCR;
KW antiasthmatic; antirheumatic; antiarthritic; neuroprotective.

XX Homo sapiens.

XX US2003064923-A1.

XX 03-APR-2003.

XX 13-JUL-2001; 2001US-00905348.

XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065933P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066456P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 02-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

XX Aehkenazi A, Botstein D, Desnoyers L, Baton DL, Ferrara N;
PI Flivaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-567190/53.

XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
XX antagonists of polypeptide, and as molecular weight markers.
XX
PS Example 33; Page 98; 471pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC polypeptides are useful for detecting PRO polypeptides and for linking a
CC bioactive molecule to a cell expressing the polypeptides, where the
CC bioactive molecule is a toxin, radiolabel or an antibody. The bioactive
CC material causes the death of the cell. The polypeptides or antibodies
CC specific to the polypeptides are useful for modulating at least one
CC biological activity of a cell expressing the polypeptides. The
CC polypeptides are useful for treating disorders associated with leukocyte
CC homing such as asthma, rheumatoid arthritis, psoriasis and multiple
CC sclerosis, repair of acute and chronic mucosal lesions such as
CC enterocolitis and Zollinger Ellison syndrome and for identifying agonists
CC or antagonists of the polypeptides. The polynucleotides are useful as
CC hybridization probes, in chromosome and gene mapping, in generation of
CC antisense RNA and DNA, in the preparation of PRO polypeptides and for
CC generating probes for polymerase chain reaction (PCR), Northern analysis,
CC Southern analysis and Western analysis. This sequence represents a PCR
CC primer used in isolation of a human PRO polynucleotide of the invention
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0
QY 5 CCTTCTTGTA^{CTCTCTCTGCTC} 26
||| || ||||| ||||| |||||
DB 24 CCTACTACTACT^{CTCTCTGCTC} 3
RESULT 32
ADBT7730/c
ID ADBT7730 standard; DNA; 24 BP.
XX ADBT7730;
XX
XX 04-DEC-2003 (first entry)
XX Human secreted/transmembrane protein, #40, PCR primer #3.
DE
XX Human; PCR; primer; ss; PRO; secreted; transmembrane;
KW gastrointestinal mucosa; mucosal lesion; skin disease;
KW keratinocyte differentiation; psoriasis; Parkinson's disease;
KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;
KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;
KW antithrombotic agent; haemorrhage; endometrial bleeding
KW kidney tissue; apoptosis; therapeutic; tissue typing;
KW immunohistochemical staining; Gene therapy; nootropic; neuroprotective;
KW cytosstatic; virucide; anticoagulant.
XX
OS Homo sapiens.
XX
XX US2003077654-A1.
XX
XX 24-APR-2003.
XX
XX 10-JUL-2001; 2001US-00902759.
XX
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.

PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy NA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-765399/72.
DR
XX
XX New isolated secreted and transmembrane polypeptide, useful for treating
PT diseases, e.g. Parkinson's disease, Alzheimer's disease, amyotrophic
PT lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
XX
XX Example 33; Page 96; 467pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
CC for treating disorders associated with the preservation and maintenance
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
CC PRO polypeptides also serves as tumour specific antigens which may be
CC exploited as therapeutic targets for anti-tumour drugs, and are also
CC employed therapeutically in vivo for lessening the effects of viral
CC infection. The PRO polypeptides can be also used in assays to determine
CC if it has a role in neurodegenerative diseases or their reversal, as an
CC antithrombotic agent with reduced risk for haemorrhage as compared with
CC heparin, in treating other PRO-associated disorders, in modulating
CC endometrial bleeding angiogenesis, and may also have an effect on kidney
CC tissue. PRO polypeptides and their portions affect the expression of
CC genes which have a role in apoptosis. The polynucleotides are useful in
CC molecular biology including uses as hybridisation probes for cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC for preparing PRO polypeptides, for generating transgenic animals or
CC knockout animals which are useful in the development and screening of
CC therapeutically useful reagents, as probes and for the genetic analysis
CC of individuals with genetic disorders as well as for recombinantly
CC expressing the protein and for chromosome identification. The proteins
CC are useful as molecular marker for protein electrophoresis purposes, as
CC therapeutic agents, for screening compounds to identify those that mimic
CC the PRO polypeptide (agonists) or prevent the effect of the PRO
CC polypeptide (antagonists). The polynucleotides and proteins are useful
CC for tissue typing. PRO antibodies are useful for immunohistochemical
CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
CC diagnostic assays for PRO e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO from
CC recombinant cell culture or natural sources. The PRO genes may also be
CC used in gene therapy, particularly for replacing a defective gene. The
CC sequence presented is a PCR primer which was used to amplify a PRO
CC polynucleotide of the invention.
XX

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTCTCTGTACTCCTCCTGCTC 26
||| || ||||| |||||
Db 24 CCTACTACTACTCCTCCTGCTC 3
RESULT 33
ADB74866/C
ID ADB74866 standard; DNA; 24 BP.
XX
AC ADB74866;
XX
DT 04-DEC-2003 (first entry)
XX
XX Human secreted/transmembrane protein, #40, PCR primer #3.
XX
XX Human; PCR; primer; ss; PRO; secreted; transmembrane;
KW Gastrointestinal mucoas; mucosal lesion; skin disease;
KW keratinocyte differentiation; psoriasis; Parkinson's disease;
KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;
KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;
KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;
KW kidney tissue; apoptosis; therapeutic; tissue typing;
KW immunohistochemical staining; gene therapy; nontropic; neuroprotective;
KW cytosstatic; virucide; anticoagulant.
XX
OS Homo sapiens.
XX
XX US2003082542-A1.
FN
XX
PD 01-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907979.
XX
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063128P.
PR 24-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 03-OCT-1997; 97US-0064103P.
 PR 07-NOV-1997; 97US-0064248P.
 PR 12-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 18-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 14-SEP-1998; 98US-0100262P.
 PR 14-SEP-1998; 98US-0100262P.
 PR 16-SEP-1998; 98US-0101917P.
 PR 17-SEP-1998; 98US-0101933P.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98US-0101943P.
 PR 13-OCT-1998; 98US-0104080P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 01-DEC-1998; 98US-0109304P.
 PR 22-DEC-1998; 98US-0113298P.
 PR 07-JUL-1999; 98US-0143048P.
 PR 26-JUL-1999; 98US-0145698P.
 PR 28-JUL-1999; 98US-0146222P.
 PR 08-SEP-1999; 98US-0146222P.
 PR 13-SEP-1999; 98US-020594.
 PR 15-SEP-1999; 98US-020594.
 PR 15-SEP-1999; 98US-020594.
 PR 05-OCT-1999; 98US-020594.
 PR 29-NOV-1999; 98US-020594.
 PR 30-NOV-1999; 98US-020594.
 PR 01-DEC-1999; 98US-020594.
 PR 02-DEC-1999; 98US-020594.
 PR 16-DEC-1999; 98US-020594.
 PR 20-DEC-1999; 98US-020594.
 PR 20-DEC-1999; 98US-020594.
 PR 05-JAN-2000; 2000US-0000219.
 PR 11-FEB-2000; 2000US-0000355.
 PR 22-FEB-2000; 2000US-0000414.
 PR 02-MAR-2000; 2000US-0000504.
 PR 20-MAR-2000; 2000US-0000584.
 PR 30-MAR-2000; 2000US-0000737.
 PR 22-MAY-2000; 2000US-0000843.
 PR 02-JUN-2000; 2000US-0001404.
 PR 28-JUL-2000; 2000US-0001528.
 PR 24-AUG-2000; 2000US-0002071.
 PR 18-SEP-2000; 2000US-0002328.
 PR 18-SEP-2000; 2000US-00665350.
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Macher JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams FM, Wood WI;
 XX WPI; 2003-765412/72.
 XX
 PT Novel isolated native PRO polypeptide useful for tissue typing,
 PT modulating biological activity of cell, as molecular weight markers in
 PT protein electrophoresis, for treating enterocolitis, Zollinger-Ellison
 PT syndrome.
 XX

PS Example 33; Page 101; 475pp; English.
 XX
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides
 CC and the nucleic acid encoding them. The polypeptides can be used to raise
 CC antibodies that specifically bind to the PRO polypeptide, for linking a
 CC bioactive molecule to a cell expressing a PRO protein and for modulating
 CC at least one biological activity of a cell. PRO polypeptides are useful
 CC for detecting other PRO polypeptides in a sample and for linking a
 CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
 CC polypeptide antibodies are useful for modulating the biological activity
 CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
 CC for treating disorders associated with the preservation and maintenance
 CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
 CC lesions, skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
 CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
 CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
 CC PRO polypeptides also serve as tumour specific antigens which may be
 CC exploited as therapeutic targets for anti-tumour drugs, and are also
 CC employed therapeutically in vivo for lessening the effects of viral
 CC infection. The PRO polypeptides can be also used in assays to determine
 CC if it has a role in neurodegenerative diseases or their reversal, as an
 CC antithrombotic agent with reduced risk for haemorrhage as compared with
 CC heparin, in treating other PRO-associated disorders, in modulating
 CC endometrial bleeding angiogenesis, and may also have an effect on kidney
 CC tissue. PRO polypeptides and their portions affect the expression of
 CC genes which have a role in apoptosis. The polynucleotides are useful in
 CC molecular biology including uses as hybridisation probes for cDNA library
 CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC for preparing PRO polypeptides, for generating transgenic animals or
 CC knockout animals which are useful in the development and screening of
 CC therapeutically useful reagents, as probes and for the genetic analysis
 CC of individuals with genetic disorders as well as for recombinantly
 CC expressing the protein and for chromosome identification. The proteins
 CC are useful as molecular marker for protein electrophoresis purposes, as
 CC the PRO polypeptide (agonists) or prevent the effect of the PRO
 CC polypeptide (antagonists). The polynucleotides and proteins are useful
 CC for tissue typing. PRO antibodies are useful for immunohistochemical
 CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
 CC diagnostic assays for PRO e.g. detecting its expression in specific
 CC cells, tissues or serum and for affinity purification of PRO from
 CC recombinant cell culture or natural sources. The PRO genes may also be
 CC used in gene therapy, particularly for replacing a defective gene. The
 CC sequence presented is a PCR primer which was used to amplify a PRO
 CC polynucleotide of the invention.
 XX
 SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 Query Match 66.2%; Score 17.2; DB 10; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5 CCTTCTGTACTCCTCCTGCTC 26
 ||| || ||||| |||||
 Db 24 CCTACTACTACTCCTCCTGCTC 3
 RESULT 34
 ADC28512/C
 ID ADC28512 standard; DNA; 24 BP.
 XX
 AC ADC28512;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein, #40, PCR primer #3.
 XX
 KW Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
 KW tissue typing; immunohistochemical staining; gene therapy;
 KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
 KW endothelial cell; stimulated T-lymphocyte; retinal neuron;

rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
retinitis pigmentosa; obesity; diabete; hyperinsulinaemia;
hypoinsulinaemia; bone disorder; cartilage disorder; sport injury;
arthritis; cardiant; vulnerary; cytostatic; ophthalmological;
osteopathic; antiarthritic; anorectic.

Homo sapiens.

US2003059772-A1.

27-MAR-2003.

18-JUL-2001; 2001US-00909064.

17-SEP-1997; 97US-0059113P.

17-SEP-1997; 97US-0059115P.

17-SEP-1997; 97US-0059117P.

17-SEP-1997; 97US-0059119P.

17-SEP-1997; 97US-0059121P.

17-SEP-1997; 97US-0059122P.

17-SEP-1997; 97US-0059184P.

18-SEP-1997; 97US-0059263P.

18-SEP-1997; 97US-0059266P.

15-OCT-1997; 97US-0062125P.

17-OCT-1997; 97US-0062285P.

17-OCT-1997; 97US-0062287P.

21-OCT-1997; 97US-0063486P.

24-OCT-1997; 97US-0062814P.

24-OCT-1997; 97US-0062816P.

24-OCT-1997; 97US-0063045P.

24-OCT-1997; 97US-0063120P.

24-OCT-1997; 97US-0063121P.

24-OCT-1997; 97US-0063127P.

24-OCT-1997; 97US-0063128P.

27-OCT-1997; 97US-0063327P.

28-OCT-1997; 97US-0063329P.

28-OCT-1997; 97US-0063541P.

28-OCT-1997; 97US-0063542P.

28-OCT-1997; 97US-0063544P.

28-OCT-1997; 97US-0063549P.

28-OCT-1997; 97US-0063550P.

28-OCT-1997; 97US-0063564P.

29-OCT-1997; 97US-0063435P.

29-OCT-1997; 97US-0063704P.

29-OCT-1997; 97US-0063732P.

29-OCT-1997; 97US-0063734P.

29-OCT-1997; 97US-0063735P.

29-OCT-1997; 97US-0063738P.

31-OCT-1997; 97US-0064215P.

31-OCT-1997; 97US-0063870P.

31-OCT-1997; 97US-0064103P.

03-NOV-1997; 97US-0064248P.

07-NOV-1997; 97US-0064809P.

12-NOV-1997; 97US-0065186P.

17-NOV-1997; 97US-0065846P.

18-NOV-1997; 97US-0065933P.

21-NOV-1997; 97US-0066120P.

21-NOV-1997; 97US-0066364P.

24-NOV-1997; 97US-0066453P.

24-NOV-1997; 97US-0066466P.

24-NOV-1997; 97US-0066511P.

24-NOV-1997; 97US-0066770P.

24-NOV-1997; 97US-0066772P.

25-NOV-1997; 97US-0066840P.

12-DEC-1997; 97US-0069425P.

04-JUN-1998; 98US-0088026P.

10-SEP-1998; 98US-009803P.

10-SEP-1998; 98WO-US018824.

14-SEP-1998; 98US-0100262P.

14-SEP-1998; 98WO-US019177.

16-SEP-1998; 98WO-US019330.

17-SEP-1998; 98US-0100858P.

17-SEP-1998; 98WO-US019437.

13-OCT-1998; 98US-0104080P.

20-NOV-1998; 98US-0109304P.

01-DEC-1998; 98WO-US025108.

22-DEC-1998; 98US-0113296P.

07-JUL-1999; 99US-0143048P.

26-JUL-1999; 99US-0145698P.

28-JUL-1999; 99US-0146222P.

08-SEP-1999; 99WO-US020594.

13-SEP-1999; 99WO-US020944.

15-SEP-1999; 99WO-US021090.

15-SEP-1999; 99WO-US021547.

05-OCT-1999; 99WO-US023089.

29-NOV-1999; 99WO-US028214.

30-NOV-1999; 99WO-US028313.

01-DEC-1999; 99WO-US028301.

02-DEC-1999; 99WO-US028564.

02-DEC-1999; 99WO-US028565.

16-DEC-1999; 99WO-US030095.

20-DEC-1999; 99WO-US030911.

20-DEC-1999; 99WO-US030999.

05-JAN-2000; 2000WO-US000219.

11-FEB-2000; 2000WO-US003565.

22-FEB-2000; 2000WO-US004414.

24-FEB-2000; 2000WO-US005004.

02-MAR-2000; 2000WO-US005841.

30-MAR-2000; 2000WO-US007377.

30-MAR-2000; 2000WO-US008439.

22-MAY-2000; 2000WO-US014042.

02-JUN-2000; 2000WO-US015264.

28-JUL-2000; 2000WO-US020710.

24-AUG-2000; 2000WO-US023328.

18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

Aehkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;

Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

Williams PM, Wood WI;

WPI; 2003-540670/51.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating skin, neurodegenerative diseases, as an antithrombotic agent and for inducing endothelial cell apoptosis.

Example 33; SEQ ID NO 204; 470pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are useful for stimulating hypertrophy of neonatal heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated proliferation of endothelial cells, modulating the proliferation of stimulated T-lymphocytes, enhancing the survival or proliferation of retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial cells, modulating glucose or FFA uptake, inducing proliferation and/or re-differentiation of chondrocytes. In particular, these are useful for detecting or treating cardiac insufficiency disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. loss of sight due to retinitis pigmentosa), obesity, diabetes, hyperinsulinaemia, hypoinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or arthritis) in mammals. PRO polypeptides and their portions affect the expression of genes which have a role in cell death. The polynucleotides

CC are useful in molecular biology including uses as hybridisation probes
CC for cDNA library to isolate the full-length PRO cDNA or to isolate other
CC cDNAs, in chromosome and gene mapping, in the generation of antisense RNA
CC and DNA, for preparing PRO polypeptides, for generating transgenic
CC animals or knockout animals which are useful in the development and
CC screening of therapeutically useful reagents, as probes and for the
CC genetic analysis of individuals with genetic disorders as well as for
CC recombinantly expressing the protein and for chromosome identification.
CC The proteins are useful as molecular marker for protein electrophoresis
CC purposes, as therapeutic agents, for screening compounds to identify
CC those that mimic the PRO polypeptide (agonists) or prevent the effect of
CC the PRO polypeptide (antagonists). The polynucleotides and proteins are
CC useful for tissue typing. PRO antibodies are useful for
CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO
CC antibodies are useful in diagnostic assays for PRO e.g. detecting its
CC expression in specific cells, tissues or serum and for affinity
CC purification of PRO from recombinant cell culture or natural sources. The
CC PRO genes may also be used in gene therapy, particularly for replacing a
CC defective gene. The sequence presented is a PCR primer which was used to
CC amplify a PRO polynucleotide of the invention.

XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 10; Length 24;

Best Local Similarity 86.4%; Pred. No. 4.7e-03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTGTGACTCCCTGCTC 26

Db 24 CCTACTACTACTCTCTGCTC 3

RESULT 35

ID ADC39712/c
ID ADC39712 standard; DNA; 24 BP.

XX AC ADC39712;

XX DT 18-DEC-2003 (first entry)

XX DE Human secreted/transmembrane protein, #40, PCR primer #3.

XX Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
KW tissue typing; immunohistochemical staining; gene therapy;
KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
KW endothelial cell; stimulated T-lymphocyte; retinal neuron;
KW rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
KW cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
KW retinitis pigmentosa; obesity; diabetes; hyperinsulinaemia;
KW hypoinulinaemia; bone disorder; cartilage disorder; sport injury;
KW arthritis; cardiant; vulnary; cytostatic; ophthalmological;
KW osteopathic; antiarthritic; anorectic.

XX OS Homo sapiens.

XX XX US2003059828-A1.

XX PN 27-MAR-2003.

XX XX 13-JUL-2001; 2001US-00904553.

XX PF 17-SEP-1997; 97US-0059113P.

XX PR 17-SEP-1997; 97US-0059113P.

XX PR 17-SEP-1997; 97US-0059117P.

XX PR 17-SEP-1997; 97US-0059119P.

XX PR 17-SEP-1997; 97US-0059121P.

XX PR 17-SEP-1997; 97US-0059122P.

XX PR 17-SEP-1997; 97US-0059184P.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

XX PR 15-OCT-1997; 97US-0062125P.

XX PR 17-OCT-1997; 97US-0062285P.

XX PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066772P.
PR 24-NOV-1997; 97US-0066773P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 99WO-US030999.
PR 11-FEB-2000; 2000WO-US000219.
PR 22-FEB-2000; 2000WO-US003565.
PR 24-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.

PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
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 PI Mather JP, Pan J, Paoni NF, Roy WA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI; 2003-540675/51.
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 XX encoding them useful for treating skin, neurodegenerative diseases, as an
 PT antithrombotic agent and for inducing endothelial cell apoptosis.
 PT
 XX Example 33; SEQ ID NO 204; 477pp; English.
 PS
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 CC of a cell expressing PRO polypeptides. The PRO polypeptides or
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 CC proliferation of endothelial cells, modulating the proliferation of
 CC stimulated T-lymphocytes, enhancing the survival or proliferation of
 CC retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial
 CC cells, modulating glucose or FFA uptake, inducing proliferation and/or re
 CC -differentiation of chondrocytes. In particular, these are useful for
 CC detecting or treating cardiac insufficiency disorders, wounds, cancerous
 CC tumours, retinal disorders or injuries (e.g. loss of sight due to
 CC retinitis pigmentosa), obesity, diabetes, hyperinsulinaemia,
 CC hypoinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or
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 CC The proteins are useful as molecular marker for protein electrophoresis
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 SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 Query Match 66.2%; Score 17.2; DB 10; Length 24;
 Best Local Similarity 86.4%; Pred. NO. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTTGTTACTCCTCCTGCTC 26
 DB 24 CCTACTACTACTCCTCCTGCTC 3
 RESULT 36
 ADC40226/c
 ID ADC40226 standard; DNA; 24 BP.
 XX AC ADC40226;
 XX AC
 DT 18-DEC-2003 (first entry)
 XX Human secreted/transmembrane protein, #40, PCR primer #3.
 DE
 XX Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
 KW tissue typing; immunohistochemical staining; gene therapy;
 KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
 KW endothelial cell; stimulated T-lymphocyte; retinal neuron;
 KW rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
 KW cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
 KW retinitis pigmentosa; obesity; diabetes; hyperinsulinaemia;
 KW hypoinsulinaemia; bone disorder; cartilage disorder; sport injury;
 KW arthritis; cardiac; vulnery; cytostatic; ophthalmological;
 KW osteopathic; antiarthritic; anorectic.
 XX
 OS Homo sapiens.
 XX
 XX US2003059829-A1.
 XX
 PD 27-MAR-2003.
 XX
 XX 13-JUL-2001; 2001US-00905381.
 PF 17-SEP-1997; 97US-0059113P.
 XX 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
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 PR 17-OCT-1997; 97US-0062285P.
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 PR 21-OCT-1997; 97US-0063486P.
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 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
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 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
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 PR 29-OCT-1997; 97US-0063732P.
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 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.

XX US2003036061-A1.
PN 20-FEB-2003.
XX 18-JUL-2001; 2001US-00909204.
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
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PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-00621125P.
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PR 24-OCT-1997; 97US-00631128P.
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PR 28-OCT-1997; 97US-00633541P.
PR 28-OCT-1997; 97US-00633542P.
PR 28-OCT-1997; 97US-00633544P.
PR 28-OCT-1997; 97US-00633549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
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PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
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PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064284P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
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PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-008026P.
PR 10-SEP-1998; 98US-009803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
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PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
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PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
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PR 13-SEP-1999; 99WO-US020944.
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PR 05-JAN-2000; 2000WO-US000219.
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PR 22-FEB-2000; 2000WO-US004414.
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PR 02-MAR-2000; 2000WO-US005841.
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PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI William PM, Wood WI;
XX WPI; 2003-615762/58.
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
FT antagonists of polypeptide, and as molecular weight markers.
XX Example 33; SEQ ID NO 204; 476pp; English.
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
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RESULT 38

ADC34350/c

ID ADC34350 standard; DNA; 24 BP.

AC ADC34350;

XX 18-DEC-2003 (first entry)

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KW retinitis pigmentosa; obesity; diabetes; hyperinsulinaemia;

KW hypotension; bone disorder; cartilage disorder; sport injury;

KW arthritis; cardiac; vulvar; cytostatic; ophthalmological;

KW osteopathic; antiarthritic; anorectic.

XX Homo sapiens.

XX US2000306094-A1.

XX 20-FEB-2003.

XX 13-JUL-2001; 2001US-00904820.

XX 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059115P.

XX 17-SEP-1997; 97US-0059117P.

XX 17-SEP-1997; 97US-0059119P.

XX 17-SEP-1997; 97US-0059121P.

XX 17-SEP-1997; 97US-0059122P.

XX 17-SEP-1997; 97US-0059184P.

XX 18-SEP-1997; 97US-0059263P.

XX 15-OCT-1997; 97US-0059266P.

XX 17-OCT-1997; 97US-0062282P.

XX 17-OCT-1997; 97US-0062287P.

XX 21-OCT-1997; 97US-0063486P.

XX 24-OCT-1997; 97US-0062814P.

XX 24-OCT-1997; 97US-0062816P.

XX 24-OCT-1997; 97US-0063045P.

XX 24-OCT-1997; 97US-0063120P.

XX 24-OCT-1997; 97US-0063121P.

XX 24-OCT-1997; 97US-0063127P.

XX 24-OCT-1997; 97US-0063128P.

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PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98US-0101917P.
PR 16-SEP-1998; 98US-0101930P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0101943P.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98US-0109304P.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99US-0146222P.
PR 13-SEP-1999; 99US-0146222P.
PR 15-SEP-1999; 99US-0146222P.
PR 15-SEP-1999; 99US-0146222P.
PR 05-OCT-1999; 99US-0146222P.
PR 29-NOV-1999; 99US-0146222P.
PR 30-NOV-1999; 99US-0146222P.
PR 01-DEC-1999; 99US-0146222P.
PR 02-DEC-1999; 99US-0146222P.
PR 02-DEC-1999; 99US-0146222P.
PR 16-DEC-1999; 99US-0146222P.
PR 20-DEC-1999; 99US-0146222P.
PR 05-JAN-2000; 2000US-0000219.
PR 11-FEB-2000; 2000US-0000219.
PR 22-FEB-2000; 2000US-0000219.
PR 24-FEB-2000; 2000US-0000219.
PR 02-MAR-2000; 2000US-0000219.
PR 30-MAR-2000; 2000US-0000219.
PR 22-MAY-2000; 2000US-0000219.
PR 02-JUN-2000; 2000US-0000219.
PR 28-JUL-2000; 2000US-0000219.
PR 24-AUG-2000; 2000US-0000219.
PR 18-SEP-2000; 2000US-0000219.
XX (GETH) GENENTECH INC.

XX PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
XX PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX PI Williams PM, Wood WI;
XX DR WPI; 2003-615763/58.
XX PT Novel secreted and transmembrane polypeptides and polynucleotides
XX PT encoding them useful for treating cancers, asthma, rheumatoid arthritis,
XX PT neurological diseases, and skin diseases.
XX PS Example 33; SEQ ID NO 204; 478pp; English.
XX CC The invention discloses isolated PRO secreted/transmembrane polypeptides
XX CC and the nucleic acid encoding them. The polypeptides can be used to raise
XX CC antibodies that specifically bind to the PRO polypeptide, for linking a
XX CC bioactive molecule to a cell expressing a PRO protein and for modulating
XX CC at least one biological activity of a cell. PRO polypeptides are useful
XX CC for detecting other PRO polypeptides in a sample and for linking a
XX CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
XX CC polypeptide antibodies are useful for modulating the biological activity
XX CC of a cell expressing PRO polypeptides. The PRO polypeptides or
XX CC polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or
XX CC bioreactors. These are useful for stimulating hypertrophy of neonatal
XX CC heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated
XX CC proliferation of endothelial cells, modulating the proliferation of
XX CC stimulated T-lymphocytes, enhancing the survival or proliferation of
XX CC retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial
XX CC cells, modulating glucose or FFA uptake, inducing proliferation and/or re
XX CC differentiation of chondrocytes. In particular, these are useful for
XX CC detecting or treating cardiac insufficiency disorders, wounds, cancerous
XX CC tumours, retinal disorders or injuries (e.g. loss of sight due to
XX CC retinitis pigmentosa), obesity, diabetes, hyperinsulinaemia,
XX CC hypoinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or
XX CC arthritis) in mammals. PRO polypeptides and their portions affect the
XX CC expression of genes which have a role in cell death. The polynucleotides
XX CC are useful in molecular biology including uses as hybridisation probes
XX CC for cDNA library to isolate the full-length PRO cDNA or to isolate other
XX CC cDNAs, in chromosome and gene mapping, in the generation of antisense RNA
XX CC and DNA, for preparing PRO polypeptides, for generating transgenic
XX CC animals or knockout animals which are useful in the development and
XX CC screening of therapeutically useful reagents, as probes and for the
XX CC genetic analysis of individuals with genetic disorders as well as for
XX CC recombinantly expressing the protein and for chromosome identification.
XX CC The proteins are useful as molecular marker for protein electrophoresis
XX CC purposes, as therapeutic agents, for screening compounds to identify
XX CC those that mimic the PRO polypeptide (agonists) or prevent the effect of
XX CC the PRO polypeptide (antagonists). The polynucleotides and proteins are
XX CC useful for tissue typing. PRO antibodies are useful for
XX CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO
XX CC antibodies are useful in diagnostic assays for PRO e.g. detecting its
XX CC expression in specific cells, tissues or serum and for affinity
XX CC purification of PRO from recombinant cell culture or natural sources. The
XX CC PRO genes may also be used in gene therapy, particularly for replacing a
XX CC defective gene. The sequence presented is a PCR primer which was used to
XX CC amplify a PRO polynucleotide of the invention.

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5 CCTTCTGTACTCTCTCTGTC 26

Db 24 CCTACTACTCTCTCTGTC 3

RESULT 39

ADC29405/C

ID ADC29405 standard; DNA; 24 BP.

XX AC ADC29405;
XX DT 18-DEC-2003 (first entry)
XX DE Human secreted/transmembrane protein, #40, PCR primer #3.
XX KW Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
XX KW tissue typing; immunohistochemical staining; gene therapy;
XX KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
XX KW endothelial cell; stimulated T-lymphocyte; retinal neuron;
XX KW rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
XX KW cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
XX KW retinitis pigmentosa; obesity; diabetes; hyperinsulinaemia;
XX KW hypoinsulinaemia; bone disorder; cartilage disorder; sport injury;
XX KW arthritis; cartilage; vulnery; cytostatic; ophthalmological;
XX KW osteopathic; antiarthritic; anorectic.
XX OS Homo sapiens.
XX PN US2003049676-A1.
XX PD 13-MAR-2003.
XX PF 10-JUL-2001; 2001US-00902736.
XX PR 17-SEP-1997; 97US-0059113P.
XX PR 17-SEP-1997; 97US-0059115P.
XX PR 17-SEP-1997; 97US-0059117P.
XX PR 17-SEP-1997; 97US-0059119P.
XX PR 17-SEP-1997; 97US-0059121P.
XX PR 17-SEP-1997; 97US-0059122P.
XX PR 17-SEP-1997; 97US-0059184P.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
XX PR 15-OCT-1997; 97US-0062125P.
XX PR 17-OCT-1997; 97US-0062285P.
XX PR 17-OCT-1997; 97US-0062287P.
XX PR 21-OCT-1997; 97US-0063486P.
XX PR 24-OCT-1997; 97US-0062814P.
XX PR 24-OCT-1997; 97US-0062816P.
XX PR 24-OCT-1997; 97US-0063045P.
XX PR 24-OCT-1997; 97US-0063120P.
XX PR 24-OCT-1997; 97US-0063121P.
XX PR 24-OCT-1997; 97US-0063127P.
XX PR 24-OCT-1997; 97US-0063128P.
XX PR 27-OCT-1997; 97US-0063327P.
XX PR 27-OCT-1997; 97US-0063329P.
XX PR 28-OCT-1997; 97US-0063541P.
XX PR 28-OCT-1997; 97US-0063542P.
XX PR 28-OCT-1997; 97US-0063544P.
XX PR 28-OCT-1997; 97US-0063549P.
XX PR 28-OCT-1997; 97US-0063550P.
XX PR 28-OCT-1997; 97US-0063564P.
XX PR 29-OCT-1997; 97US-0063435P.
XX PR 29-OCT-1997; 97US-0063704P.
XX PR 29-OCT-1997; 97US-0063732P.
XX PR 29-OCT-1997; 97US-0063734P.
XX PR 29-OCT-1997; 97US-0063735P.
XX PR 29-OCT-1997; 97US-0063718P.
XX PR 29-OCT-1997; 97US-0064215P.
XX PR 31-OCT-1997; 97US-0063870P.
XX PR 31-OCT-1997; 97US-0064103P.
XX PR 03-NOV-1997; 97US-0064248P.
XX PR 07-NOV-1997; 97US-0064809P.
XX PR 12-NOV-1997; 97US-0065186P.
XX PR 12-NOV-1997; 97US-0065846P.
XX PR 18-NOV-1997; 97US-0065693P.
XX PR 21-NOV-1997; 97US-0066120P.
XX PR 21-NOV-1997; 97US-0066364P.
XX PR 24-NOV-1997; 97US-0066453P.
XX PR 24-NOV-1997; 97US-0066466P.
XX PR 24-NOV-1997; 97US-0066511P.

24-NOV-1997; 97US-0066770P.
25-NOV-1997; 97US-0066772P.
25-NOV-1997; 97US-0066840P.
12-DEC-1997; 97US-0069425P.
04-JUN-1998; 98US-0088026P.
10-SEP-1998; 98US-0098038P.
10-SEP-1998; 98WO-US018824.
14-SEP-1998; 98US-0100262P.
14-SEP-1998; 98WO-US019177.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98US-0100858P.
17-SEP-1998; 98WO-US019437.
13-OCT-1998; 98US-0104080P.
20-NOV-1998; 98US-0109304P.
01-DEC-1998; 98WO-US025108.
22-DEC-1998; 98US-0113296P.
07-JUL-1999; 98US-0143048P.
26-JUL-1999; 98US-0145698P.
28-JUL-1999; 98US-0146222P.
08-SEP-1999; 99WO-US020594.
13-SEP-1999; 99WO-US020944.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
05-OCT-1999; 99WO-US023089.
29-NOV-1999; 99WO-US028313.
30-NOV-1999; 99WO-US028301.
01-DEC-1999; 99WO-US028564.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
PA (GETH) GENENTECH INC.
XX
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Ann Roy M, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX
DR WPI; 2003-585107/55.
XX
PT Novel isolated PRO polypeptides e.g. PRO234 (useful for treating
PT rheumatoid arthritis, psoriasis and multiple sclerosis) and PRO187
PT (useful for treating Alzheimer's disease, cancer).
XX
XX
PS Example 33; SEQ ID NO 204; 451pp; English.
PS
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. The PRO polypeptides or
CC polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. These are useful for stimulating hypertrophy of neonatal
CC heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated
CC proliferation of endothelial cells, modulating the proliferation of
CC stimulated T-lymphocytes, enhancing the survival or proliferation of
CC retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial
CC cells, modulating glucose or FFA uptake, inducing proliferation and/or re
CC differentiation of chondrocytes. In particular, these are useful for
CC detecting or treating cardiac insufficiency disorders, wounds, cancerous
CC tumours, retinal disorders or injuries (e.g. loss of sight due to
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CC hypopinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or
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CC are useful in molecular biology including uses as hybridisation probes
CC for cDNA library to isolate the full-length PRO cDNA or to isolate other
CC cDNAs, in chromosome and gene mapping, in the generation of antisense RNA
CC and DNA, for preparing PRO polypeptides, for generating transgenic
CC animals or knockout animals which are useful in the development and
CC screening of therapeutically useful reagents, as probes and for the
CC genetic analysis of individuals with genetic disorders as well as for
CC recombinantly expressing the protein and for chromosome identification.
CC The proteins are useful as molecular marker for protein electrophoresis
CC purposes, as therapeutic agents, for screening compounds to identify
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CC expression in specific cells, tissues or serum and for affinity
CC purification of PRO from recombinant cell culture or natural sources. The
CC PRO genes may also be used in gene therapy, particularly for replacing a
CC defective gene. The sequence presented is a PCR primer which was used to
CC amplify a PRO polynucleotide of the invention.
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CCTCTGTGACTCTCTCTGCTC 26
DB 24 CCTACTACTACTCTCTGCTC 3
RESULT 40
ADC28936/c
ID ADC28936 standard; DNA; 24 BP.
XX
XX AC ADC28936;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #40, PCR primer #3.
XX
KW Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
KW tissue typing; immunohistochemical staining; gene therapy;
KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
KW endothelial cell; stimulated T-lymphocyte; retinal neuron;
KW rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
KW cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
KW retinitis pigmentosa; obesity; diabetes; hyperinsulinaemia;
KW hypopinsulinaemia; bone disorder; cartilage disorder; sport injury;
KW arthritis; cardiac; vulnary; cytostatic; ophthalmological;
KW osteopathic; antiarthritic; anorectic.
XX
XX OS Homo sapiens.
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XX US2003049677-A1.
XX
PD 13-MAR-2003.
XX
PF 17-JUL-2001; 2001US-00907794.
XX
XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
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PR 15-OCT-1997; 97US-0062128P.
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PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
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PR 21-NOV-1997; 97US-0066364P.
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PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
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PR 26-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
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PI Williams PM, Wood WI;
XX WPI; 2003-615797/58.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating skin, neurodegenerative diseases, as an
PT antithrombotic agent and for inducing endothelial cell apoptosis.
XX
PS Example 33; SEQ ID NO 204; 470pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
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Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTGTACTCTCTGCTC 26
||| || |||||
Db 24 CCTACTACTACTCTCTGCTC 3

Search completed: November 18, 2005, 11:52:33
Job time : 181.034 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1243.65 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCTCCTCTTGTGACTCTCTCTGCTC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	71.5	49	8	AZ407440 1M0178H15
2	18	69.2	27	8	AZ435323 1M0079M16
3	17	65.4	33	8	AZ435186 1M0222E03
4	17	65.4	35	8	AZ421500 1M0199J13
5	17	65.4	36	8	AZ479840 1M0300P16
6	17	65.4	37	8	AZ623276 1M0460M16
7	17	65.4	44	8	AZ968544 2M0240J20
8	17	65.4	45	8	AZ843544 2M0142022
9	17	65.4	50	8	AZ397298 1M0162A13
10	16.6	63.8	41	1	AU256766 AU256766
11	16.4	63.1	41	8	AZ450486 1M0249D13
12	16.2	62.3	27	8	AZ835139 2M0129P09
13	16.2	62.3	37	1	A1966611 sc53c11.y
14	16	61.5	50	9	CR235166 Forward s
15	15.6	60.0	43	1	A1570014 tr91a09.x
16	15.4	59.2	31	8	AZ500072 1M0338A14
17	15.4	59.2	32	8	AZ792853 2M0045C07
18	15.4	59.2	33	8	AZ783357 2M0025B05
19	15.4	59.2	34	1	AV847122 AV847122
20	15.4	59.2	37	8	AZ392980 1M0155P13
21	15.4	59.2	37	8	AZ761912 1M0356D02
22	15.4	59.2	40	8	AZ345503 1M0080G05
23	15.4	59.2	46	1	A1088341 qb07a07.x
24	15.4	59.2	49	1	AA388129 vc86f05.x

c	25	15.4	59.2	50	1	AU102295
	26	15	57.7	29	8	AZ854411 2M0158B05
c	27	15	57.7	40	8	AZ537227
c	28	15	57.7	45	5	BQ590260 E012843-0
c	29	14.8	56.9	26	8	AZ942099 2M0202C09
c	30	14.8	56.9	44	8	AZ456843 1M0259J24
c	31	14.8	56.9	50	8	AZ767297 1M0566G21
c	32	14.6	56.2	39	1	AJ794161 AJ794161
c	33	14.6	56.2	50	7	CF329688 NACL-05-
c	34	14.4	55.4	38	2	BE736376 601306S13
c	35	14.4	55.4	40	7	CF319095 HD--09-H1
c	36	14.4	55.4	43	7	CF292564 30DGS--01
c	37	14.4	55.4	48	8	AZ443723 1M0238D11
c	38	14.4	55.4	50	9	AL943250 Arabidops
c	39	14.2	54.6	21	8	AZ45564 1M0511C13
c	40	14.2	54.6	39	7	CO783803 BL279A_A0
c	41	14.2	54.6	42	7	R39311 yd01c07.s1
c	42	14.2	54.6	43	7	W86565 zh63h03.r1
c	43	14.2	54.6	46	1	A1124130 SMOVL3CAN
c	44	14.2	54.6	48	8	BH629491 1007073A0
c	45	14.2	54.6	49	1	AA719607 zh37a05.s

ALIGNMENTS

RESULT 1
AZ407440 49 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0178H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0178H15 F, genomic survey sequence.
ACCESSION AZ407440
VERSION AZ407440.1 GI:10531549
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0178 row: H column: 15
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 49.
Location/Qualifiers
1. 49
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0178H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 33;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CCTCCTTCTGTACTCTCTCTCTC 26
||||| ||| ||||| |||
Db 32 CCTCCTCTCTATCTCTCTCTC 8

RESULT 4

AZ421500/c
LOCUS AZ421500 35 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0199J13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0199J13 R, genomic survey sequence.

ACCESSION AZ421500
VERSION AZ421500.1 GI:10545513
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 35)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0199 row: J column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 35.

Location/Qualifiers

FEATURES

source

FEATURES

source

1..35

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0199J13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 35;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CCTCCTTCTGTACTCTCTCTCTC 26
||||| ||| ||||| |||
Db 33 CCTCCTCTCTCTCTCTCTCTC 9

RESULT 5

AZ479840/c

LOCUS AZ479840 36 bp DNA linear GSS 04-OCT-2000

DEFINITION IM0300P16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0300P16 R, genomic survey sequence.

ACCESSION AZ479840

VERSION AZ479840.1 GI:10640854

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 36)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0300 row: P column: 16

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 36.

Location/Qualifiers

1..36

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0300P16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 36;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 34 CCTCTCTCTCTCTCTCTCTCTCTC 10

RESULT 6

AZ623276/c
LOCUS 37 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0460M16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0460M16 R, genomic survey sequence.

ACCESSION AZ623276
VERSION AZ623276.1 GI:11745466

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 37)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0460 row: M column: 16

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 37.

FEATURES

source

1..37

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0460M16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 37;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 35 CCTCTCTCTCTCTCTCTCTCTCTC 11

RESULT 7

AZ968544/c
LOCUS 44 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0240J20R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0240J20 R, genomic survey sequence.

ACCESSION AZ968544
VERSION AZ968544.1 GI:13839771

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 44)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0240 row: J column: 20

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 44.

FEATURES

source

1..44

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0240J20"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 44;
Best Local Similarity 80.0%; Pred. No. 4.4e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CCTCTCTTGTACTCTCTCTCTC 26
DB 42 CCTCTCTCTCTCTCTCTCTCTC 18

RESULT 8
LOCUS AZ843544
DEFINITION 2M0142022F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0142022 F, genomic survey sequence.
ACCESSION AZ843544
VERSION AZ843544.1 GI:13013452
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 45)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0142 row: 0 column: 22

Seq primer: CTTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

FEATURES

source

1. 45
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0142022"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 45;
Best Local Similarity 80.0%; Pred. No. 4.4e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CCTCTCTTGTACTCTCTCTCTC 26
DB 11 CCTCTCTCTCTCTCTCTCTCTC 35

RESULT 9

LOCUS

AZ397298
DEFINITION 1M0162A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0162A13 F, genomic survey sequence.
ACCESSION AZ397298
VERSION AZ397298.1 GI:10512370
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 50)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0162 row: A column: 13

Seq primer: CTTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 50.

Location/Qualifiers

FEATURES

source

1. 50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0162A13"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 50;
Best Local Similarity 80.0%; Pred. No. 4.4e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCCTCTCTGTACTCCTCCTGCTC 26
||||||| | ||||| |||

Db 26 CCTCCTTCACATCCTCCTCCTCCTC 50
||||||| | ||||| |||

RESULT 10

AU256766/c 41 bp mRNA linear EST 25-APR-2002
LOCUS AU256766 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION BED0008949 3', mRNA sequence.

ACCESSION

VERSION AU256766

KEYWORDS

SOURCE AU256766.1 GI:20320746

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)

AUTHORS

CONTACT: Kikuya Kato

Graduate School of Biological Sciences

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8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkatoo@nara.ac.jp, /BED/index.html.

URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES

Location/Qualifiers
1..41
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0008949"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"

ORIGIN

Query Match 63.8%; Score 16.6; DB 1; Length 41;
Best Local Similarity 82.6%; Pred. No. 6.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CCTCCTCTCTGTACTCCTCCTGCTC 24
||||||| | ||||| |||

Db 40 CCTCCTCTCTGTACTCCTCCTGCTC 18
||||||| | ||||| |||

RESULT 11

AZ450486 41 bp DNA linear GSS 04-OCT-2000
LOCUS AZ450486
DEFINITION 1M0249D13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0249D13 F, genomic survey sequence.

AZ450486

VERSION AZ450486.1 GI:10605322

KEYWORDS GSS.

SOURCE

ORGANISM Mus musculus (house mouse)

REFERENCE

AUTHORS

1 (bases 1 to 41)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0249 row: D column: 13

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 41.

Location/Qualifiers

1..41

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0249D13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 63.1%; Score 16.4; DB 8; Length 41;
Best Local Similarity 76.9%; Pred. No. 7.2e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCCTCTCTGTACTCCTCCTGCTC 26
||||||| | ||||| |||

Db 2 CCTCCTCTCTGTACTCCTCCTGCTC 27
||||||| | ||||| |||

RESULT 12

AZ835139 27 bp DNA linear GSS 20-FEB-2001
LOCUS AZ835139
DEFINITION 2M0129P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0129P09 F, genomic survey sequence.

ACCESSION
AZ835139
VERSION
AZ835139.1 GI:13005047
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0129 row: P column: 09

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 27.

Location/Qualifiers

1..27

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0129P09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 62.3%; Score 16.2; DB 8; Length 27;

Best Local Similarity 85.7%; Pred. No. 8.2e+04;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCTCCTCTTGTACTCCTCT 22

||||| ||| ||| ||| |||

Db 7 CCTCCTCTTGTACTCCTCT 27

RESULT 13

AI966611/c

LOCUS

DEFINITION sc53c11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

AI966611 37 bp mRNA linear EST 12-JUL-2004

Gm-c1015-1293 5' similar to TR:004132 004132 SRC1.; mRNA
sequence.

ACCESSION
AI966611
VERSION
AI966611.1 GI:5761248

KEYWORDS
EST.

SOURCE
Glycine max (soybean)

ORGANISM
Glycine max

REFERENCE
AUTHORS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 37)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,

Bowers, Y., Person, B., Swaller, T., Gibbons, M., Fape, D., Harvey, N.,

Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this

clone is listed in the 'Other ESTs on clone' field. Trace

considered overall poor quality Possible reversed clone: similarity

on wrong strand This clone is available through: Biogenetic

Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423

4163; email: info@biogeneticservices.com)

Seq primer: -40RP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..37

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Williams 82"

/db_xref="taxon:3947"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-1293"

/tissue_type="Mature flowers, field grown plants"

/lab_host="XL10-Gold"

/clone_lib="Gm-c1015"

/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:

XhoI; This cDNA library was constructed from mRNA isolated

from mature flowers of field grown plants. The cDNA

library was prepared using the Stratagene pBluescript II

XR cDNA library construction kit. Complementary DNA was

synthesized from mRNA using a primer consisting of a poly

(dT) sequence with a XhoI restriction site. EcoRI adaptors

were ligated to the blunt-ended cDNA fragments followed by

XhoI digestion. The cDNA fragments were directionally

cloned into the EcoRI-XhoI restriction site of the

pBluescript vector. The ligated cDNA fragments were

transformed into XL10-Gold host cells. This library was

constructed by Dr. Randy Shoemaker and Dr. John

Erpelding."

ORIGIN

Query Match 62.3%; Score 16.2; DB 1; Length 37;

Best Local Similarity 85.7%; Pred. No. 8.4e+04;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCTCCTCTTGTACTCCTCT 22

||||| ||| ||| ||| |||

Db 35 CCTCCTCTTGTACTCCTCT 15

RESULT 14

CR235166

LOCUS

DEFINITION CR235166 50 bp DNA linear GSS 06-JUL-2004

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 31;
 Best Local Similarity 76.0%; Pred. No. 1.6e+05;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 CCTCCTCTCTGACTCTCTCTCTCTC 26
 ||||| || ||||| |||||
 Db 25 CCTCCTCTCTCATCTCTCTCTCTC 1

RESULT 17
 AZ792853/c
 LOCUS
 DEFINITION 2M0045C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0045C07 R, genomic survey sequence.

ACCESSION AZ792853
 VERSION AZ792853.1 GI:12937209

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 32)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: C column: 07

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

FEATURES

source

1..32
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0045C07"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptored DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 32;
 Best Local Similarity 76.0%; Pred. No. 1.6e+05;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 CCTCCTCTCTGACTCTCTCTCTCTC 26
 ||||| || ||||| |||||
 Db 32 CCTCCTCTCTCTCTCTCTCTCTC 8

RESULT 18
 AZ783357
 LOCUS
 DEFINITION 2M0025B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0025B05 F, genomic survey sequence.

ACCESSION AZ783357
 VERSION AZ783357.1 GI:12918011

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 33)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0025 row: B column: 05

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 33.

Location/Qualifiers

FEATURES

source

1..33
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0025B05"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptored DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 33;
Best Local Similarity 76.0%; Pred. No. 1.6e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCTCCTCTTGTACTCCTCTGCTC 26
||||| | | | | | | | | |
Db 3 CCTCCTCTCTCTCCCTCTCTCTC 27

RESULT 19

AV847122 34 bp mRNA linear EST 08-NOV-2001
LOCUS AV847122 Nori Satoh unpublished cDNA library, egg Ciona
DEFINITION intestinalis cDNA clone rcieg9fi4 3', mRNA sequence.
ACCESSION AV847122
VERSION AV847122.1 GI:16827179
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis

REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 34)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoheascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers
1..34
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcieg9fi4"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

FEATURES

source

ORIGIN

Query Match 59.2%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 1.6e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCTCCTCTTGTACTCCTCTGCTC 26
||||| | | | | | | | | |
Db 8 CTTCCTCTTGTCTCTCTCTGATC 32

RESULT 20

AZ392980/C 37 bp DNA linear GSS 03-OCT-2000
LOCUS AZ392980 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0155P13 R, genomic survey sequence.
ACCESSION AZ392980
VERSION AZ392980.1 GI:10508052
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
AUTHORS

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Kelly,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0155 row: P column: 13
Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 37.

Location/Qualifiers
1..37
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0155P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [G14732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 37;
Best Local Similarity 76.0%; Pred. No. 1.7e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCTCCTCTTGTACTCCTCTGCTC 26
||||| | | | | | | | | |
Db 26 CCTCCTCTCTCTCTCTCTCTCTC 2

RESULT 21

AZ761912/C 37 bp DNA linear GSS 16-FEB-2001
LOCUS AZ761912 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0556D02 R, genomic survey sequence.
ACCESSION AZ761912
VERSION AZ761912.1 GI:12871332
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0556 row: D column: 02
 Seq primer: CACACAGGAAAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 37.
 Location/Qualifiers
 1. .37

FEATURES

source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0556D02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 37;
 Best Local Similarity 76.0%; Pred. No. 1.7e+05;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCTCTCTTGTGACCTCTCTCTCTC 26

Db 37 CCTCTCTCTCTCTCTCTCTCTCTC 13

RESULT 22
 A2345503
 LOCUS
 DEFINITION 1M0080C05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080G05 F, genomic survey sequence.
 ACCESSION A2345503
 VERSION A2345503.1 GI:10424740
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 40)
 REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE

JOURNAL COMMENT

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: G column: 05
 Seq primer: CTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 40.
 Location/Qualifiers
 1. 40

FEATURES

source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080G05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 40;
 Best Local Similarity 76.0%; Pred. No. 1.7e+05;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCTCTTGTGACTCTCTCTCTGCT 25

Db 8 CCTCTCTCTCTCTCTCTCTCTCT 32

RESULT 23
 A1088341
 LOCUS
 DEFINITION qb07a07.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:1695540 3' similar to TR:Q19985 Q19985 F40E10.6 ;, mRNA sequence.
 ACCESSION A1088341
 VERSION A1088341.1 GI:3427400
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 46)
 REFERENCE

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG04811"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 59.2%; Score 15.4; DB 1; Length 50;
Best Local Similarity 94.1%; Pred. No. 1.7e+05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCTCTTCTGTACTCC 18
||||| ||||| |||||
Db 34 CCTCTCTGTACTCC 18

RESULT 26
AZ854411 29 bp DNA linear GSS 21-FEB-2001
LOCUS
DEFINITION 2M0158B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0158B05 F, genomic survey sequence.

ACCESSION AZ854411
VERSION AZ854411.1 GI:13043500
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0158 row: B column: 05

Seq primer: CGTGTAAACGACGGCAGT
Class: plasmid ends

High quality sequence stop: 29.

FEATURES

Location/Qualifiers

1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0158B05"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated

ORIGIN

Query Match 57.7%; Score 15; DB 8; Length 29;
Best Local Similarity 78.3%; Pred. No. 2.3e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 TCCTCTGTACTCTCTCTGCTC 26
||||| ||||| ||||| |||||
Db 5 TCCTCTGTACTCTCTCTGTTT 27

RESULT 27
AZ537227/c

LOCUS
DEFINITION AST-2P03013 Genetrapp PC-3 Human Prostatic Carcinoma Library Homo
sapiens genomic 5', genomic survey sequence.

ACCESSION AZ537227
VERSION AZ537227.1 GI:11114155
KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)

REFERENCE
AUTHORS Henkel, G., Iiyanaage, M., Pratt, E., Huang, D., Riley, M.,
Bernardino, A., Durick, K. and Pollok, B.

TITLE Exon-trap tags from a PC-3 GenomeScreen(TM) Library
Unpublished (2000)

COMMENT Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkel@aurorabio.com

Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
preceded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAmp-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
Class: exon-trapped.

FEATURES

Location/Qualifiers

1..40
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Adenocarcinoma"
/cell_type="Epithelial"
/cell_line="PC-3"
/clone_lib="Genetrapp PC-3 Human Prostatic Carcinoma
Library"
/note="Organ: Prostate; Vector: pAmp-1; 3' RACE of total
RNA from genetrapp pools; shotgun clone in pAmp-1 and used
to transform DH5-alpha competent bacteria."

ORIGIN

Query Match 57.7%; Score 15; DB 8; Length 40;
Best Local Similarity 78.3%; Pred. No. 2.3e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CTCCTCTTGTACTCTCTCTGCT 25
||||| ||||| ||||| |||||
Db 30 CTCCTCTTGTCTCCACTCTCTGCT 8

with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 44)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0259 row: J column: 24
 Seq primer: CACACAGAAACAGTATGACC
 Class: plasmid ends
 High quality sequence stop: 44.
FEATURES
 Location/Qualifiers
 1..44
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0259J24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN
 Query Match 56.9%; Score 14.8; DB 8; Length 44;
 Best Local Similarity 73.1%; Pred. NO. 2.8e+05;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 CCCTCCTCTTGTACTCTCTCTGCTC 26
 Db 41 CCCTCCTCTTGTACTCTCTCTCTCC 16
RESULT 31
 AZ767297
 LOCUS AZ767297 50 bp DNA linear GSS 16-FEB-2001
 DEFINITION IM0566221F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0566221 F, genomic survey sequence.
 ACCESSION AZ767297
 VERSION AZ767297.1 GI:12885248

KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 50)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0566 row: G column: 21
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 50.
FEATURES
 Location/Qualifiers
 1..50
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0566G21"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN
 Query Match 56.9%; Score 14.8; DB 8; Length 50;
 Best Local Similarity 73.1%; Pred. NO. 2.8e+05;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 CCCTCCTCTTGTACTCTCTCTGCTC 26
 Db 7 CTCCCCCTTCTTACCCCTCTCTCCCTC 32
RESULT 32
 AZ794161/c
 LOCUS AZ794161 39 bp mRNA linear EST 11-AUG-2004
 DEFINITION AZ794161 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018.3.04 h20, mRNA sequence.
 ACCESSION AZ794161
 VERSION AZ794161.1 GI:51109489

KEYWORDS	RT-PCR."
SOURCE	ORIGIN
ORGANISM	Query Match
	Best Local Similarity 56.2%; Score 14.6; DB 7; Length 50;
	Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
REFERENCE	QY 1 CCTCTCTTCTGTACTCTCTCC 21
AUTHORS	DB 30 CTCCTCTTCTGTACTCTCTCC 50
TITLE	
JOURNAL	
COMMENT	
FEATURES	RESULT 34
source	BE736376 38 bp mRNA linear EST 15-SEP-2000
	601306513P1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640802 5',
	mRNA sequence.
	ACCESSION BE736376
	VERSION BE736376.1 GI:10150368
	KEYWORDS EST.
	SOURCE Homo sapiens (human)
	ORGANISM Homo sapiens
	REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	1 (bases 1 to 38) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	AUTHORS NIH-MGC http://mgc.nci.nih.gov/ .
	TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
	JOURNAL Unpublished (1999)
	COMMENT Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-remail.nih.gov
	Tissue Procurement: ATCC
	cDNA Library Preparation: Ling Hong/Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/LLNL at:
	http://image.llnl.gov
	Plate: LLCM345 row: j column: 03
	High quality sequence stop: 38.
	FEATURES Location/Qualifiers
	source
	1..38
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:3640802"
	/tissue_type="adenocarcinoma"
	/lab_host="DH10B (phage-resistant)"
	/clone_lib="NIH_MGC_39"
	/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
	Site 2: EcoRI; cDNA made by oligo-dT priming.
	Directionally cloned into EcoRI/XhoI sites using the
	following 5' adaptor: GCACGAG(G). Library constructed
	by Ling Hong in the laboratory of Gerald M. Rubin
	(University of California, Berkeley) using ZAP-cDNA
	synthesis kit (Stratagene) and Superscript II RT (Life
	Technologies)."
	ORIGIN
	Query Match
	Best Local Similarity 55.4%; Score 14.4; DB 2; Length 38;
	Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
	QY 2 CCTCTCTTCTGTACTCTCTCTGCT 25
	DB 38 CCCCTCTCTCTCTCTCTCTCCAGCT 15
	RESULT 35
	CF319095
	LOCUS CF319095/c
	DEFINITION HD--09-H17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
	library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
	HD--09-H17, mRNA sequence.
	KEYWORDS
	SOURCE
	ORGANISM
REFERENCE	1 (bases 1 to 39)
AUTHORS	Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.
TITLE	Antirrhinum EST collection
JOURNAL	Unpublished (2003)
COMMENT	Contact: Schwarz-Sommer Z
	Molekulare Pflanzen-genetik
	MPI fuer Zuechtungs-forschung
	Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES	Location/Qualifiers
source	1..39
	/organism="Antirrhinum majus"
	/mol_type="mRNA"
	/db_xref="taxon:4151"
	/clone="018.3.04.h20"
	/tissue_type="whole plant"
	/clone_lib="Antirrhinum majus whole plant"
ORIGIN	
Query Match	56.2%; Score 14.6; DB 1; Length 39;
Best Local Similarity	81.0%; Pred. No. 3.3e+05;
Matches	17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 CCTCTCTTCTGTACTCTCTCT 22	
DB 37 CCTCTCTCTGTCTCACCTCT 17	
RESULT 33	
CF329688	
LOCUS	
DEFINITION	CF329688 50 bp mRNA linear EST 18-AUG-2003
	NACL--05-B16.b1 Rice callus plasmid cDNA library (NACL) Oryza
	sativa (japonica cultivar-group) cDNA clone NACL--05-B16, mRNA
	sequence.
ACCESSION	CF329688
VERSION	CF329688.1 GI:33807590
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
	Ehrhartoideae; Oryzeae; Oryza.
REFERENCE	1 (bases 1 to 50)
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
	Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
	Large-scale Sequencing Analysis of Rice ESTs
	Unpublished (2003)
TITLE	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
JOURNAL	of Bioscience and Bioinformatics, Myongji University
COMMENT	Yongin, Kyeonggi, Korea
	Tel: 82 31 330 6193
	Fax: 82 31 321 6355
	Email: bhnam@bio.com , bhnam@bio.myongji.ac.kr .
FEATURES	Location/Qualifiers
source	1..50
	/organism="Oryza sativa (japonica cultivar-group)"
	/mol_type="mRNA"
	/cultivar="Nackdong"
	/db_xref="taxon:39947"
	/clone="NACL--05-B16"
	/tissue_type="callus"
	/dev_stage="proliferated callus on 2N6 media for 30 days"
	/lab_host="E.coli DH10B"
	/clone_lib="Rice callus plasmid cDNA library (NACL)"
	/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
	with oligoribonucleotides and then used as templates for

```

ACCESSION   CF319095
VERSION     CF319095.1
KEYWORDS    GI:33690856
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..40
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--01-G23"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

ORIGIN
Query Match      55.4%; Score 14.4; DB 7; Length 43;
Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGTACTCTCTCTCTC 26
    |||||
Db 43 CTCCTCTCTGTCTCTCTCTCTC 20
    |||||

RESULT 37
LOCUS      AZ443723/c
DEFINITION AZ443723 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0238D11 F, genomic survey sequence.
ACCESSION  AZ443723
VERSION    1
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1 (bases 1 to 48)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: dunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0238 row: D column: 11
            Seq primer: CGTTGTAACGACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 48.
            Location/Qualifiers
     source           1..48
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0238D11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA

ACCESSION   CF292564
VERSION     CF292564.1
KEYWORDS    GI:33661597
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE   1 (bases 1 to 43)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..40
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--09-H17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

ORIGIN
Query Match      55.4%; Score 14.4; DB 7; Length 40;
Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCTCTCTGTACTCTCTCTCTC 24
    |||||
Db 32 CCTCTCTCTGTGTCTCTCTCTC 9
    |||||

RESULT 36
LOCUS      CF292564/c
DEFINITION CF292564 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--01-G23, mRNA
            sequence.
ACCESSION  CF292564
VERSION    1
KEYWORDS   CF292564.1 GI:33661597
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE   1 (bases 1 to 43)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```


was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.4%; Score 14.4; DB 8; Length 48;
Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CTCCTCTCTGTACTCTCTCTGCT 25
||||| ||||| ||||| ||||| ||
Db 46 CTCCTCTCTCTCTCTCTCTCTCT 23

RESULT 38
AL943250 50 bp DNA linear GSS 31-MAR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-272H06-015096,
DEFINITION genomic survey sequence.
ACCESSION AL943250
VERSION AL943250.1 GI:24399848
KEYWORDS GSS.

ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL MEDLINE 22755829
PUBMED 12874060
REFERENCE 2

ROSSO, M.G., LI, Y., STRIZHOV, N., REISS, B., DEKKER, K. and
WEISSHAAR, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
JOURNAL MEDLINE 14682050
PUBMED 14756321
REFERENCE 4

(Bases 1 to 50)
Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
Details on the protocols used for generation of the sequence are
described in References 1-3. Re-examination of the source from
which this sequence has been produced indicates that the sequence
is of low reliability. Therefore, no information on a potential
insertion site is deduced. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source

1. .50
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-272H06-015096"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (Ti) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 55.4%; Score 14.4; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGTACTCTCTCTGCTC 26
||||| ||||| ||||| ||||| ||
Db 24 CTCCTCTATGTACCACTCTGCTC 47

RESULT 39
AZ645664 21 bp DNA linear GSS 14-DEC-2000
LOCUS clone UUGC1M0511C13 F, genomic survey sequence.
DEFINITION

ACCESSION AZ645664
VERSION AZ645664.1 GI:11775376
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (Bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 13
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

1. .21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0511C13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 54.6%; Score 14.2; DB 8; Length 21;
 Best Local Similarity 84.2%; Pred. NO. 4.3e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCCTTCTTGTACTCTCTCT 22
 ||||| |||||
 Db 1 TCCTCTATTACTCTCTCT 19

RESULT 40

CO783803/c

LOCUS

DEFINITION BL279A_A01 6-Day Axolotl Tail Blastema (6DaxBL) Ambystoma mexicanum
 CDNA 5' similar to hypothetical protein, mRNA sequence.

ACCESSION CO783803

VERSION CO783803.1 GI:50999783

KEYWORDS

EST.

SOURCE

Ambystoma mexicanum (axolotl)

Ambystoma mexicanum

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;

Ambystoma.

1 (bases 1 to 39)

Habermaun,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,

Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.

An Ambystoma mexicanum EST sequencing project: Analysis of 17,352

expressed sequence tags from embryonic and regenerating blastema

CDNA libraries

Genome Biol. (2004) In press

Contact: Elly M. Tanaka

Tanaka Lab

Max Planck Institute of Molecular Cell Biology and Genetics,

Dresden

Pfotenhauserstrasse 108, 01307 Dresden, Germany

Tel: 0049 351 210 2620

Fax: 0049 351 210 1489

Email: tanaka@mpi-cbg.de

Plate: BL279A row: 01 column: A

Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES

source

1..39

/organism="Ambystoma mexicanum"

/mol_type="mRNA"

/db_xref="taxon:8296"

/tissue_type="Tail Blastema"

/cell_type="regenerating tail blastema"

/clone_lib="6-Day Axolotl Tail Blastema (6DaxBL)"

/note="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;

Unnormalized cDNA plasmid library prepared by Invitrogen.

Size fractionated mRNA was polydT primed and cloned into

NotI-SalI site of pCMVSPORT6. Bacterial host is

EMDH10B-TONA. Average insert size is 1.67 kb.
 TAG_LIB=6DaxBL"

ORIGIN

Query Match 54.6%; Score 14.2; DB 7; Length 39;
 Best Local Similarity 84.2%; Pred. NO. 4.6e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCCTTCTTGTACTCTCTCC 21
 ||||| |||||
 Db 20 CTCCTTCTTGTACTCTCTCC 2

Search completed: November 18, 2005, 21:12:54
 Job time : 1246.65 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 50.5171 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCTCTCTTGTGACTCTCTCTGCTC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	1	US-07-989-160-8
2	17.2	66.2	24	4	US-09-907-794A-204
3	17.2	66.2	24	4	US-09-905-125A-204
4	17.2	66.2	24	4	US-09-902-775A-204
5	17.2	66.2	24	4	US-09-906-700-204
6	17.2	66.2	24	4	US-09-903-603A-204
7	17.2	66.2	24	4	US-09-904-920A-204
8	17.2	66.2	24	4	US-09-909-064-204
9	17.2	66.2	24	4	US-09-905-381A-204
10	17.2	66.2	24	4	US-09-906-618-204
11	17	65.4	30	1	US-08-068-747-4
12	17	65.4	30	3	US-08-589-109A-12
13	17	65.4	39	1	US-08-068-747-9
14	17	65.4	48	3	US-09-580-923-34
15	17	65.4	50	3	US-08-860-038-17
16	17	65.4	50	3	US-09-580-923-17
17	17	65.4	50	3	US-09-371-489-4
18	16.6	63.8	25	4	US-09-866-108A-13556
19	16.6	63.8	25	4	US-09-866-108A-13557
20	16.6	63.8	25	4	US-09-866-108A-13558
21	16.6	63.8	42	1	US-08-391-000-36
22	16.6	63.8	42	2	US-08-741-931-36
23	16.6	63.8	48	3	US-09-012-515A-7
24	16.6	63.8	48	3	US-08-360-144A-7
25	16.6	63.8	48	3	US-09-012-504A-7
26	16.6	63.8	48	4	US-09-012-399A-7
27	16.6	63.8	48	5	PCT-US95-06722-7

c	28	16.4	63.1	28	3	US-08-993-008A-2	Sequence 2, Appli
c	29	16.4	63.1	28	3	US-08-993-008A-3	Sequence 3, Appli
c	30	16.4	63.1	40	1	US-08-361-920-41	Sequence 41, Appl
c	31	16.4	63.1	40	1	US-08-361-920-52	Sequence 52, Appl
c	32	16.4	63.1	40	1	US-08-479-939-41	Sequence 41, Appl
c	33	16.4	63.1	40	1	US-08-479-939-52	Sequence 52, Appl
c	34	16.4	63.1	40	1	US-08-483-432-41	Sequence 41, Appl
c	35	16.4	63.1	40	1	US-08-483-432-52	Sequence 52, Appl
c	36	16.4	63.1	43	1	US-08-324-001-19	Sequence 19, Appl
c	37	16.4	63.1	43	1	US-08-324-001-20	Sequence 20, Appl
c	38	16.4	63.1	50	1	US-08-324-001-10	Sequence 10, Appl
c	39	16.4	63.1	50	1	US-08-324-001-11	Sequence 11, Appl
c	40	15.6	60.0	24	4	US-09-362-842-38	Sequence 38, Appl
c	41	15.6	60.0	25	4	US-09-866-108A-13555	Sequence 13555, A
c	42	15.6	60.0	25	4	US-09-866-108A-13559	Sequence 13559, A
c	43	15.6	60.0	25	4	US-09-396-196G-62750	Sequence 62750, A
c	44	15.6	60.0	37	4	US-08-899-367-10	Sequence 10, Appl
c	45	15.6	60.0	37	4	US-08-899-367-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-07-989-160-8
; Sequence 8, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-07-989-160-8

Query Match 100.0%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTCTCTTGTGACTCTCTCTGCTC 26
|||||

Db 1 CCTCTCTTTGTACTCTCTCTGCTC 26

RESULT 2

US-09-907-794A-204/c

; Sequence 204, Application US/09907794A

; Patent No. 6635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 204

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide probe

US-09-907-794A-204

Query Match 66.2%; Score 17.2; DB 4; Length 24;

Best Local Similarity 86.4%; Pred. No. 9.1e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTCTTTGTACTCTCTCTGCTC 26

Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 3

US-09-905-125A-204/c

; Sequence 204, Application US/09905125A

; Patent No. 6664376

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,125A

; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

APPLICANT: Genentech, Inc.	US 09/904,920
APPLICANT: Ashkenazi, Avi	US 09/904,920
APPLICANT: Botstein, David	US 09/904,920
APPLICANT: Desnoyers, Luc	US 09/904,920
APPLICANT: Eaton, Dan L.	US 09/904,920
APPLICANT: Ferrara, Napoleone	US 09/904,920
APPLICANT: Filvaroff, Ellen	US 09/904,920
APPLICANT: Fong, Sherman	US 09/904,920
APPLICANT: Gao, Wei-Qiang	US 09/904,920
APPLICANT: Gerber, Hanspeter	US 09/904,920
APPLICANT: Gerritsen, Mary E.	US 09/904,920
APPLICANT: Goddard, A.	US 09/904,920
APPLICANT: Godowski, Paul J.	US 09/904,920
APPLICANT: Grimaldi, Christopher J.	US 09/904,920
APPLICANT: Gurney, Austin L.	US 09/904,920
APPLICANT: Hillan, Kenneth, J.	US 09/904,920
APPLICANT: Khlavin, Ivar J.	US 09/904,920
APPLICANT: Mather, Jennie P.	US 09/904,920
APPLICANT: Pan, James	US 09/904,920
APPLICANT: Paoni, Nicholas F.	US 09/904,920
APPLICANT: Roy, Margaret Ann	US 09/904,920
APPLICANT: Stewart, Timothy A.	US 09/904,920
APPLICANT: Tumas, Daniel	US 09/904,920
APPLICANT: Williams, P. Mickey	US 09/904,920
APPLICANT: Wood, William, I.	US 09/904,920
TITLE OF INVENTION: Secreted and Transmembrane Proteins	US 09/904,920
TITLE OF INVENTION: Acids Encoding the Secreted Proteins	US 09/904,920
FILE REFERENCE: 10466-14	US 09/904,920
CURRENT APPLICATION NUMBER: US 09/904,920	US 09/904,920
CURRENT FILING DATE: 2001-07-13	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US00/04414	US 09/904,920
PRIOR FILING DATE: 2000-02-22	US 09/904,920
PRIOR APPLICATION NUMBER: US 60/143,048	US 09/904,920
PRIOR FILING DATE: 1999-07-07	US 09/904,920
PRIOR APPLICATION NUMBER: US 60/145,698	US 09/904,920
PRIOR FILING DATE: 1999-07-26	US 09/904,920
PRIOR APPLICATION NUMBER: US 60/146,222	US 09/904,920
PRIOR FILING DATE: 1999-07-28	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/20594	US 09/904,920
PRIOR FILING DATE: 1999-09-08	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/20944	US 09/904,920
PRIOR FILING DATE: 1999-09-13	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/21090	US 09/904,920
PRIOR FILING DATE: 1999-09-15	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/21547	US 09/904,920
PRIOR FILING DATE: 1999-09-15	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/23089	US 09/904,920
PRIOR FILING DATE: 1999-10-05	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/28214	US 09/904,920
PRIOR FILING DATE: 1999-11-29	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/28313	US 09/904,920
PRIOR FILING DATE: 1999-11-30	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/28564	US 09/904,920
PRIOR FILING DATE: 1999-12-02	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/28565	US 09/904,920
PRIOR FILING DATE: 1999-12-02	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/30095	US 09/904,920
PRIOR FILING DATE: 1999-12-16	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/30911	US 09/904,920
PRIOR FILING DATE: 1999-12-20	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US99/30999	US 09/904,920
PRIOR FILING DATE: 1999-12-20	US 09/904,920
PRIOR APPLICATION NUMBER: PCT/US00/00219	US 09/904,920

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: ROY, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 204
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
US-09-906-618-204

Query Match 66.2%; Score 17.2; DB 4; Length 24;
Best Local Similarity 86.4%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCTCTCTGCTC 26
||| ||| ||| ||| ||| ||| ||| |||
Db 24 CCTACTACTCTCTCTGCTC 3

RESULT 11
US-08-068-747-4/c
Sequence 4, Application US/08068747
Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.

TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-08-068-747-4

Query Match 65.4%; Score 17; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTTGTGTACTCTCTCTGCTC 26
||| ||| ||| ||| ||| ||| ||| |||
Db 30 CCTCTCTCTCTCTCTCTCTCTC 6

RESULT 12
US-08-589-109A-12
Sequence 12, Application US/08589109A
Patent No. 6365344
GENERAL INFORMATION:
APPLICANT: No. 6365344an, Garry P.
APPLICANT: Rothenberg, Michael S.
TITLE OF INVENTION: Methods for Screening for Transdominant
TITLE OF INVENTION: Effector Peptides and RNA Molecules
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Honbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,109A
FILING DATE: 23-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.

REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-64259/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONES: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cdna
US-08-589-109A-12

Query Match 65.4%; Score 17; DB 3; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTTCTTGTACTCTCTCGTGC 26
Db 1 CCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 13

US-08-068-747-9
Sequence 9, Application US/08068747
Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Houseman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-08-068-747-9

Query Match 65.4%; Score 17; DB 1; Length 39;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTTCTTGTACTCTCTCGTGC 26
Db 1 CCTCTCTCTCTCTCTCTCTCTCTC 25

Db 1 CCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 14

US-09-580-923-34/c
Sequence 34, Application US/09580923
Patent No. 6319672
GENERAL INFORMATION:
APPLICANT: Crouzet, Joel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILE REFERENCE: 03804.0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/860,038
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/FR95/01468
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotide
US-09-580-923-34

Query Match 65.4%; Score 17; DB 3; Length 48;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTTCTTGTACTCTCTCGTGC 26
Db 47 CCTCTCTCTCTCTCTCTCTCTCTC 23

RESULT 15

US-08-860-038-17/c
Sequence 17, Application US/08860038
Patent No. 6287762
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, Pierre
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,038
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/15162
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO FR95/01468
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST94090-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-17

Query Match 65.4%; Score 17; DB 3; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGTACTCTCTCTCTC 26
||||| ||| ||| ||| ||| ||| |||
Db 49 CCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 16
US-09-580-923-17/c
; Sequence 17, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
; APPLICANT: Crouzet, Joel
; APPLICANT: Scherman, Daniel
; APPLICANT: Wills, Pierre
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
; FILE REFERENCE: 03804.0138-01
; CURRENT APPLICATION NUMBER: US/09/580,923
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 08/860,038
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/FR95/01468
; PRIOR FILING DATE: 1995-11-08
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-580-923-17

Query Match 65.4%; Score 17; DB 3; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGTACTCTCTCTCTC 26
||||| ||| ||| ||| ||| ||| |||
Db 49 CCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 17
US-09-371-489-4/c
; Sequence 4, Application US/09371489
; Patent No. 6355803
; GENERAL INFORMATION:
; APPLICANT: Anand Natrajan

; APPLICANT: Qingping Jiang
; APPLICANT: David Sharpe
; APPLICANT: Say-Jong Law
; TITLE OF INVENTION: NEAR INFRARED CHEMILUMINESCENT
; FILE REFERENCE: CCDDT-258XX
; CURRENT APPLICATION NUMBER: US/09/371,489
; CURRENT FILING DATE: 1999-08-10
; EARLIER APPLICATION NUMBER: 60/096,073
; EARLIER FILING DATE: 1998-08-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (223)...(223)
; OTHER INFORMATION: VANCO B PMP-PROBE 496.20 (ON PMP) IN EXAMPLE 16
US-09-371-489-4

Query Match 65.4%; Score 17; DB 3; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGTACTCTCTCTCTC 26
||||| ||| ||| ||| ||| ||| |||
Db 26 CCTCTCTCTCTCTCTCTCTCTCTC 2

RESULT 18
US-09-866-108A-13556/c
; Sequence 13556, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13556
; LENGTH: 25

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13556

Query Match      63.8%; Score 16.6; DB 4; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGTACTCTCTCTGCT 25
    ||||| ||||| ||||| ||||| |||||
Db 25 CTCCTCTCTGTACTCTCTCTGCT 3

RESULT 19
US-09-866-108A-13557/c
; Sequence 13557, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13558

Query Match      63.8%; Score 16.6; DB 4; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGTACTCTCTCTGCT 25
    ||||| ||||| ||||| ||||| |||||
Db 25 CTCCTCTCTGTACTCTCTCTGCT 1

RESULT 21
US-08-391-000-36/c
; Sequence 36, Application US/08391000
; Patent No. 5723752
; GENERAL INFORMATION:
; APPLICANT: HOUTZ, Robert L.
; TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF
; TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/391,000
FILING DATE: 21-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 028750-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-391-000-36

Query Match 63.8%; Score 16.6; DB 1; Length 42;
Best Local Similarity 82.6%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTTGTTACTCTCTCTGCTC 26
||||| | | | | | | | | |
Db 33 TCCTTCTTGTTACTCTCTCTGCTC 11

RESULT 22

US-08-741-931-36/c
Sequence 36, Application US/08741931
Patent No. 5866394
GENERAL INFORMATION:
APPLICANT: HOUTZ, Robert L.
TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF
TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
SUBUNIT N-METHYLTRANSFERASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,931
FILING DATE: 31-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/391,000
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 028750-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-741-931-36

Query Match 63.8%; Score 16.6; DB 2; Length 42;
Best Local Similarity 82.6%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTTGTTACTCTCTCTGCTC 26
||||| | | | | | | | | |
Db 33 TCCTTCTTGTTACTCTCTCTGCTC 11

RESULT 23

US-09-012-515A-7/c
Sequence 7, Application US/09012515A
Patent No. 6127521
GENERAL INFORMATION:
APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,515A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/360,144
FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-036.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-012-515A-7

Query Match 63.8%; Score 16.6; DB 3; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTTGTTACTCTCTCTGCTC 26
||||| | | | | | | | | |
Db 42 TTCTACTGTACTCTCTCCACCTC 20

RESULT 24

US-08-360-144A-7/c
Sequence 7, Application US/08360144A
Patent No. 6150137
GENERAL INFORMATION:
APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique

;; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
;; STREET: One Post Office Square
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109-2170
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/360,144A
;; FILING DATE: 20-DEC-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Vincent, Matthew P.
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: APV-036.02
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-832-1000
;; TELEFAX: 617-832-7000
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 48 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-360-144A-7

Query Match 63.8%; Score 16.6; DB 3; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTGTACTCTCTCTGCTC 26
Db 42 TTCTACTTGTACTCTCCACCTC 20

RESULT 25

US-09-012-504A-7/c
; Sequence 7, Application US/09012504A
; Patent No. 6464974
; GENERAL INFORMATION:
; APPLICANT: Berlin, V.
; APPLICANT: Chiu, I.
; APPLICANT: Cottarel, G.
; APPLICANT: Damagnez, V.
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; FILE REFERENCE: APBI-P05-036
; CURRENT APPLICATION NUMBER: US/09/012,504A
; CURRENT FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 08/360,144
; PRIOR FILING DATE: 1994-12-20
; PRIOR APPLICATION NUMBER: 08/250,795
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide coding strand
US-09-012-504A-7

Query Match 63.8%; Score 16.6; DB 3; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTGTACTCTCTCTGCTC 26
Db 42 TTCTACTTGTACTCTCCACCTC 20

RESULT 26

US-09-012-399A-7/c
; Sequence 7, Application US/09012399A
; Patent No. 6509152
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, Maria Isabel
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Damagnez, Veronique
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,399A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/360,144
; FILING DATE: 20-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: APV-036.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-012-399A-7

Query Match 63.8%; Score 16.6; DB 4; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTGTACTCTCTCTGCTC 26
Db 42 TTCTACTTGTACTCTCCACCTC 20

RESULT 27

PCT-US95-06722-7/c
; Sequence 7, Application PC/TUS9506722
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Immunosuppressant Target Proteins
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06722
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/250,795
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/250,795
; FILING DATE: 20-DEC-1994
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; PCT-US95-06722-7

Query Match 63.8%; Score 16.6; DB 5; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTGTACTCTCTCTGTC 26
Db 42 TTCTACTTGTACTCTCCACCTC 20

RESULT 28
US-08-993-008A-2/c
; Sequence 2, Application US/08993008A
; Patent No. 6153596
; GENERAL INFORMATION:
; APPLICANT: Liotta, Dennis C.
; APPLICANT: Petros, John A.
; APPLICANT: Wey, Shioh-Jyi
; APPLICANT: Karr, Joan F.
; APPLICANT: Pohl, Jan
; TITLE OF INVENTION: Polycationic Oligomers
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,008A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,436
; FILING DATE: 18-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sullivan, Sally A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 33-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-993-008A-3

Query Match 63.8%; Score 16.4; DB 3; Length 28;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGTC 26
Db 28 CCCTCCTCTCCACCTCTCTCTCTC 3

RESULT 29
US-08-993-008A-3
; Sequence 3, Application US/08993008A
; Patent No. 6153596
; GENERAL INFORMATION:
; APPLICANT: Liotta, Dennis C.
; APPLICANT: Petros, John A.
; APPLICANT: Wey, Shioh-Jyi
; APPLICANT: Karr, Joan F.
; APPLICANT: Pohl, Jan
; TITLE OF INVENTION: Polycationic Oligomers
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,008A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,436
; FILING DATE: 18-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sullivan, Sally A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 33-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-993-008A-3

Query Match 63.8%; Score 16.4; DB 3; Length 28;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGTC 26
Db 1 CCCTCCTCTCCACCTCTCTCTCTC 26

RESULT 30
US-08-361-920-41/c
```

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;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-993-008A-2

Query Match 63.8%; Score 16.4; DB 3; Length 28;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGTC 26
Db 28 CCCTCCTCTCCACCTCTCTCTCTC 3

RESULT 29
US-08-993-008A-3
; Sequence 3, Application US/08993008A
; Patent No. 6153596
; GENERAL INFORMATION:
; APPLICANT: Liotta, Dennis C.
; APPLICANT: Petros, John A.
; APPLICANT: Wey, Shioh-Jyi
; APPLICANT: Karr, Joan F.
; APPLICANT: Pohl, Jan
; TITLE OF INVENTION: Polycationic Oligomers
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,008A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,436
; FILING DATE: 18-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sullivan, Sally A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 33-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-993-008A-3

Query Match 63.8%; Score 16.4; DB 3; Length 28;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGTC 26
Db 1 CCCTCCTCTCCACCTCTCTCTCTC 26

RESULT 30
US-08-361-920-41/c
```

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; Sequence 41, Application US/08361920
; Patent No. 5457046
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 54570460 No. 5457046disk of No. 5457046th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-361-920-41

Query Match 63.1%; Score 16.4; DB 1; Length 40;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGCTC 26
Db 30 CCCTGCCTCTGGTGTCTCTGCTC 5

RESULT 31
US-08-361-920-52/c
; Sequence 52, Application US/08361920
; Patent No. 5457046
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 54570460 No. 5457046disk of No. 5457046th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-361-920-41

Query Match 63.1%; Score 16.4; DB 1; Length 40;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGCTC 26
Db 30 CCCTGCCTCTGGTGTCTCTGCTC 5

RESULT 32
US-08-479-939-41/c
; Sequence 41, Application US/08479939
; Patent No. 5686593
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,939
```



```

/ APPLICATION NUMBER: PCT/DK91/00124
/ FILING DATE: 08-MAY-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lambiris, Elias J.
/ REGISTRATION NUMBER: 33,728
/ REFERENCE/DOCKET NUMBER: 3435.204-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-867-0123
/ TELEFAX: 212-867-0298
/ INFORMATION FOR SEQ ID NO: 52:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 40 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/
US-08-479-939-52

Query Match 63.1%; Score 16.4; DB 1; Length 40;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCTCCTTCTTGTACTCCTCTGCTC 26
    ||||| ||||| ||||| |||||
DB 30 CCCTGCTCTGCTGTTCTCTGCTC 5

RESULT 34
US-08-483-432-41/c
/ Sequence 41, Application US/08483432
/ Patent No. 5763254
/ GENERAL INFORMATION:
/ APPLICANT: Woelldike, Helle F.
/ APPLICANT: Hagen, Frederick
/ APPLICANT: Hjort, Carsten M.
/ APPLICANT: Sven, Hastrup
/ TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
/ TITLE OF INVENTION: or Hemicellulose
/ NUMBER OF SEQUENCES: 85
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: No. 5763254o No. 5763254disk of No. 5763254th America, Inc.
/ STREET: 405 Lexington Avenue, 62nd Floor
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States of America
/ ZIP: 10174-6201
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/483,432
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/361,920
/ FILING DATE:
/ APPLICATION NUMBER: US 07/940,860
/ FILING DATE: 28-OCT-1992
/ APPLICATION NUMBER: DK 1158/90
/ FILING DATE: 09-MAY-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/DK91/00124
/ FILING DATE: 08-MAY-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lambiris, Elias J.
/ REGISTRATION NUMBER: 33,728
/ REFERENCE/DOCKET NUMBER: 3435.204-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-867-0123
/ TELEFAX: 212-867-0298
/ INFORMATION FOR SEQ ID NO: 41:

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SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-483-432-41

Query Match 63.1%; Score 16.4; DB 1; Length 40;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCCTCTGCTC 26
||||| ||||| ||||| ||||| |||||
Db 30 CCCTGCCTCTGTGTCTCTGCTC 5

RESULT 35

US-08-483-432-52/c
Sequence 52, Application US/08483432
Patent No. 5763254
GENERAL INFORMATION:
APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57632540 No. 5763254disk of No. 5763254th America, Inc.
STREET: 405 Lexington Avenue, 52nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,432
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-483-432-52

Query Match 63.1%; Score 16.4; DB 1; Length 40;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CCCTCCTTCTGTACTCCTCTGCTC 26
||||| ||||| ||||| ||||| |||||
Db 30 CCCTGCCTCTGTGTCTCTGCTC 5

RESULT 36

US-08-324-001-19
Sequence 19, Application US/08324001
Patent No. 5624803
GENERAL INFORMATION:
APPLICANT: NOONBERG, SARAH B.
APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSN FOERSSFO
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-324-001-19

Query Match 63.1%; Score 16.4; DB 1; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCCTCTGCTC 26
||||| ||||| ||||| ||||| |||||
Db 8 CCCTCCTCTCCACCTCCTCTCTC 33

RESULT 37

US-08-324-001-20/c
Sequence 20, Application US/08324001
Patent No. 5624803
GENERAL INFORMATION:
APPLICANT: NOONBERG, SARAH B.
APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
US-08-324-001-20

; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,001
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, GLADYS H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 22000-20544.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSN FOERSSFO
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-324-001-20

Query Match 63.1%; Score 16.4; DB 1; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||
Db 36 CCTCTCTCTCCACCTCTCTCTCTC 11
||||| ||| ||||| |||

RESULT 38
US-08-324-001-10
; Sequence 10, Application US/08324001
; Patent No. 5624803
; GENERAL INFORMATION:
; APPLICANT: NOONBERG, SARAH B.
; APPLICANT: HUNT, C. ANTHONY
; TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
; TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
; TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,001
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, GLADYS H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 22000-20544.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSN FOERSSFO

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-324-001-10

Query Match 63.1%; Score 16.4; DB 1; Length 50;
Best Local Similarity 76.9%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||
Db 23 CCTCTCTCTCCACCTCTCTCTCTC 48
||||| ||| ||||| |||

RESULT 39
US-08-324-001-11/c
; Sequence 11, Application US/08324001
; Patent No. 5624803
; GENERAL INFORMATION:
; APPLICANT: NOONBERG, SARAH B.
; APPLICANT: HUNT, C. ANTHONY
; TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
; TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
; TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,001
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONROY, GLADYS H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 22000-20544.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSN FOERSSFO
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-324-001-11

Query Match 63.1%; Score 16.4; DB 1; Length 50;
Best Local Similarity 76.9%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||
Db 28 CCTCTCTCTCCACCTCTCTCTCTC 3
||||| ||| ||||| |||

RESULT 40
US-09-362-842-38/c
; Sequence 38, Application US/09362842
; Patent No. 6511824

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; GENERAL INFORMATION:
; APPLICANT: Buchman et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK
; FILE REFERENCE: 7326-104
; CURRENT APPLICATION NUMBER: US/09/362,842
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/270,767
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-362-842-38

Query Match      60.0%; Score 15.6; DB 4; Length 24;
Best Local Similarity 81.8%; Pred. No. 3.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 TCCTTCTTGTACTCCTCTGCT 25
Db      22 TCCTTCTTGGAATCGCCTACT 1

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Search completed: November 18, 2005, 11:22:02
Job time : 51.5171 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 349.468 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCTCCTCTTGTACTCTCCTGCTC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:**

- 1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	8	US-08-469-172-8
2	26	100.0	26	20	US-10-788-779-8
3	17.8	68.5	25	24	US-10-843-527-11341
4	17.8	68.5	25	24	US-10-843-527-12315
5	17.8	68.5	25	24	US-10-843-527-224398

c	6	17.8	68.5	25	24	US-10-843-527-225372	Sequence 225372,
c	7	17.6	67.7	25	26	US-11-036-317-60793	Sequence 60793, A
c	8	17.2	66.2	24	9	US-09-909-320-204	Sequence 204, App
c	9	17.2	66.2	24	9	US-09-909-088B-204	Sequence 204, App
c	10	17.2	66.2	24	9	US-09-905-231A-204	Sequence 204, App
c	11	17.2	66.2	24	9	US-09-902-853-204	Sequence 204, App
c	12	17.2	66.2	24	9	US-09-907-824-204	Sequence 204, App
c	13	17.2	66.2	24	9	US-09-907-841-204	Sequence 204, App
c	14	17.2	66.2	24	10	US-09-904-011-204	Sequence 204, App
c	15	17.2	66.2	24	10	US-09-903-640-204	Sequence 204, App
c	16	17.2	66.2	24	10	US-09-908-093-204	Sequence 204, App
c	17	17.2	66.2	24	10	US-09-906-742-204	Sequence 204, App
c	18	17.2	66.2	24	10	US-09-906-838-204	Sequence 204, App
c	19	17.2	66.2	24	10	US-09-907-613-204	Sequence 204, App
c	20	17.2	66.2	24	10	US-09-907-942-204	Sequence 204, App
c	21	17.2	66.2	24	10	US-09-904-859-204	Sequence 204, App
c	22	17.2	66.2	24	10	US-09-909-204-204	Sequence 204, App
c	23	17.2	66.2	24	10	US-09-904-820-204	Sequence 204, App
c	24	17.2	66.2	24	10	US-09-904-786-204	Sequence 204, App
c	25	17.2	66.2	24	10	US-09-906-646-204	Sequence 204, App
c	26	17.2	66.2	24	10	US-09-906-700-204	Sequence 204, App
c	27	17.2	66.2	24	10	US-09-903-786-204	Sequence 204, App
c	28	17.2	66.2	24	10	US-09-902-903-204	Sequence 204, App
c	29	17.2	66.2	24	10	US-09-903-749A-204	Sequence 204, App
c	30	17.2	66.2	24	10	US-09-904-119-204	Sequence 204, App
c	31	17.2	66.2	24	10	US-09-904-956-204	Sequence 204, App
c	32	17.2	66.2	24	10	US-09-902-736-204	Sequence 204, App
c	33	17.2	66.2	24	10	US-09-907-794-204	Sequence 204, App
c	34	17.2	66.2	24	10	US-09-903-943-204	Sequence 204, App
c	35	17.2	66.2	24	10	US-09-904-462-204	Sequence 204, App
c	36	17.2	66.2	24	10	US-09-907-925-204	Sequence 204, App
c	37	17.2	66.2	24	10	US-09-902-692-204	Sequence 204, App
c	38	17.2	66.2	24	10	US-09-903-520-204	Sequence 204, App
c	39	17.2	66.2	24	10	US-09-905-056-204	Sequence 204, App
c	40	17.2	66.2	24	10	US-09-909-064-204	Sequence 204, App
c	41	17.2	66.2	24	10	US-09-904-553-204	Sequence 204, App
c	42	17.2	66.2	24	10	US-09-905-381-204	Sequence 204, App
c	43	17.2	66.2	24	10	US-09-904-485-204	Sequence 204, App
c	44	17.2	66.2	24	10	US-09-905-348-204	Sequence 204, App
c	45	17.2	66.2	24	10	US-09-905-088-204	Sequence 204, App

ALIGNMENTS

RESULT 1
US-08-469-172-8
; Sequence 8, Application US/08469172
; Publication No. US200300543A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-469-172-8

Query Match 100.0%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.73; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGCTC 26
Db 1 CCCTCCTTCTGTACTCTCTCTGCTC 26

RESULT 2
US-10-788-779-8
; Sequence 8, Application US/10788779
; Publication No. US2004015212A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-10-788-779-8

Query Match 100.0%; Score 26; DB 20; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.73; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGCTC 26
Db 1 CCCTCCTTCTGTACTCTCTCTGCTC 26

RESULT 3
US-10-843-527-11341
; Sequence 11341, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 11341
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-11341

Query Match 68.5%; Score 17.8; DB 24; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCCTCTTGTACTCTCTCTG 23
Db 2 CTCCTCTTGTACTCTCTG 22

RESULT 4
US-10-843-527-12315
; Sequence 12315, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 12315
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-12315

Query Match 68.5%; Score 17.8; DB 24; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCCTCTTGTACTCTCTCTG 23
Db 4 CTCCTCTTGTCTCTCTG 24
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RESULT 5
US-10-843-527-224398/c
; Sequence 224398, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 224398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-224398

Query Match      68.5%; Score 17.8; DB 24; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CTCCTTCTTGACTCTCTCTG 23
Db      22 CTCCTTCTTGACTCTCTCTG 2

RESULT 6
US-10-843-527-225372/c
; Sequence 225372, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 225372
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-225372

Query Match      68.5%; Score 17.8; DB 24; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CTCCTTCTTGACTCTCTCTG 23
Db      24 CTCCTTCTTGACTCTCTCTG 4

RESULT 7
US-11-036-317-60793/c
; Sequence 60793, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 60793
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-60793

Query Match      67.7%; Score 17.6; DB 26; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CCCTCTCTTCTTGACTCTCTCTG 24
Db      25 CGTCCTTCTTGACTCTCTCTG 2

RESULT 8
US-09-909-320-204/c
; Sequence 204, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mathier, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
```

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US-09-305-291A-204/c
; Sequence 204, Application US/09905291A
; Patent No. US20030160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botschein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F

```


; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-905-291A-204

Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCTCTCGTCTC 26
Db 24 CCTACTACTCTCTCTCGTCTC 3

RESULT 11
US-09-902-853-204/c
; Sequence 204, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide Probe
US-09-902-853-204

Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTGTACTCTCTCGTCTC 26


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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-907-841-204

Query Match          66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5 CCTTCTTGTAAGTCTCTCTGCTC 26
    ||| || ||||| |||||
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 14
US-09-904-011-204/c
; Sequence 204, Application US/09904011
; Publication No. US2003003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
```

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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-011-204

Query Match          66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5 CCTTCTTGTAAGTCTCTCTGCTC 26
    ||| || ||||| |||||
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 15
US-09-903-640-204/c
; Sequence 204, Application US/09903640
; Publication No. US20030017463A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,640
; CURRENT FILING DATE: 2001-07-11
```

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; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-903-640-204

Query Match          66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCTCTCGTCTC 26
    ||| || ||||| ||||| |||
Db 24 CCTACTACTACTCTCTCGTCTC 3

RESULT 16
US-09-908-093-204/c
; Sequence 204, Application US/09908093
; Publication No. US20030017498A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/908,093
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
```

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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-908-093-204

Query Match          66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCTCTCGTCTC 26
    ||| || ||||| ||||| |||
Db 24 CCTACTACTACTCTCTCGTCTC 3

RESULT 17
US-09-906-742-204/c
; Sequence 204, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
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RESULT 18
US - 93-906-838-204/c
; Sequence 204, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Garber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.

RESULT 19
US-09-907-613-204/c
; Sequence 204, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-907-613-204

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTGTGTACTCCTCCTGCTC 26
||| || ||||| |||||
Db 24 CCTACTACTACTCCTCCTGCTC 3

RESULT 20
US-09-907-942-204/c
; Sequence 204, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16

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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
; OTHER INFORMATION: oligonucleotide probe
US-09-907-942-204

```

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTA^{CT}CCTCCTGCTC 26
Db 24 CCTACTACTACTCCTCCTGCTC 3

RESULT 21
US-09-904-859-204/c
; Sequence 204, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:

APPLICANT:	Genentech, Inc.
APPLICANT:	Ashkenazi, Avi
APPLICANT:	Botstein, David
APPLICANT:	Desnoyers, Luc
APPLICANT:	Eaton, Dan L.
APPLICANT:	Ferrara, Napoleone
APPLICANT:	Filvaroff, Ellen
APPLICANT:	Fong, Sherman
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gerber, Hanspeter
APPLICANT:	Garritsen, Mary E.
APPLICANT:	Goddard, A.
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, Christoph
APPLICANT:	Gurney, Austin L.
APPLICANT:	Hillan, Kenneth, J
APPLICANT:	Kijavlin, Ivar J.
APPLICANT:	Mather, Jennie P.
APPLICANT:	Pan, James
APPLICANT:	Paoni, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Stewart, Timothy A
APPLICANT:	Tumas, Daniel
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William, I.

```

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

```

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; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
;

```

```

, PRIOR FILING DATE: 1999-09-13
, PRIOR APPLICATION NUMBER: PCT/US99/21090
, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/21547
, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/23089
, PRIOR FILING DATE: 1999-10-05
, PRIOR APPLICATION NUMBER: PCT/US99/28214
, PRIOR FILING DATE: 1999-11-29
, PRIOR APPLICATION NUMBER: PCT/US99/28313
, PRIOR FILING DATE: 1999-11-30
, PRIOR APPLICATION NUMBER: PCT/US99/28564
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/28565
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: 1999-12-16
, PRIOR APPLICATION NUMBER: PCT/US99/30911
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 204
, LENGTH: 24
, TYPE: DNA
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Synthetic Oligonucleotide
US-99-904-859-204

```

Query Match 66.2%; Score 17.2; DB 10;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels

Qy 5 CCTTCTTGTA

RESULT 22
US-09-909-204-204/c
; Sequence 204, Application US/0909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grittsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Tra
; TITLE OF INVENTION: Acids Encoding

```
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,204
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-909-204-204
```

```
Query Match          66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 5 CCTCTTGTTACTCTCTCTGCTC 26
   ||| ||| ||| ||| ||| ||| |||
Db 24 CCTACTACTACTCTCTCTGCTC 3
```

```
RESULT 23
US-09-904-820-204/c
; Sequence 204, Application US/09904820
; Publication No. US2003036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
```

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-820-204
```

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Query Match          66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 5 CCTCTTGTTACTCTCTCTGCTC 26
   ||| ||| ||| ||| ||| ||| |||
Db 24 CCTACTACTACTCTCTCTGCTC 3
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RESULT 24


```

US-09-904-786-204/c
; Sequence 204, Application US/09904786
; Publication No. US2003003996A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transcribed Nucleic Acid Sequences
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904786
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-904-786-204

Query Match          66.2%   Score
Best Local Similarity 86.4%   Pred:
Matches 19; Conservative 0; Mismatch 1

QY    5 CCTCTTTGTACTCCTCTCGTC 26
      |||||T|||||T|||||T|||||
Db    24 CCTACTACTACTCCTCTCGTC 3

RESULT 25
US-09-906-646-204/c
; Sequence 204, Application US/09906646
; Publication No. US2003003997A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

```

GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/306,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe

US-09-906-700-204
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTCTCTGTACTCTCTCTGCTC 26
||| || ||||| |||||
Db 24 CCTACTACTACTCTCTGCTC 3
RESULT 27
US-09-903-786-204/c
; Sequence 204, Application US/09903786
; Publication No. US2003004793A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,786
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565

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, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: 1999-12-16
, PRIOR APPLICATION NUMBER: PCT/US99/30911
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 204
, LENGTH: 24
, TYPE: DNA
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Synthetic Oligonucleotide
US-09-903-786-204

```

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels

Qy 5 CCTCTTGTACTCCTCCTGCTC 26
 ||| ||| ||| ||| ||| ||| |||
Db 24 CCTACTACTACTCCTCCTGCTC 3

RESULT 28

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US-09-902-903-204/c
; Sequence 204, Application US/09902903
; Publication No. US2003004489A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Garber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mathew, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transcribed Nucleic Acid Sequences
; TITLE OF INVENTION: Acids Encoding Proteins
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902903
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/00489A
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 6/143,143
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 6/145,645
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 6/146,246
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/202903
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/202903

```

```

, PRIOR FILING DATE: 1998-09-13
, PRIOR APPLICATION NUMBER: PCT/US99/21090
, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/21547
, PRIOR FILING DATE: 1999-09-15
, PRIOR APPLICATION NUMBER: PCT/US99/23089
, PRIOR FILING DATE: 1999-10-05
, PRIOR APPLICATION NUMBER: PCT/US99/28214
, PRIOR FILING DATE: 1999-11-29
, PRIOR APPLICATION NUMBER: PCT/US99/28313
, PRIOR FILING DATE: 1999-11-30
, PRIOR APPLICATION NUMBER: PCT/US99/28564
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/28565
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: 1999-12-16
, PRIOR APPLICATION NUMBER: PCT/US99/30911
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 204
, LENGTH: 24
, TYPE: DNA
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Description of Artificial
, OTHER INFORMATION: oligonucleotide probe
US-09-902-903-204

```

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels

Qy 5 CCTTCTTGTA

RESULT 29

US-09-903-749A-204/c
; Sequence 204, Application US/09903749A
; Publication No. US20030045693A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

```

RESULT 30
US-904-119-204/c
; Sequence 204, Application US/09904119
; Publication No. US2003009621A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Garber, Hanspeter
; APPLICANT: Geritsen, Mary E.

```

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Query Match      66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 31
US-09-904-956-204/c
; Sequence 204, Application US/09904956
; Publication No. US20030049622A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,956
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-904-956-204

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTTGTACTCTCTCTGCTC 26
DB 24 CCTACTACTCTCTCTGCTC 3

RESULT 32
US-09-902-736-204/c
; Sequence 204, Application US/09902736
; Publication No. US20030049676A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,736
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
```

```
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-902-736-204

Query Match      66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTTACTCTCTCGTCTC 26
    ||| || ||||| ||||| |||||
Db 24 CCTACTACTACTCTCTCGTCTC 3

RESULT 33
US-09-907-794-204/c
; Sequence 204, Application US/09907794
; Publication No. US20030049677A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
```

```
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-794-204

Query Match      66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTTACTCTCTCGTCTC 26
    ||| || ||||| ||||| |||||
Db 24 CCTACTACTACTCTCTCGTCTC 3

RESULT 34
US-09-903-943-204/c
; Sequence 204, Application US/09903943
; Publication No. US20030054349A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
```

```
0; Gaps 0;
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```
QY      5  CCTCTCTGTAAGTCTCTCTCTGTC 26
      |||||
Db     24  CCTACTACTACTCTCTCTGTC 3

RESULT 36
; Sequence 204, Application US/09907925
; Publication No. US20030054352A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,925
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
```

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; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-925-204

Query Match      66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5  CCTCTCTGTAAGTCTCTCTCTGTC 26
      |||||
Db     24  CCTACTACTACTCTCTCTGTC 3

RESULT 37
US-09-902-692-204/c
; Sequence 204, Application US/09902692
; Publication No. US20030054400A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,692
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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RESULT 38
US-09-903-520-204/c
; Sequence 204, Application US/09903520
; Publication No. US20030054401A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Garber, Hanspeter
; APPLICANT: Grøitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Tra
; FILE OF INVENTION: Acids Encoding
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/90
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350

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Query Match	66.2%	Score 17.2;	DB 10;	Length 24;
Best Local Similarity	86.4%	Pred. No. 2.4e+03;		
Matches 19: Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

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; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,056
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
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; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-905-056-204

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 24 CCTACTACTACTCTCTCGTCTC 3

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; Sequence 204, Application US/0909064
; Publication No. US2003005972A1
; GENERAL INFORMATION:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-909-064-204
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Query Match 66.2%; Score 17.2; DB 10; Length 24;
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 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 24 CCTACTACTACTCTCTCTGCTC 3

Search completed: November 18, 2005, 15:41:09
 Job time : 351.468 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 693.631 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-9

Perfect score: 25

Sequence: 1 CAACTCATCACCACTCTCTCCATC 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

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10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	25	100.0	25	6	112902	112902 Sequence 9
C 2	18.6	74.4	41	6	BD217302	BD217302 Mammalian
C 3	18.2	72.8	47	6	AR291854	AR291854 Sequence
C 4	17.6	70.4	41	6	BD217295	BD217295 Mammalian
5	16.2	64.8	46	6	AR0233959	AR0233959 Sequence
6	16.2	64.8	46	6	I15460	I15460 Sequence 38
7	16	64.0	42	6	AX080737	AX080737 Sequence
C 8	15.4	61.6	25	6	AR561920	AR561920 Sequence
C 9	15.2	60.8	20	6	AR002284	AR002284 Sequence
C 10	15.2	60.8	20	6	AR053135	AR053135 Sequence
11	14.8	59.2	42	6	AX078405	AX078405 Sequence
12	14.8	59.2	22	6	AX923032	AX923032 Sequence
C 13	14.8	59.2	24	6	CQ767675	CQ767675 Sequence
14	14.6	58.4	21	6	BD061255	BD061255 A method
15	14.6	58.4	31	6	E27249	E27249 Novel physi
C 16	14.6	58.4	50	3	GIAC270	L49327 STS of NotI
17	14.4	57.6	41	6	AX327047	AX327047 Sequence
18	14.4	57.6	41	6	AX327048	AX327048 Sequence
19	14.4	57.6	47	6	AR289466	AR289466 Sequence

C 20	14.2	56.8	20	6	AX496861	AX496861 Sequence
C 21	14.2	56.8	24	6	AR072405	AR072405 Sequence
C 22	14.2	56.8	24	6	I26516	I26516 Sequence 20
C 23	14.2	56.8	25	6	AX511858	AX511858 Sequence
24	14.2	56.8	41	6	AX521320	AX521320 Sequence
C 25	14	56.0	22	6	AR082996	AR082996 Sequence
C 26	14	56.0	22	6	BD005994	BD005994 An optima
C 27	14	56.0	22	6	BD070465	BD070465 Methods f
C 28	14	56.0	24	6	AX494081	AX494081 Sequence
C 29	14	56.0	25	6	AX610677	AX610677 Sequence
C 30	14	56.0	31	6	AX248216	AX248216 Sequence
C 31	14	56.0	31	6	AX249206	AX249206 Sequence
C 32	14	56.0	32	6	CQ786866	CQ786866 Sequence
C 33	13.8	55.2	20	6	E59389	E59389 Method for
C 34	13.8	55.2	20	6	AX118076	AX118076 Sequence
C 35	13.8	55.2	27	6	BD197187	BD197187 Method an
C 36	13.8	55.2	29	6	BD252384	BD252384 Regulatio
C 37	13.8	55.2	29	6	AX300835	AX300835 Sequence
38	13.8	55.2	29	6	AX300839	AX300839 Sequence
39	13.8	55.2	31	6	BD235713	BD235713 Targeted
40	13.8	55.2	33	6	BD235714	BD235714 Targeted
C 41	13.8	55.2	33	6	AR401446	AR401446 Sequence
C 42	13.8	55.2	33	6	AR401452	AR401452 Sequence
C 43	13.8	55.2	33	6	AR401454	AR401454 Sequence
C 44	13.8	55.2	33	6	AR453285	AR453285 Sequence
C 45	13.8	55.2	33	6	AR453291	AR453291 Sequence

ALIGNMENTS

RESULT 1
112902
LOCUS 112902 25 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 9 from patent US 5429923.
ACCESSION 112902
VERSION 112902.1 GI:910879
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 9 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..25
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Best Local Similarity 100.0%; Pred. No. 5.9;
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Qy 1 CAACTCATCACCACTCTCTCCATC 25
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Db 1 CAACTCATCACCACTCTCTCCATC 25
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RESULT 2
BD217302/c
LOCUS BD217302 41 bp DNA linear PAT 17-JUL-2003
DEFINITION Mammalian DED-caspase homolog usurin.
ACCESSION BD217302
VERSION BD217302.1 GI:33027072
KEYWORDS JP 2002520025-A/17.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 41)

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AUTHORS      Nicholson,D.W., Rasper,D.M., Xanthoudakis,S. and Roy,S.
TITLE        Mammalian DED-caspase homolog usurpin
JOURNAL      Patent: JP 2002520025-A 17 09-JUL-2002;
COMMENT      MERCK FROST CANADA AND CO
             OS Homo sapiens (human)
             PN JP 2002520025-A/17
             PD 09-JUL-2002
             PF 07-JUL-1999 JP 2000559244
             PR 08-JUL-1998 US 60/092005
             PI DONALD W NICHOLSON,DITA M RASPER,STEVE XANTHOUDAKIS,SOPHIE ROY
             PC D12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
             ,C12N5/10,C12Q1/02
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Best Local Similarity 84.0%; Pred. No. 3.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 41 CAATCTCTCACCAATCTCTGCCATC 17

RESULT 3
AR291854/c AR291854 47 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 3589 from patent US 6537751.
ACCESSION AR291854
VERSION AR291854.1 GI:31679138
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
        disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 3589 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..47
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Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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RESULT 4
BD217295/c BD217295 41 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Mammalian DED-caspase homolog usurpin.
ACCESSION BD217295
VERSION BD217295.1 GI:33027065
KEYWORDS JP 2002520025-A/10.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 41)
AUTHORS Nicholson,D.W., Rasper,D.M., Xanthoudakis,S. and Roy,S.
TITLE Mammalian DED-caspase homolog usurpin
JOURNAL Patent: JP 2002520025-A 10 09-JUL-2002;
COMMENT      MERCK FROST CANADA AND CO
             OS Homo sapiens (human)
             PN JP 2002520025-A/10
             PD 09-JUL-2002
             PF 07-JUL-1999 JP 2000559244
             PR 08-JUL-1998 US 60/092005
             PI DONALD W NICHOLSON,DITA M RASPER,STEVE XANTHOUDAKIS,SOPHIE ROY
             PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
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             CC Mammalian DED-caspase homolog usurpin
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Best Local Similarity 83.3%; Pred. No. 8.3e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 40 CAATCTCTCACCAATCTCTGCCAT 17

RESULT 5
AR023959 AR023959 46 bp DNA linear PAT 05-DEC-1998
LOCUS
DEFINITION Sequence 38 from patent US 5795762.
ACCESSION AR023959
VERSION AR023959.1 GI:3977253
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Abramson,R.D. and Gelfand,D.H.
TITLE 5' to 3' exonuclease mutations of thermostable DNA polymerases
JOURNAL Patent: US 5795762-A 38 18-AUG-1998;
FEATURES Location/Qualifiers
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Best Local Similarity 85.7%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 17 CTCATCCCACTCTTTCAT 37

RESULT 6
II5460 II5460 46 bp DNA linear PAT 02-APR-1996
LOCUS
DEFINITION Sequence 38 from patent US 5466591.
ACCESSION II5460
VERSION II5460.1 GI:1250368
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Abramson,R.D. and Gelfand,D.H.
TITLE 5' to 3' exonuclease mutations of thermostable DNA polymerases
JOURNAL Patent: US 5466591-A 38 14-NOV-1995;
FEATURES
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ORIGIN
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Best Local Similarity 85.7%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTCTTCCAT 24
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Db 17 CTCATCCCACTCTTTTCCAT 37

RESULT 7
AX080737 42 bp DNA linear PAT 27-FEB-2001
LOCUS AX080737
DEFINITION Sequence 14 from Patent WO0109189.
ACCESSION AX080737
VERSION AX080737.1 GI:13169725
KEYWORDS
    synthetic construct
    other sequences; artificial sequences.
ORGANISM
    synthetic construct
REFERENCE 1
AUTHORS Bodary,S.C. and Fisher,K.L.
TITLE Compositions and methods for the treatment of tumors
JOURNAL Patent: WO 0109189-A 14 08-FEB-2001;
Genentech, Inc. (US)
FEATURES
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                /note="PCR primer"

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Best Local Similarity 79.2%; Pred. No. 4e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACTCATCACCACCTCTCTTCCATC 25
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RESULT 8
AR561920/c 25 bp DNA linear PAT 08-OCT-2004
LOCUS AR561920
DEFINITION Sequence 147 from patent US 6759198.
ACCESSION AR561920
VERSION AR561920.1 GI:53975571
KEYWORDS
    Unknown.
    Unassigned.
ORGANISM
    Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kris,R.M. and Felder,S.
TITLE High throughput assay system
JOURNAL Patent: US 6759198-A 147 06-JUL-2004;
FEATURES
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ORIGIN
Query Match 61.6%; Score 15.4; DB 6; Length 25;

Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Abramson,R.D. and Gelfand,D.H.
TITLE 5' to 3' exonuclease mutations of thermostable DNA polymerases
JOURNAL Patent: US 5466591-A 38 14-NOV-1995;
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Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTCTTCCAT 24
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Db 17 CTCATCCCACTCTTTTCCAT 37

RESULT 7
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LOCUS AX080737
DEFINITION Sequence 14 from Patent WO0109189.
ACCESSION AX080737
VERSION AX080737.1 GI:13169725
KEYWORDS
    synthetic construct
    other sequences; artificial sequences.
ORGANISM
    synthetic construct
REFERENCE 1
AUTHORS Bodary,S.C. and Fisher,K.L.
TITLE Compositions and methods for the treatment of tumors
JOURNAL Patent: WO 0109189-A 14 08-FEB-2001;
Genentech, Inc. (US)
FEATURES
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QY 2 AACTCATCACCACCTCTCTTCCATC 25
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Db 6 AATGCATCAAGACTCTCTGCCATC 29

RESULT 8
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LOCUS AR561920
DEFINITION Sequence 147 from patent US 6759198.
ACCESSION AR561920
VERSION AR561920.1 GI:53975571
KEYWORDS
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    Unassigned.
ORGANISM
    Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kris,R.M. and Felder,S.
TITLE High throughput assay system
JOURNAL Patent: US 6759198-A 147 06-JUL-2004;
FEATURES
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Best Local Similarity 76.0%; Pred. No. 7.7e+04;
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RESULT 9
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LOCUS AR002284
DEFINITION Sequence 23 from patent US 5741645.
ACCESSION AR002284
VERSION AR002284.1 GI:3963838
KEYWORDS
    Unknown.
    Unassigned.
ORGANISM
    Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE Gene sequence for spinocerebellar ataxia type 1 and method for diagnosis
JOURNAL Patent: US 5741645-A 23 21-APR-1998;
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QY 1 CAATCATCACCACCTCTCTT 20
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Db 20 CAACTCATGACCCCTCTCCT 1

RESULT 10
AR053135/c 20 bp DNA linear PAT 29-SEP-1999
LOCUS AR053135
DEFINITION Sequence 41 from patent US 5834183.
ACCESSION AR053135
VERSION AR053135.1 GI:5977997
KEYWORDS
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    Unassigned.
ORGANISM
    Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE Gene sequence for spinocerebellar ataxia type 1 and method for diagnosis
JOURNAL Patent: US 5834183-A 41 10-NOV-1998;
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ORIGIN
Query Match 60.8%; Score 15.2; DB 6; Length 20;
Best Local Similarity 85.0%; Pred. No. 9.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAATCATCACCACCTCTCTT 20
    ||||| ||||| ||||| |||||
Db 20 CAACTCATGACCCCTCTCCT 1

RESULT 11
AR078405 42 bp DNA linear PAT 31-AUG-2000
LOCUS AR078405
DEFINITION Sequence 24 from patent US 5962636.
ACCESSION AR078405
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VERSION AR078405.1 GI:10005151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 42)
AUTHORS Bachmaier,K., Hessel,A.John., Neu,N. and Penninger,J.Martin.
TITLE Peptides capable of modulating inflammatory heart disease
JOURNAL Patent: US 5962636-A 24 05-OCT-1999;
FEATURES
    source
        Location/Qualifiers
            1..42
                /organism="unknown"
                /mol_type="unassigned DNA"

ORIGIN
    Query Match 60.8%; Score 15.2; DB 6; Length 42;
    Best Local Similarity 85.0%; Pred. No. 8.8e+04;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTC 21
    ||||| ||||| ||||| |||||
Db 8 AGCTCATGCCACCTCTCTTC 27

RESULT 12
AX923032 AX923032 22 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 1372 from Patent WO02068649.
ACCESSION AX923032
VERSION AX923032.1 GI:40216120
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS other sequences; artificial sequences.
JOURNAL
FEATURES
    source
        Location/Qualifiers
            1..22
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Description of Artificial Sequence: Ag4532 Forward"

ORIGIN
    Query Match 59.2%; Score 14.8; DB 6; Length 22;
    Best Local Similarity 88.9%; Pred. No. 1.4e+05;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCATC 25
    ||||| ||||| ||||| |||||
Db 3 TCACCTCTCTCTCCATC 20

RESULT 13
CQ767675/c CQ767675 24 bp DNA linear PAT 04-MAR-2004
LOCUS Sequence 142 from Patent EP1386931.
ACCESSION CQ767675
VERSION CQ767675.1 GI:45107802
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS other sequences; artificial sequences.
JOURNAL Wood,W.I., Goddard,A., Gurney,A., Yuan,J., Baker,K.P. and Chen,J.
TITLE Human neutrotrimin homologue
JOURNAL Patent: EP 1386931-A 142 04-FEB-2004;
FEATURES
    source
        Location/Qualifiers
            1..24
                /organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial Sequence"

ORIGIN
    Query Match 59.2%; Score 14.8; DB 6; Length 24;
    Best Local Similarity 88.9%; Pred. No. 1.4e+05;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTC 21
    ||||| ||||| ||||| |||||
Db 23 CACATCACCACCTCTTC 6

RESULT 14
BD061255 BD061255 21 bp DNA linear PAT 27-AUG-2002
LOCUS A method to identify and breed corn with increased kernel oil
DEFINITION concentration.
ACCESSION BD061255
VERSION BD061255.1 GI:22606861
KEYWORDS JP 2001517951-A/72.
SOURCE Medicago sativa
ORGANISM Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 21)
AUTHORS Reiter,R.S.
TITLE A method to identify and breed corn with increased kernel oil
JOURNAL
COMMENT Patent: JP 2001517951-A 72 09-OCT-2001;
EI DU PONT DE NEMOURS & CO
PN JP 2001517951-A/72
PD 09-OCT-2001
PF 19-MAR-1998 JP 1998544487
PR 24-MAR-1997 US 60/041515
PI ROBERT STEFAN REITER
PC C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
PH Key Location/Qualifiers.
FEATURES
    source
        Location/Qualifiers
            1..21
                /organism="Medicago sativa"
                /mol_type="genomic DNA"
                /db_xref="taxon:3879"

ORIGIN
    Query Match 58.4%; Score 14.6; DB 6; Length 21;
    Best Local Similarity 81.0%; Pred. No. 1.7e+05;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTCCATC 25
    ||||| ||||| ||||| |||||
Db 1 TCATCAGCTCTCTCTTCAAC 21

RESULT 15
E27249 E27249 31 bp DNA linear PAT 18-JUN-2001
LOCUS Novel physiologically active substance, process for producing the
DEFINITION same and utilization thereof.
ACCESSION E27249
VERSION E27249.1 GI:13025266
KEYWORDS JP 1999009286-A/40.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 31)
AUTHORS Shuji,H. and Shoji,F.
TITLE Novel physiologically active substance, process for producing the

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same and utilization thereof
 Patent: JP 1999009286-A 40 19-JAN-1999;
 TAKEDA CHEM IND LTD
 OS Unidentified
 PN JP 1999009286-A/40
 PD 19-JAN-1999
 PF 27-APR-1998 JP 1998117189
 PR
 PI SHUJI HINUMA, SHOJI FUKUZUMI
 PC C12N15/09, A01K67/027, A61K38/00, A61K38/00, C07K14/47, C07K16/18,
 PC C12N1/21,
 PC C12N5/10, C12P21/02, G01N33/53, G01N33/577//C12P21/08, (C12N15/09,
 PC C12R1:91),
 PC (C12N1/21, C12R1:19), (C12N5/10, C12R1:91), (C12P21/02, C12R1:19),
 PC C12N15/00,
 PC A61K37/02, A61K37/02, C12N5/00, (C12N15/00, C12R1:91), (C12N5/00,
 PC C12R1:91)
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key
 FT source 1. .31 Location/Qualifiers
 FT /organism='Unidentified'.
 FEATURES
 source
 1. .31
 Location/Qualifiers
 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'
 ORIGIN
 Query Match 58.4%; Score 14.6; DB 6; Length 31;
 Best Local Similarity 81.0%; Pred. No. 1.7e+05;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CAACTCATCACCACCTCTCTTC 21
 Db 3 CGACTCAGCAGCACTGTCTTC 23
 RESULT 16
 GIAC270/c 50 bp DNA linear INV 19-DEC-2001
 LOCUS STS of NotI segment E of chromosome 5 in Giardia duodenalis strain
 WB-1B.
 ACCESSION L49327
 VERSION L49327.1 GI:1100084
 KEYWORDS
 SOURCE Giardia intestinalis
 ORGANISM Giardia intestinalis
 Eukaryota; Diplomonadida; Hexamitidae; Giardia.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Upcroft, J.A., Chen, N. and Upcroft, P.
 TITLE Mapping variation in chromosome homologues of different Giardia strains
 JOURNAL Mol. Biochem. Parasitol. 76 (1-2), 135-143 (1996)
 MEDLINE 97077435
 PUBMED 8920002
 COMMENT Original source text: Giardia lamblia DNA.
 FEATURES
 source
 1. .50
 Location/Qualifiers
 /organism='Giardia intestinalis'
 /mol_type='genomic DNA'
 /db_xref='taxon:5741'
 ORIGIN
 Query Match 58.4%; Score 14.6; DB 3; Length 50;
 Best Local Similarity 81.0%; Pred. No. 1.6e+05;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 TCATCACCACCTCTCTTCATC 25
 Db 26 TCATCAACACTCTCATCGTTC 6

RESULT 17
 AX327047 41 bp DNA linear PAT 07-JAN-2002
 LOCUS Sequence 243 from Patent WO0178894.
 DEFINITION AX327047
 ACCESSION AX327047
 VERSION AX327047.1 GI:18097758
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Keith, T.
 TITLE Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
 JOURNAL Patent: WO 0178894-A 243 25-OCT-2001;
 GENOME Therapeutics Corp. (US)
 FEATURES
 source
 1. .41
 Location/Qualifiers
 /organism='Homo sapiens'
 /mol_type='unassigned DNA'
 /db_xref='taxon:9606'
 ORIGIN
 Query Match 57.6%; Score 14.4; DB 6; Length 41;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CAACTCATCACCACCTCTCTTCAT 24
 Db 4 CATCTCAGCTCCACACTCTTCTT 27
 RESULT 18
 AX327048 41 bp DNA linear PAT 07-JAN-2002
 LOCUS Sequence 244 from Patent WO0178894.
 DEFINITION AX327048
 ACCESSION AX327048
 VERSION AX327048.1 GI:18097759
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Keith, T.
 TITLE Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
 JOURNAL Patent: WO 0178894-A 244 25-OCT-2001;
 GENOME Therapeutics Corp. (US)
 FEATURES
 source
 1. .41
 Location/Qualifiers
 /organism='Homo sapiens'
 /mol_type='unassigned DNA'
 /db_xref='taxon:9606'
 ORIGIN
 Query Match 57.6%; Score 14.4; DB 6; Length 41;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CAACTCATCACCACCTCTCTTCAT 24
 Db 5 CATCTCAGCTCCACACTCTTCTT 28
 RESULT 19
 AR289466 47 bp DNA linear PAT 12-JUN-2003
 LOCUS Sequence 1201 from patent US 6537751.
 DEFINITION AR289466
 ACCESSION AR289466
 VERSION AR289466.1 GI:31676750
 KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 47)
TITLE        Cohen,D., Chumakov,I. and Blumenfeld,M.
              Biallelic markers for use in constructing a high density
              disequilibrium map of the human genome
JOURNAL      Patent: US 6537751-A 1201 25-MAR-2003;
FEATURES     Location/Qualifiers
              1..47
              /organism="unknown"
              /mol_type="genomic DNA"

ORIGIN

Query Match      57.6%; Score 14.4; DB 6; Length 47;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTC 21
Db 25 CTCCTCATCACTCTCTKC 42

RESULT 20
AX496861/c
LOCUS      AX496861                20 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 3 from Patent WO205749.
ACCESSION  AX496861
VERSION     AX496861.1 GI:23342381
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
              other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Ho,S.P.
TITLE        Crf 2? ligands in combination therapy
JOURNAL      Patent: WO 0205749-A 3 24-JAN-2002;
              Bristol-Myers Squibb Pharma Company (US)
FEATURES     Location/Qualifiers
              1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Antisense Oligonucleotide"

ORIGIN

Query Match      56.8%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCC 22
Db 19 CTCATCACCACCTTCATCC 1

RESULT 21
AR072405/c
LOCUS      AR072405                24 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 208 from patent US 5948611.
ACCESSION  AR072405
VERSION     AR072405.1 GI:9999169
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
              Unclassified.
REFERENCE    1 (bases 1 to 24)
AUTHORS      Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvaniemi,P.,
              Baldwin,C., Hopkins,I. and Ahmad,N.Nina.
TITLE        Primers and methods for detecting mutations in the procollagen II
              gene (COL2A1) that indicate a genetic predisposition for a
              COL2A1-associated disease
JOURNAL      Patent: US 5948611-A 208 07-SEP-1999;
FEATURES     Location/Qualifiers

SOURCE      1..24
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN

Query Match      56.8%; Score 14.2; DB 6; Length 24;
Best Local Similarity 84.2%; Pred. No. 2.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATCACCACCTCTCTTCCAT 24
Db 24 CATCACCCCTCTTTCCCAT 6

RESULT 22
I26516/c
LOCUS      I26516                24 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 208 from patent US 5558988.
ACCESSION  I26516
VERSION     I26516.1 GI:1606386
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
              Unclassified.
REFERENCE    1 (bases 1 to 24)
AUTHORS      Prockop,D.J., Ala-Kokko,L. and Ritvaniemi,P.
TITLE        Primers and methods for detecting mutations in the procollagen II
              gene that indicate a genetic predisposition for osteoarthritis
JOURNAL      Patent: US 5558988-A 208 24-SEP-1996;
FEATURES     Location/Qualifiers
              1..24
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN

Query Match      56.8%; Score 14.2; DB 6; Length 24;
Best Local Similarity 84.2%; Pred. No. 2.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATCACCACCTCTCTTCCAT 24
Db 24 CATCACCCCTCTTTCCCAT 6

RESULT 23
AX511858/c
LOCUS      AX511858                25 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 265 from Patent WO02055705.
ACCESSION  AX511858
VERSION     AX511858.1 GI:23392558
KEYWORDS   .
SOURCE      synthetic construct
              synthetic construct
              other sequences; artificial sequences.
ORGANISM    synthetic construct
              other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Mezes,P.S., Rastelli,L., Herrmann,J.L., Macdougall,J.R., Zhong,H.,
              Casman,S.J., Boldog,F., Shinkets,R.A., Gorman,L., Crasta,O.R.,
              Mysore,K.K., Folkerts,O., Martin,G.B., Eisen,A., Spaderma,S.K.,
              Vernet,C.A., Bergh,C., Spytek,K.A., Dipippo,V.A., Zerhusen,B.D.,
              Peyman,J.A., Ellerman,K., Stone,D.J., Grosse,W.M., Alsobrook,J.P.,
              Lepley,D.M., Rieger,D.K., Burgess,C.E. and Edinger,S.
              Proteins and nucleic acids encoding same
              Patent: WO 02055705-A 265 18-JUL-2002;
              Curagen Corporation (US)
FEATURES     Location/Qualifiers
              1..25
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="oligonucleotide primer"

ORIGIN

Query Match      56.8%; Score 14.2; DB 6; Length 25;

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Best Local Similarity 84.2%; Pred. No. 2.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACTCATCACCACCTCTCT 19
DB 22 CAACTAATCACCATGCTCT 4

RESULT 24
AX521320
LOCUS AX521320 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 7518 from Patent WO20052044.
ACCESSION AX521320
VERSION AX521320.1 GI:23572190
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
Detection of genetic polymorphisms
TITLE
JOURNAL Patent: WO 02052044-A 7518 04-JUL-2002;
Riken (JP)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 56.8%; Score 14.2; DB 6; Length 41;
Best Local Similarity 84.2%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACTCATCACCACCTCTCTTC 21
DB 1 ACTCATTATCACTGTCTTC 19

RESULT 25
AR082996/c
LOCUS AR082996 22 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 22 from patent US 5976798.
ACCESSION AR082996
VERSION AR082996.1 GI:10009786
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 22)
Parker, W. Davis., Herrnstadt, C., Ghosh, S. and Fahy, E.D.
AUTHORS Methods for detecting mitochondrial mutations diagnostic for
TITLE Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid
JOURNAL Patent: US 5976798-A 22 02-NOV-1999;
FEATURES Location/Qualifiers
source
1..22
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 22;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTCTTCATC 25
DB 22 CTCACACACCACTCTCTTCGACC 1

RESULT 26
BD005994/c
LOCUS BD005994 22 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods for detecting mitochondrial mutations diagnostic for
ACCESSION BD005994
VERSION BD005994.1 GI:18634365
KEYWORDS
SOURCE Unidentified.
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 22)
Herrnstadt, C., Ghosh, S., Fahy, E.D. and Davis, R.E.
AUTHORS An optimal procedure for isolation of mutant mitochondrial alleles
TITLE An optimal procedure for isolation of mutant mitochondrial alleles
JOURNAL Patent: JP 2001500020-A 2 09-JAN-2001;
MITOKOR
COMMENT OS Unidentified
PN JP 2001500020-A/2
PD 09-JAN-2001
PF 26-NOV-1997 JP 1998524745
PR 27-NOV-1996 US 08/757438
PI CORINNA HERRNSTADT, SOUMITRA GHOSH, EOIN D FAHY, ROBERT E DAVIS
PC C07H21/04, C12Q1/68, C12P19/34
CC Strandedness: Double;
CC Topology: Linear;
CC Location/Qualifiers
FH key
FT source
1..22
/organism="Unidentified"
LOCATION/Qualifiers
1..22
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 22;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTCTTCATC 25
DB 22 CTCACACCACTCTCTTCGACC 1

RESULT 27
BD070465/c
LOCUS BD070465 22 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods for detecting mitochondrial mutations diagnostic for
ACCESSION BD070465
VERSION BD070465.1 GI:22616068
KEYWORDS
SOURCE Unidentified.
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 22)
Parker, W.D., Herrnstadt, C., Ghosh, S. and Fahy, E.D.
AUTHORS Methods for detecting mitochondrial mutations diagnostic for
TITLE Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid
JOURNAL Patent: JP 2001514500-A 22 11-SEP-2001;
MITOKOR
COMMENT OS Unidentified
PN JP 2001514500-A/22
PD 11-SEP-2001
PF 27-FEB-1998 JP 1998537738
PR 28-FEB-1997 US 08/810599
PI WILLIAM DAVIS PARKER, CORINNA HERRNSTADT, SOUMITRA GHOSH, EOIN D
PC C12Q1/68, C07H21/04
CC Strandedness: Double;
CC Topology: Linear;
CC Methods for detecting mitochondrial mutations diagnostic for
CC Alzheimer's
CC disease and methods for determining heteroplasmy of CC

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CC acid
FH key Location/Qualifiers
FT source 1..22
FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 22;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCATC 25
||||| ||||| ||||| |||||
Db 22 CTCACACCACTTCTTGACC 1

RESULT 28
AX494081/c
LOCUS AX494081 24 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1055 from Patent WO02059355.
ACCESSION AX494081
VERSION AX494081.1 GI:23339713
KEYWORDS
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Fieldhouse,D. and Kobler,D.
TITLE Polynucleotides for use as tags and tag complements, manufacture and use thereof
JOURNAL Patent: WO 02059355-A 1055 01-AUG-2002;
TM BIOSCIENCE CORP (CA)
FEATURES
source 1..24
Location/Qualifiers
/morganism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially Synthesized DNA Sequence"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 24;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCCA 23
||||| ||||| ||||| |||||
Db 24 AACTCATAACAACTTCTTACAA 3

RESULT 29
AX610677/c
LOCUS AX610677 25 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 1702 from Patent WO02072882.
ACCESSION AX610677
VERSION AX610677.1 GI:28406106
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cullen,P. and Seedorf,U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 1702 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
source 1..25
Location/Qualifiers
/morganism="Homo sapiens"

/mitochondrial nucleic
acid
key Location/Qualifiers
source 1..22
/morganism='Unidentified'.
Location/Qualifiers
source 1..22
/morganism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 22;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCATC 25
||||| ||||| ||||| |||||
Db 22 CTCACACCACTTCTTGACC 1

RESULT 28
AX494081/c
LOCUS AX494081 24 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1055 from Patent WO02059355.
ACCESSION AX494081
VERSION AX494081.1 GI:23339713
KEYWORDS
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Fieldhouse,D. and Kobler,D.
TITLE Polynucleotides for use as tags and tag complements, manufacture and use thereof
JOURNAL Patent: WO 02059355-A 1055 01-AUG-2002;
TM BIOSCIENCE CORP (CA)
FEATURES
source 1..24
Location/Qualifiers
/morganism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially Synthesized DNA Sequence"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 24;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCCA 23
||||| ||||| ||||| |||||
Db 24 AACTCATAACAACTTCTTACAA 3

RESULT 29
AX610677/c
LOCUS AX610677 25 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 1702 from Patent WO02072882.
ACCESSION AX610677
VERSION AX610677.1 GI:28406106
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cullen,P. and Seedorf,U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 1702 19-SEP-2002;
OGHAM GmbH (DE)
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Location/Qualifiers
/morganism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTCTCTTCCAT 24
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Db 25 ACTCTTCCCAGTCACCTTACAT 4

RESULT 30
AX248216/c
LOCUS AX248216 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 295 from Patent WO0166800.
ACCESSION AX248216
VERSION AX248216.1 GI:15862839
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 295 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
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Location/Qualifiers
/morganism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3e+05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACCACCTCTCTTCCAT 24
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Db 30 CACCACACTCTTCCT 15

RESULT 31
AX249206/c
LOCUS AX249206 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1285 from Patent WO0166800.
ACCESSION AX249206
VERSION AX249206.1 GI:15863829
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1285 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
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Location/Qualifiers
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ORIGIN
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Best Local Similarity 87.5%; Pred. No. 3e+05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACCACCTCTCTTCCAT 24
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Db 30 CACCACACTCTTCCT 15

RESULT 31
AX249206/c
LOCUS AX249206 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1285 from Patent WO0166800.
ACCESSION AX249206
VERSION AX249206.1 GI:15863829
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1285 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
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/mol_type="unassigned DNA"
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ORIGIN
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Best Local Similarity 87.5%; Pred. No. 3e+05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACCACCTCTCTTCCAT 24
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Db 30 CACCACACTCTTCCT 15

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Db          30 CACCACACTCTTCCT 15
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Query Match          55.2%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.8e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 32
CQ786866
LOCUS          32 bp DNA linear PAT 24-MAR-2004
DEFINITION    Sequence 43 from Patent WO2004021010.
ACCESSION     CQ786866
VERSION       CQ786866.1 GI:45721858
KEYWORDS
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE
AUTHORS       Nakamura,Y. and Furukawa,Y.
TITLE         Method of diagnosing colon and gastric cancers
JOURNAL       Patent: WO 2004021010-A 43 11-MAR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
FEATURES
LOCATION/Qualifiers
1..32
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Artificially synthesized primer sequence for
RT-PCR"
ORIGIN
Query Match          56.0%; Score 14; DB 6; Length 32;
Best Local Similarity 77.3%; Pred. No. 3e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY          2 AACTCATCACCACACTCTCTCCA 23
|||||
Db          10 AAGTCATTGTCACACTCTCATCCA 31
|||||

RESULT 33
E59389/c
LOCUS          20 bp DNA linear PAT 31-JAN-2002
DEFINITION    Method for differentiating varieties of pig by DNA sequence
polymorphism.
ACCESSION     E59389
VERSION       E59389.1 GI:18622524
KEYWORDS      JP 2000350586-A/13.
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE
AUTHORS       Mitsuhashi,T. and Okumura,N.
TITLE         Method for differentiating varieties of pig by DNA sequence
JOURNAL       Patent: JP 2000350586-A 13 19-DEC-2000;
LINESTOCK EXPERIMENT STATION MINISTRY OF AGRICULTURE FORESTRY AND
FISHERIES, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY
AND FISHERIES, TADAYOSHI MITSUHASHI
COMMENT       OS Artificial Sequence
PN JP 2000350586-A/13
PD 19-DEC-2000
PF 11-JUN-1999 JP 1999165269
PR TADAYOSHI MITSUHASHI,NAOHIKO OKUMURA
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC
FH Key Location/Qualifiers
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Query Match          55.2%; Score 13.8; DB 6; Length 27;
Best Local Similarity 88.2%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          3 ACTCATCACCACACTCTCT 19
|||||
Db          17 AGTCATCACCACACTCTCCT 1
|||||

RESULT 35
BD197187/c
LOCUS          29 bp RNA linear PAT 17-JUL-2003
DEFINITION    Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION     BD197187
VERSION       BD197187.1 GI:33006957
KEYWORDS      JP 2002509721-A/213.
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE
AUTHORS       Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Meswigen,J.A.
TITLE         Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL       Patent: JP 2002509721-A 213 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT       OS Artificial Sequence
PN JP 2002509721-A/213
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00

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CC      Synthesized Hammerhead Ribozyme
CC      The letter 'n' stands for any base or bases forming a loop or
CC      stem-loop
CC      that may contain multiple nucleic acid analogues or 2'- CC
        deoxynucleotides.
FH      Key
FT      Location/Qualifiers
FT      source
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Query Match      55.2%; Score 13.8; DB 6; Length 29;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CAACTCATCAGCACTCTC 18
Db      19 CGNCTCATCAGCACTCTC 2

RESULT 36
BD252384/c
LOCUS      29 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION      Regulation of repressor genes using nucleic acid molecules.
ACCESSION      BD252384
VERSION      BD252384.1 GI:33062154
KEYWORDS      JP 2002541795-A/177.
SOURCE      unidentified
            unclassified.
REFERENCE      1 (bases 1 to 29)
AUTHORS      Blatt L., Zwick M., Pavco P. and Mcswiggen J.
TITLE      Regulation of repressor genes using nucleic acid molecules
JOURNAL      Patent: JP 2002541795-A 177 10-DEC-2002;
COMMENT      RIBOZYME PHARMACEUTICALS INC
            OS      Eukaryote
            PN      JP 2002541795-A/177
            PD      10-DEC-2002
            PF      11-APR-2000 JP 2000611654
            PR      12-APR-1999 US 60/129390
            PI      LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
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            PC      (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC      A61K37/02,
            PC      (C12N5/00,C12R1:91)
            CC      N in position 17 represents stem II region of a HH ribozyme.
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Query Match      55.2%; Score 13.8; DB 6; Length 29;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CAACTCATCAGCACTCTC 18
Db      19 CGNCTCATCAGCACTCTC 2

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RESULT 37
AX300835/c
LOCUS      29 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION      Sequence 4 from Patent WO0185955.
ACCESSION      AX300835
VERSION      AX300835.1 GI:17382113
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1
AUTHORS      Bahr,G., Cocude,C. and Capron,A.
TITLE      Rh16 polypeptides and its fragments and polynucleotides encoding
            said polypeptides and therapeutic uses
JOURNAL      Patent: WO 0185955-A 4 15-NOV-2001;
            Istac (FR) ; INSTITUT PASTEUR DE LILLE (FR)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Query Match      55.2%; Score 13.8; DB 6; Length 29;
Best Local Similarity 88.2%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 TCATCACCACCTCTCTTC 21
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Db      18 TCATCACCACCTCTCTC 2

RESULT 38
AX300839
LOCUS      29 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION      Sequence 8 from Patent WO0185955.
ACCESSION      AX300839
VERSION      AX300839.1 GI:17382117
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Bahr,G., Cocude,C. and Capron,A.
TITLE      Rh16 polypeptides and its fragments and polynucleotides encoding
            said polypeptides and therapeutic uses
JOURNAL      Patent: WO 0185955-A 8 15-NOV-2001;
            Istac (FR) ; INSTITUT PASTEUR DE LILLE (FR)
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Best Local Similarity 88.2%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 TCATCACCACCTCTCTTC 21
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Db      12 TCATCACCACCTCTCTC 28

RESULT 39
BD235713
LOCUS      31 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Targeted alphavirus and alphaviral vectors.
ACCESSION      BD235713
VERSION      BD235713.1 GI:33045483
KEYWORDS      JP 2002523053-A/16.

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SOURCE
ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 31)
AUTHORS      Dropulic, B., Dropulic, L. and Hardwick, M.J.
TITLE        Targeted alphavirus and alphaviral vectors
JOURNAL      Patent: JP 2002523053-A 16 30-JUL-2002;
              JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT      OS Artificial Sequence
              PN JP 2002523053-A/16
              PD 30-JUL-2002
              PF 30-JUL-1999 JP 2000566453
              PR 30-JUL-1998 US 60/095138
              PI BORO DROPULIC, LESIA DROPULIC, MARIE J HARDWICK PC
              C12N15/09, A61K35/76, A61K38/00, A61P35/00, C12N7/00, PC
              C12Q1/02,
              PC G01N33/48// (C12N7/00, C12R1:92), (C12Q1/02, C12R1:92), C12N15/00,
              PC A61K37/02
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Best Local Similarity 88.2%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 TCATCACCACCTCTCTTC 21
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Db      10 TCAACAGCACTCTCTTC 26

RESULT 40
BD235714
LOCUS      BD235714      33 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Targeted alphavirus and alphaviral vectors.
ACCESSION  BD235714
VERSION    BD235714.1 GI:33045484
KEYWORDS   JP 2002523053-A/17.
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 33)
AUTHORS    Dropulic, B., Dropulic, L. and Hardwick, M.J.
TITLE      Targeted alphavirus and alphaviral vectors
JOURNAL    Patent: JP 2002523053-A 17 30-JUL-2002;
              JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT    OS Artificial Sequence
              PN JP 2002523053-A/17
              PD 30-JUL-2002
              PF 30-JUL-1999 JP 2000566453
              PR 30-JUL-1998 US 60/095138
              PI BORO DROPULIC, LESIA DROPULIC, MARIE J HARDWICK PC
              C12N15/09, A61K35/76, A61K38/00, A61P35/00, C12N7/00, PC
              C12Q1/02,
              PC G01N33/48// (C12N7/00, C12R1:92), (C12Q1/02, C12R1:92), C12N15/00,
              PC A61K37/02
              CC Description of Artificial Sequence: primer
              FH Key
              FT source
              FT Location/Qualifiers
              /organism='Artificial Sequence'.
              /db_xref="taxon:32630"

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            /mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 88.2%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 TCATCACCACCTCTCTTC 21
      ||| ||| ||| ||| ||| ||| |||
Db      10 TCAACAGCACTCTCTTC 26

SOURCE
ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 31)
AUTHORS      Dropulic, B., Dropulic, L. and Hardwick, M.J.
TITLE        Targeted alphavirus and alphaviral vectors
JOURNAL      Patent: JP 2002523053-A 16 30-JUL-2002;
              JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT      OS Artificial Sequence
              PN JP 2002523053-A/16
              PD 30-JUL-2002
              PF 30-JUL-1999 JP 2000566453
              PR 30-JUL-1998 US 60/095138
              PI BORO DROPULIC, LESIA DROPULIC, MARIE J HARDWICK PC
              C12N15/09, A61K35/76, A61K38/00, A61P35/00, C12N7/00, PC
              C12Q1/02,
              PC G01N33/48// (C12N7/00, C12R1:92), (C12Q1/02, C12R1:92), C12N15/00,
              PC A61K37/02
              CC Description of Artificial Sequence: primer
              FH Key
              FT source
              FT Location/Qualifiers
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Query Match      55.2%; Score 13.8; DB 6; Length 33;
Best Local Similarity 88.2%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 TCATCACCACCTCTCTTC 21
      ||| ||| ||| ||| ||| ||| |||
Db      16 TCAACAGCACTCTCTTC 32

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OM nucleic - nucleic search, using sw model

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Title: US-10-788-779-9

Perfect score: 25

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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	25	100.0	25	9	ACA63119 Human bet
3	25	100.0	25	13	ADR05305 Human bet
C 4	18.6	74.4	41	3	AaZ57003 Forward a
C 5	18.6	74.4	47	3	AaZ569233 Human map
C 6	17.6	70.4	41	3	AaZ56996 Forward a
7	16.2	64.8	46	2	AaQ24360 Oligonule
8	16	64.0	42	4	AaF30389 Human ADA
C 9	15.6	62.4	33	6	ABQ83617 Human lys
C 10	15.6	62.4	41	6	ABQ83619 Human lys
C 11	15.4	61.6	25	8	ABZ72744 Attenuati
C 12	15.4	61.6	33	6	AaL50996 Human act
13	15.4	61.6	36	12	ADL23552 Worm tors
C 14	15.2	60.8	20	2	AaQ95137 Spinocere
15	15.2	60.8	42	2	AaZ28187 Human alp
16	15.2	60.8	42	3	AaZ99170 Human pep
C 17	15	60.0	41	6	ABQ83620 Human lys
18	15	60.0	50	6	ABZ06975 Human leu
C 19	15	60.0	50	6	ABZ06585 Human leu
20	14.8	59.2	22	6	ADL17836 Forward P

21	14.8	59.2	22	12	ADN42918	Adn42918 Human NOV
C 22	14.8	59.2	24	2	AAZ34011	Aaz34011 Human PRO
C 23	14.8	59.2	24	3	AAZ78692	Aaz78692 Human PRO
C 24	14.8	59.2	24	8	ACA63579	Acac63579 Novel hum
C 25	14.8	59.2	24	8	ACA71743	Acac71743 Human PRO
C 26	14.8	59.2	24	8	ABX92383	Abx92383 Human PRO
C 27	14.8	59.2	24	8	ACA66124	Acac66124 Human sec
C 28	14.8	59.2	24	9	ADA24681	Ada24681 Secreted
C 29	14.8	59.2	24	9	ACD29725	Acad29725 Novel hum
C 30	14.8	59.2	24	9	ADA12342	Ada12342 Human sec
C 31	14.8	59.2	24	9	ACD29140	Acad29140 Novel hum
C 32	14.8	59.2	24	10	ADB73648	Adb73648 Human PRO
C 33	14.8	59.2	24	10	ADB76364	Adb76364 Human PRO
C 34	14.8	59.2	24	10	ADC43790	Adc43790 Human PRO
C 35	14.8	59.2	24	10	ADC61550	Adc61550 Human PRO
C 36	14.8	59.2	24	10	ADC63514	Adc63514 Human PRO
C 37	14.8	59.2	24	10	ADC66614	Adc66614 Human PRO
C 38	14.8	59.2	24	10	ADC68738	Adc68738 Human PRO
C 39	14.8	59.2	24	10	ADC62798	Adc62798 Human PRO
C 40	14.8	59.2	24	10	ADC67863	Adc67863 Human PRO
C 41	14.8	59.2	24	10	ADC41183	Adc41183 Human PRO
C 42	14.8	59.2	24	10	ADC67238	Adc67238 Human PRO
C 43	14.8	59.2	24	10	ADC62174	Adc62174 Human PRO
C 44	14.8	59.2	24	10	ADC41807	Adc41807 Human PRO
C 45	14.8	59.2	24	10	ADE49176	Ade49176 Human PRO

ALIGNMENTS

RESULT 1

AAQ91129

ID AAQ91129 standard; cDNA; 25 BP.

XX AC AAQ91129;

XX DT 19-FEB-1996 (first entry)

XX DE Beta-cardiac myosin heavy chain PCR primer B9.1F.

XX KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;

XX KW diagnosis; primer; mutation; detection; ss.

XX OS Synthetic.

XX PN USS429923-A.

XX PD 04-JUL-1995.

XX PF 11-DEC-1992; 92US-00989160.

XX PR 11-DEC-1992; 92US-00989160.

XX PA (HARD) HARVARD COLLEGE.

XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX PI (GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA.

XX PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX DR WPI; 1995-245715/32.

XX PT Non-invasive method for diagnosis of hypertrophic cardio-myopathy -

XX PT useful for testing asymptomatic individual(s).

XX PS Example 1; Col 10; 22pp; English.

XX CC AAQ91121-091130 are nested PCR primers used for the amplification and

XX CC identification of beta-cardiac myosin heavy-chain RNA. They are used in a

XX CC new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),

XX CC the method involves detecting the presence or absence of specific HC- from

XX CC associated mutations in the beta-cardiac myosin heavy-chain obtained from

XX CC a blood sample. The method may be used to diagnose familial or sporadic

XX CC HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria
 CC
 SQ Sequence 25 BP; 6 A; 12 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.55;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACATCATCACCACCTCTCTTCATC 25

Db 1 CAACATCATCACCACCTCTCTTCATC 25

RESULT 2

ACA63119

ID ACA63119 standard; DNA; 25 BP.

XX AC

ACA63119;

XX 28-AUG-2003 (first entry)

XX Human beta cardiac myosin heavy chain PCR primer B9.1F.

DE Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;

XX familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;

KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;

KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;

KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

OS US2003054343-A1.

XX 20-MAR-2003.

XX 06-JUN-1995; 95US-00469172.

XX 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.

PA (SEID/) SEIDMAN J.

PA (WATK/) WATKINS H.

PA (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

PI WPI; 2003-512374/48.

DR Detecting a presence or absence of a mutation associated with

PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or

PT hemophilia, by detecting a mutation in an amplified product of a beta

PT cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

PS The invention relates to detecting the presence or absence of a mutation

CC associated with hypertrophic cardiomyopathy (sporadic or familial, SHC

CC and FHC) comprises detecting a mutation associated with hypertrophic

CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy

CC chain DNA. The mutations associated with SHC/FHC are detected in the

CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-

CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect

CC sample). FHC associated point mutation can be classified and used to

CC determine life expectancy in affected individuals e.g. using a Kaplan-

CC Meier curve for the classified type of FHC causing point mutation. Also

CC included are an RNA probe comprising ribonucleotides arranged in a

CC sequence which is complementary to at least a portion of beta-cardiac

CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for

CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
 CC chain gene containing an FHC-associated mutation

XX SQ Sequence 25 BP; 6 A; 12 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.55;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACATCATCACCACCTCTCTTCATC 25

Db 1 CAACATCATCACCACCTCTCTTCATC 25

RESULT 3

ADR05305

ID ADR05305 standard; DNA; 25 BP.

XX AC

ADR05305;

XX 21-OCT-2004 (first entry)

XX Human beta cardiac myosin heavy chain mutation detection primer B9.1F.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;

KW familial hypertrophic cardiomyopathy;

KW sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

XX US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

PA (SEID/) SEIDMAN J.

PA (WATK/) WATKINS H.

PA (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

PI WPI; 2004-592586/57.

DR Detecting mutations associated with hypertrophic cardiomyopathy to

PT diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac

PT myosin heavy-chain DNA and detecting the mutation in the amplified

PT product.

XX Claim 18; SEQ ID NO 9; 22pp; English.

CC The invention relates to detecting the presence or absence of a mutation

CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,

CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,

CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an

CC amplified product, and detecting the presence or absence of a mutation

CC associated with hypertrophic cardiomyopathy in the amplified product,

CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also

CC included are a set of DNA oligonucleotide primers for amplifying beta-

CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

XX
SQ Sequence 25 BP; 6 A; 12 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATCATCACCACTCTCTTCATC 25
||| ||||| ||||| ||||| |||||
DB 1 CAATCATCACCACTCTCTTCATC 25

RESULT 4
AAZ57003/C
ID AAZ57003 standard; DNA; 41 BP.
XX AAZ57003;
XX
XX 12-MAY-2000 (first entry)
XX
XX Forward amplicon for generating usurpin constructs.
XX
XX Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
KW caspase; cytostatic; antiParkinsonian; antidiabetic; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200003023-A1.
XX
XX 20-JAN-2000.
XX
XX 07-JUL-1999; 99WO-CA000615.
XX
XX 08-JUL-1998; 98US-0092005P.
XX
XX (MERI) MERCK FROSST CANADA INC.
XX
XX Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
PI WPI; 2000-160929/14.
XX
XX Novel recombinant DNA molecules and polypeptides for treating apoptosis
PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
PT disease.
XX
XX Example 7; Page 33; 69pp; English.

CC The invention provides recombinant nucleic acid molecules encoding
CC usurpin-alpha (lacking the first death effector domain (DED) or its
CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
CC useful in vitro and in vivo identification of usurpin-procaspase-8
CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity
CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
CC is useful for treating diseases like autoimmune diabetes, cancer and
CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
CC interaction are also useful for treating various diseases mediated by
CC apoptosis. Usurpin provides an attractive model for modulating caspase
CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
CC regulated at several levels in the presence of usurpin, conferring
CC resistance to Fas-ligand cell death. The present sequence represents a
CC forward amplicon for generating usurpin-alpha, delDED-A usurpin
CC constructs for transfection into human cells

XX
SQ Sequence 41 BP; 9 A; 5 C; 16 G; 11 T; 0 U; 0 Other;

Query Match 74.4%; Score 18.6; DB 3; Length 41;
Best Local Similarity 84.0%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAATCATCACCACTCTCTTCATC 25
||| ||||| ||||| ||||| |||||
DB 41 CAATCTCTCACCAATCTCTGCATC 17

RESULT 5
AAZ69233/C
ID AAZ69233 standard; DNA; 47 BP.
XX AAZ69233;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human map-related biallelic marker SEQ ID NO:3589.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation; diagnosis;
KW single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT variation replace(24,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
PI WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 3; Page 996; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

XX SQ Sequence 47 BP; 15 A; 9 C; 14 G; 9 T; 0 U; 0 Other;

Query Match 74.4%; Score 18.6; DB 3; Length 47;
 Best Local Similarity 84.0%; Pred. No. 2.9e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAACCTCATCACCACCTCTCTTCCATC 25
 |||||
 Db 32 CACCTCATCAGCACTGCTTCTCTTC 8

RESULT 6

AAZ56996/C
 ID AAZ56996 standard; DNA; 41 BP.

XX AC

XX AAZ56996;

XX DT 12-MAY-2000 (first entry)

XX DE Forward amplicon for generating delDED-A usurin construct.

XX Usurin-alpha; death effector domain; DBD; prodomain; usurin-beta;
 KW usurin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
 KW caspase; cytostatic; antiparkinsonian; antidiabetic; PCR primer; ss.

XX OS Homo sapiens.

XX FN WO200003023-A1.

XX PD 20-JAN-2000.

XX PF 07-JUL-1999; 99WO-CA000615.

XX PR 08-JUL-1998; 98US-0092005P.

XX PA (MERI) MERCK FROSST CANADA INC.

XX PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;

XX DR WPI; 2000-160929/14.

XX Novel recombinant DNA molecules and polypeptides for treating apoptosis
 PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 PT disease.

XX PS Example 7; Page 31; 69pp; English.

XX The invention provides recombinant nucleic acid molecules encoding
 CC usurin-alpha (lacking the first death effector domain (DED) or its
 CC prodomain), usurin-beta or usurin-gamma. Usurin polypeptides are
 CC useful for in vitro and in vivo identification of usurin-procaspase-8
 CC interaction inhibitor. Usurin is useful as modulator of the sensitivity
 CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
 CC regulated at several levels in the presence of usurin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents a
 CC forward amplicon for generating delDED-A usurin constructs

XX SQ Sequence 41 BP; 9 A; 7 C; 15 G; 10 T; 0 U; 0 Other;
 Query Match 70.4%; Score 17.6; DB 3; Length 41;
 Best Local Similarity 83.3%; Pred. No. 7.4e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAACCTCATCACCACCTCTCTTCCAT 24
 |||||
 Db 40 CAAATCCTCACCACCTCTCTTCCAT 17

RESULT 7

AAQ24360

ID AAQ24360 standard; DNA; 46 BP.

XX AC

XX AAQ24360;

XX DT 26-OCT-1992 (first entry)

XX DE Oligonucleotide primer TAFR01.

XX Tag polymerase; mutant; thermostable; DNA polymerase; exonuclease; PCR;
 KW amplification; reverse primer; ss.

XX OS Synthetic.

XX FN WO9206200-A.

XX PD 16-APR-1992.

XX PF 30-SEP-1991; 91WO-US007035.

XX PR 28-SEP-1990; 90US-00590213.

XX PR 28-SEP-1990; 90US-00590466.

XX PR 28-SEP-1990; 90US-00590490.

XX PA (CETU) CETUS CORP.

XX Gelfand DH, Abramson RD;

XX WPI; 1992-150885/18.

XX Thermostable DNA polymerases with altered 5'-3' exo nuclease activity -
 PT having conserved regions mutated or deleted, for use in e.g. PCR,
 PT sequencing and detection assays.

XX PS Example 10; Page 102; 185pp; English.

XX The primer was used in conjunction with primer TAFI285 (see AAQ24359) to
 CC obtain a DNA fragment encoding a 5'-3' exonuclease deficient thermostable
 CC DNA polymerase from Thermophilus africanus. A portion of the DNA
 CC polymerase gene comprising amino acids 285-892 was selectively amplified
 CC using the two PCR primers and the purified prod. isolated. The purified
 CC protein is deficient in 5'-3' exo- nuclease activity, is more
 CC thermoresistant than the corresp. native enzyme and is partic. useful in
 CC PCR of G+C rich templates. See also AAQ23993-Q24013, AAQ24320-36 and
 CC AAQ24343-59

XX SQ Sequence 46 BP; 12 A; 17 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 64.8%; Score 16.2; DB 2; Length 46;
 Best Local Similarity 85.7%; Pred. No. 2.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCAT 24
 |||||
 Db 17 CTCATCACCACCTCTCTTCCAT 37

RESULT 8

AAF30389

ID AAF30389 standard; DNA; 42 BP.

```

XX AAF30389;
AC
XX
XX
DT 14-MAY-2001 (first entry)
XX
DE Human ADAM8 cDNA forward primer ST239A8MF.
XX
XX ADAM8; human; tumour; cancer; therapy; diagnosis; antitumour; PCR primer;
KW ss.
XX
XX Homo sapiens.
OS
XX WO200109189-A2.
XX
XX PD 08-FEB-2001.
XX
XX PF 27-JUL-2000; 2000WO-US020731.
XX
XX PR 28-JUL-1999; 99US-0146217P.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Bodary SC, Fisher KL;
XX
XX DR WPI; 2001-182943/18.
XX
XX Antibodies against ADAM8 polypeptides, useful e.g. for diagnosis and
PT treatment of tumors and inflammation.
PT
XX Example 6; Page 75; 117pp; English.
XX
XX The present sequence is that of forward PCR primer ST239A8MF, which was
CC used with reverse primer ST239A8TCR (see AAF30390) for the PCR
CC amplification of human full-length ADAM8 cDNA (see AAF30377). The forward
CC primer includes an NsiI restriction site toward the 5' end followed by
CC the sequence at the beginning of the mature sequence of ADAM8. The PCR
CC product was used in the construction of plasmid pST239.ADM8mat for
CC expression of mature ADAM8 protein (see AAB20251) in Escherichia coli
CC strain 583 cells. The ADAM8 gene is amplified in the genome of certain
CC tumour cells. Such gene amplification is associated with overexpression
CC of ADAM8 protein and contributes to tumourigenesis. ADAM8 is therefore a
CC useful target for the diagnosis and/or treatment of certain cancers.
CC Therapeutic agents may take the form of antagonists of ADAM8, such as
CC anti-ADAM8 antibodies, or may be ADAM8 antisense constructs
XX
XX Sequence 42 BP; 12 A; 16 C; 7 G; 7 T; 0 U; 0 Other;
SQ
Query Match 64.0%; Score 16; DB 4; Length 42;
Best Local Similarity 79.2%; Pred. No. 3.5e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AACTCATCACCACCTCTCTCCATC 25
Db ||||| ||||| ||||| |||||
6 AATGCATCAAGACTCTCTGCCATC 29
RESULT 9
ABQ83617/c
ID ABQ83617 standard; DNA; 33 BP.
XX
XX AC ABQ83617;
XX
XX 26-JAN-2003 (first entry)
DT
XX Human lysyl oxidase 46.31 PCR primer 3 SEQ ID NO:5.
DE
XX Human; lysyl oxidase 46.31; enzyme; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; HIV infection; inflammation;
KW immunological disease; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX CN1345944-A.
XX

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```

XX 24-APR-2002.
PD
XX
XX 26-SEP-2000; 2000CN-00125428.
PF
XX
XX 26-SEP-2000; 2000CN-00125428.
PR
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX PA Mao Y, Xie Y;
XX
XX WPI; 2002-539343/58.
XX
XX New polypeptide-human lysyl oxidase 46.31 for treating malignant tumor,
PT hemopathy, human immunodeficiency virus infection, immunological disease
PT and various inflammations.
XX
XX Example 4; Page 17 (Disclosure); 33pp; Chinese.
XX
XX The present invention describes human lysyl oxidase 46.31 (I). Also
CC described is a process for producing (I) using DNA recombination
CC technology. (I) can be used in the treatment of several diseases, such as
CC malignant tumour, haemopathy, human immunodeficiency virus (HIV)
CC infection, immunological disease and various inflammations. The present
CC sequence represents a PCR primer for (I), which is used in an example
CC from the present invention
XX
XX Sequence 33 BP; 12 A; 4 C; 11 G; 6 T; 0 U; 0 Other;
SQ
Query Match 62.4%; Score 15.6; DB 6; Length 33;
Best Local Similarity 81.8%; Pred. No. 5e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CTCATCACCACCTCTCTCCATC 25
Db ||||| ||||| ||||| |||||
33 CTCATTCCCACTCTCTCCATC 12
RESULT 10
ABQ83619/c
ID ABQ83619 standard; DNA; 41 BP.
XX
XX AC ABQ83619;
XX
XX 26-JAN-2003 (first entry)
DT
XX Human lysyl oxidase 46.31 probe 1 SEQ ID NO:8.
DE
XX Human; lysyl oxidase 46.31; enzyme; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; HIV infection; inflammation;
KW immunological disease; probe; ss.
XX
XX Homo sapiens.
OS
XX CN1345944-A.
XX
XX 24-APR-2002.
PD
XX 26-SEP-2000; 2000CN-00125428.
PF
XX
XX 26-SEP-2000; 2000CN-00125428.
PR
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX PA Mao Y, Xie Y;
XX
XX WPI; 2002-539343/58.
XX
XX New polypeptide-human lysyl oxidase 46.31 for treating malignant tumor,
PT hemopathy, human immunodeficiency virus infection, immunological disease
PT and various inflammations.
XX
XX Example 6; Page 19 (Disclosure); 33pp; Chinese.
XX

```

XX The present invention describes human lysyl oxidase 46.31 (I). Also
CC described is a process for producing (I) using DNA recombination
CC technology. (I) can be used in the treatment of several diseases, such as
CC malignant tumour, haemopathy, human immunodeficiency virus (HIV)
CC infection, immunological disease and various inflammations. The present
CC sequence represents a probe for (I), which is used in an example from the
CC present invention
XX
SQ Sequence 41 BP; 15 A; 7 C; 13 G; 6 T; 0 U; 0 Other;

Query Match 62.4%; Score 15.6; DB 6; Length 41;
Best Local Similarity 81.8%; Pred. No. 5.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCATC 25
||| ||||| ||||| |||||
Db 23 CTCATTCCACTCTCTTCCATC 2

RESULT 11

ABZ72744/C
ID ABZ72744 standard; DNA; 25 BP.
XX AC ABZ72744;
XX
DT 09-APR-2003 (first entry)
XX

DE Attenuation factor oligonucleotide SEQ ID NO:147.

XX High throughput assay system; nucleic acid detection; anchor; target;
KW linker; ss.

XX Synthetic.

XX WO2003002750-A2.

XX 09-JAN-2003.

XX 26-JUN-2002; 2002WO-US020039.

XX 26-JUN-2001; 2001US-00888413.

XX (HIGH-) HIGH THROUGHPUT GENOMICS INC.

XX Kris RM, Felder S;

XX WPI; 2003-201508/19.

XX Detecting nucleic acid target in sample by using combination comprising
PT multiple regions each of which has two different loci of anchors in
PT association with a bifunctional linker that has portion specific for
PT anchor.

XX Example 30; Page 114; 129pp; English.

XX The present invention describes a method for detecting a nucleic acid
CC target (I) in a sample (S). The method involves: (a) contacting (S) which
CC may comprise the target(s) with a nuclease protection fragment(s) (I)
CC specific for and which binds to the target(s), exposing the (S) to a
CC nuclease effective to digest remaining single stranded nucleic acid, and
CC then contacting the resultant (S) with a combination (II) which
CC comprises, before addition of (S), a surface comprising multiple
CC spatially discrete regions, at least two of which are substantially
CC identical, each region comprising at least two different loci of anchors,
CC the anchors at each locus, each in association with a bifunctional linker
CC which has a first portion that is specific for the anchor, and a second
CC portion that comprises a probe which is specific for one of the (I),
CC under conditions effective for the (I) to bind to the combination, where
CC two or more of the anchors located at a first locus of a region are in
CC association with different bifunctional linkers, having different target
CC specificities; and (b) detecting the bound protection fragment(s), and
CC where the regions are tubes, and the loci of anchors are arranged in a

CC linear array in the tubes. Such an assay can be termed a multi array
CC plate screen (MAPS) method or assay. When the probes are
CC oligonucleotides, the MAPS can be used for diagnosing the presence of
CC genetic variations or defects e.g. polymorphisms or specific mutations
CC associated with disease such as cystic fibrosis or pathogenic organisms.
CC When the probes are antigen binding molecules, the assays can be used for
CC screening variant proteins or protein expression patterns. The assay can
CC also be used for mapping expressed sequences tags (ESTs). ABZ72599 to
CC ABZ72762, and ABP5611, represent sequences used in the exemplification
CC of the present invention
XX

SQ Sequence 25 BP; 4 A; 1 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 61.6%; Score 15.4; DB 8; Length 25;
Best Local Similarity 76.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAACTCATCACCACCTCTCTTCCATC 25
||| ||||| ||||| |||||
Db 25 CACCTCATAGCACTCTCAACCACC 1

RESULT 12

AAL50996/C
ID AAL50996 standard; DNA; 33 BP.

XX AC AAL50996;

XX 13-FEB-2003 (first entry)

XX Human actin 21-34 PCR primer #3.

XX Human; PCR; primer; ss; actin; 21.34; zinc finger; PHD structural domain;
KW malignant tumour; haemopathy; HIV; immunological disease; inflammation.

XX Homo sapiens.

XX CN1345794-A.

XX 24-APR-2002.

XX 22-SEP-2000; 2000CN-00125360.

XX 22-SEP-2000; 2000CN-00125360.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2002-548937/59.

XX Novel polypeptide-human actin 21.34 contained zinc finger and PHD finger
PT structural domain and its encoding polynucleotide useful for treating
PT e.g., HIV infection.

XX Example 4; Page 20; 33pp; Chinese.

XX The invention comprises the amino acid and coding sequence of the human
CC actin 21.34 protein (which contains a zinc finger and a PHD structural
CC domain). The 21.34 DNA and protein sequences are useful for treating:
CC malignant tumour; haemopathy; HIV; immunological disease; and
CC inflammations. The present DNA sequence represents a PCR primer for the
CC human actin 21.34 gene
XX

SQ Sequence 33 BP; 8 A; 7 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 61.6%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAACTCATCACCACCTCTCTTCCATC 25
||| ||||| ||||| |||||
Db 33 CGACTCGTACCCGCTCTCTTCCATC 9

```
RESULT 13
ADL23552
ID ADL23552 standard; DNA; 36 BP.
XX
AC ADL23552;
XX
DT 20-MAY-2004 (first entry)
XX
DE Worm torsin-2 RT-PCR primer seqid 12.
XX
KW notropic; neuroprotective; antiparkinsonian; anticonvulsant;
KW protein aggregates formation suppressor; gene therapy; tor-1; tor-2;
KW torsin; protein-aggregation-associated disease; Alzheimer's disease;
KW Parkinson's disease; prion disease; taupathy; Huntington's disease;
KW polyglutamine disease; dystonia; familial amyotrophic lateral sclerosis;
KW worm; tor-2; reverse transcriptase PCR; primer; ss; torsin-2.
XX
OS Caenorhabditis elegans.
XX
PN US2003235823-A1.
XX
PD 25-DEC-2003.
XX
PF 24-JUN-2002; 2002US-00177104.
XX
PR 24-JUN-2002; 2002US-00177104.
XX
PA (UYAL-) UNIV ALABAMA.
XX
PI Caldwell GA, Caldwell KA;
XX
DR WPI; 2004-070571/07.
XX
PT Novel isolated tor-1, tor-2 polypeptides, useful for treating protein-
PT aggregation-associated diseases e.g. Alzheimer's disease, Parkinson's
PT disease, prion disease, taupathy and Huntington's disease.
XX
PS Example; SEQ ID NO 12; 48pp; English.
XX
XX The invention describes isolated tor-1, tor-2 polypeptides (I). A vector
XX comprising a polynucleotide (II) encoding (I) is useful for making a
XX torsin polypeptide which involves culturing the vector for a duration of
XX time under conditions suitable for expression of the torsin polypeptide.
XX A polynucleotide that is 70-90% or more identical to (II) is useful for
XX detecting a polynucleotide encoding a polypeptide having 70% or more
XX homology to (I) or a polypeptide having torsin activity. The
XX polynucleotides and polypeptides of the invention are useful for treating
XX symptoms or treating one or more protein-aggregation-associated disease
XX which involves administering the polynucleotides or polypeptides to a
XX human being or an animal in need. The one or more protein-aggregation-
XX associated disease is chosen from Alzheimer's disease, Parkinson's
XX disease, prion disease, taupathy, Huntington's disease, polyglutamine
XX disease, dystonia, and familial amyotrophic lateral sclerosis. (I) is
XX useful for controlling expression of one or more isolated polypeptides
XX having amino acid sequence identical to (I) in an organism. This sequence
XX represents a reverse transcriptase PCR primer used in the isolation of
XX cDNA encoding worm torsin-2 (tor-2).
XX
SQ Sequence 36 BP; 10 A; 11 C; 3 G; 12 T; 0 U; 0 Other;
Query Match 61.6%; Score 15.4; DB 12; Length 36;
Best Local Similarity 76.0%; Pred. No. 6.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCATCTCTTCCATC 25
Db 11 CAACTCATCATTAACACTCTTCTTC 35
RESULT 14
AAQ95137/c
AAQ95137 standard; DNA; 20 BP.
XX
AC AAQ95137;
XX
DT 25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
DE Spinocerebellar ataxia type 1 LR40A PCR primer.
XX
KW Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis;
KW LR40A PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9501437-A2.
XX
PD 12-JAN-1995.
XX
PF 29-JUN-1994; 94WO-US007336.
XX
PR 29-JUN-1993; 93US-00084365.
XX
PR 28-JUN-1994; 94US-00267803.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Orr HT, Chung M, Zoghbi HY;
XX
DR WPI; 1995-061001/08.
XX
PT New autosomal dominant spinocerebellar ataxia type 1 nucleic acid - used
PT to develop prods. for detection or presymptomatic diagnosis of a SCA1
PT disorder.
XX
PS Example I; Page 39; 111pp; English.
XX
XX AAQ95137 and AAQ95138 are a pair of primers for the PCR amplification of
XX AAQ84793, a new autosomal dominant spinocerebellar ataxia type 1 (SCA 1)
XX nucleic acid. The nucleic acid and its protein product (AAR71111) can be
XX used to develop products, for the presymptomatic detection of a SCA 1
XX disorder. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 5 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
Query Match 60.8%; Score 15.2; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCATCTCTT 20
Db 20 CAACTCATGACCCCTCTCCT 1
RESULT 15
AAZ28187
ID AAZ28187 standard; DNA; 42 BP.
XX
AC AAZ28187;
XX
DT 20-DEC-1999 (first entry)
XX
DE Human alpha myosin heavy chain-derived peptide M7A-alpha homologue DNA.
XX
KW Heart disease; inflammatory; autoimmune; cardiomyopathy; myosin;
KW Chlamydia; induction; vaccine; ds.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN US5962636-A.
XX
PD 05-OCT-1999.
XX
PF 12-AUG-1998; 98US-00133774.
```

XX 12-AUG-1998; 98US-00133774.
 XX (AMGE-) AMGEN CANADA INC.
 XX PI Bachmaier K, Hessel AJ, Penninger JM, Neu N;
 XX WPI; 1999-589735/50.
 DR P-PSDB; AAY42731.
 XX Peptides that induce or suppress inflammatory cardiomyopathy.
 XX Example 1; Col 20; 17pp; English.
 XX This sequence represents DNA encoding the human homologue of the murine
 CC alpha myosin heavy chain-derived peptide, M7A-alpha (AAY42723). Like M7A-
 CC alpha, the human homologue induces inflammatory cardiomyopathy (ICM) via
 CC an autoimmune response in mice immunised with it. It contains an amino
 CC acid sequence motif MxxxxS (AAY42722) which appears to be required for
 CC the induction of this disease. The motif was originally identified in M7A
 CC -alpha when it was compared with a peptide derived from a homologous
 CC region of the murine beta myosin heavy chain, M7A-beta (AAY42724) which
 CC did not cause the disease. Several peptide fragments containing the motif
 CC were identified from a database and were found to be fragments of
 CC cysteine rich outer membrane proteins from various species of Chlamydia.
 CC These peptides also induced ICM, indicating that infection with Chlamydia
 CC may be involved in the development of ICM. Inflammatory cardiomyopathy
 CC peptides are used to determine the risk of ICM by incubation with a
 CC subject's T cells and measuring the degree of proliferation (an increased
 CC degree being indicative of risk) or to raise specific antibodies which
 CC can be used therapeutically and for the detection of Chlamydia. Such
 CC peptides can also be used with an adjuvant and an excipient in a vaccine
 CC for decreasing ICM
 XX SQ Sequence 42 BP; 7 A; 19 C; 4 G; 12 T; 0 U; 0 Other;
 Query Match 60.8%; Score 15.2; DB 2; Length 42;
 Best Local Similarity 85.0%; Pred. No. 7.6e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AACTCATCCACCACTCTCTTC 21
 DB 8 AGCTCATGGCCACTCTCTTC 27
 RESULT 16
 AAZ99170
 ID AAZ99170 standard; DNA; 42 BP.
 XX AC AAZ99170;
 XX DT 21-JUN-2000 (first entry)
 XX DE Human peptide M7A-alpha coding sequence.
 XX KW Cardiant; murine alpha myosin heavy chain; inflammatory myocarditis;
 KW autoimmune inflammatory cardiomyopathy; Chlamydia; antibody; vaccine;
 KW hybridization probe; ss.
 XX OS Homo sapiens.
 XX PN US6034230-A.
 XX PD 07-MAR-2000.
 XX PF 03-MAY-1999; 99US-00303862.
 XX PR 12-AUG-1998; 98US-00133774.
 XX PA (AMGE-) AMGEN CANADA INC.
 XX PI Neu N, Penninger JM, Bachmaier K, Hessel AJ;
 XX WPI; 1999-589735/50.
 XX WPI; 2002-539343/58.

DR WPI; 2000-255712/22.
 DR P-PSDB; AAY83820.
 XX DNA molecules encoding novel myocardial peptides used for inhibiting and
 PT inducing inflammatory cardiomyopathy in vivo.
 XX Claim 1; Col 19; 17pp; English.
 XX This sequence represents the coding sequence of the human homologue of
 CC the murine M7A-alpha peptide (Y83811) derived from the murine alpha
 CC myosin heavy chain polypeptide. The peptide was used to evaluate its
 CC ability to induce autoimmune inflammatory cardiomyopathy. A similar
 CC experiment was carried out using the peptide M7A-beta (Y83821). The
 CC invention relates to the isolation of sequences coding for peptide
 CC sequences derived from bacteria and viruses which may cause inflammatory
 CC cardiomyopathy. The peptide sequences are searched based on the sequence
 CC of the M7A peptides derived from the murine alpha myosin heavy chain
 CC polypeptide. The consensus sequence of the murine M7A-alpha/beta peptides
 CC (Y83813) was used to search the PIR public database for similar bacterial
 CC and viral sequences able to cause inflammatory cardiomyopathy. The screen
 CC isolated the peptides Y83814-Y83819 and their corresponding coding
 CC sequences Z99164-Z99169. The peptides encoded by the DNAs are used, alone
 CC or in conjunction with other therapeutics, for inducing or inhibiting
 CC inflammatory cardiomyopathy in vivo, where the cardiomyopathy is
 CC autoimmune inflammatory cardiomyopathy, and inflammatory cardiomyopathy
 CC caused by Chlamydia or other bacterial or viral infections that cause
 CC inflammatory cardiomyopathy. The peptides may also be used for increasing
 CC inflammatory myocarditis in a mammal. Antibodies against the peptides and
 CC the peptides themselves are used for measuring the risk of inflammatory
 CC cardiomyopathy in a mammal. The peptides may also be used in vaccines.
 CC Nucleic acids encoding the peptides may be used as hybridization probes,
 CC e.g. in diagnostic assays to test for the presence of Chlamydia DNA
 XX SQ Sequence 42 BP; 7 A; 19 C; 4 G; 12 T; 0 U; 0 Other;
 Query Match 60.8%; Score 15.2; DB 3; Length 42;
 Best Local Similarity 85.0%; Pred. No. 7.6e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AACTCATCCACCACTCTCTTC 21
 DB 8 AGCTCATGGCCACTCTCTTC 27
 RESULT 17
 ABQ83620/c
 ID ABQ83620 standard; DNA; 41 BP.
 XX AC ABQ83620;
 XX DT 26-JAN-2003 (first entry)
 XX DE Human lysyl oxidase 46.31 probe 2 SEQ ID NO:9.
 XX KW Human; lysyl oxidase 46.31; enzyme; malignant tumour; haemopathy;
 KW human immunodeficiency virus infection; HIV infection; inflammation;
 KW immunological disease; probe; ss.
 XX OS Homo sapiens.
 XX PN CN1345944-A.
 XX PD 24-APR-2002.
 XX PF 26-SEP-2000; 2000CN-00125428.
 XX PR 26-SEP-2000; 2000CN-00125428.
 XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX PI Mao Y, Xie Y;
 XX WPI; 2002-539343/58.

XX New polypeptide-human lysyl oxidase 46.31 for treating malignant tumor,
PT hemopathy, human immunodeficiency virus infection, immunological disease
XX and various inflammations.

PS Example 6; Page 19 (Disclosure); 33pp; Chinese.

XX The present invention describes human lysyl oxidase 46.31 (I). Also
CC described is a process for producing (I) using DNA recombination
CC technology. (I) can be used in the treatment of several diseases, such as
CC malignant tumour, haemopathy, human immunodeficiency virus (HIV)
CC infection, immunological disease and various inflammations. The present
CC sequence represents a probe for (I), which is used in an example from the
XX present invention

XX Sequence 41 BP; 15 A; 8 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 60.0%; Score 15; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 CCACCTCTCTCCATC 25
Db 16 CCACCTCTCTCCATC 2

RESULT 18
ABZ06975
ID ABZ06975 standard; DNA; 50 BP.

XX AC ABZ06975;
XX AC
XX DT 09-JAN-2003 (first entry)
XX DE
XX DE Human leukocyte gene expression profiling probe SEQ ID NO 6966.
XX T7; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX OS Homo sapiens.
XX FN WO200257414-A2.
XX PD 25-JUL-2002.
XX PF 22-OCT-2001; 2001WO-US047856.
XX PR 20-OCT-2000; 2000US-0241994P.
XX PR 08-JUN-2001; 2001US-0296764P.
XX PA (BIOC-) BIOCARDIA INC.
XX PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quettermous T, Johnson F;
XX WPI; 2002-636525/68.
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.

PS Claim 1; Page 53; Opp; English.

XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08132) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual.

XX The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX Sequence 50 BP; 10 A; 23 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 60.0%; Score 15; DB 6; Length 50;
Best Local Similarity 78.3%; Pred. No. 9.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 AACTCATCACCATCTCTTCCAT 24
Db 24 AACTCATCTCGAATCTCTCAT 46

RESULT 19
ABZ06585/c
ID ABZ06585 standard; DNA; 50 BP.

XX AC ABZ06585;
XX AC
XX DT 09-JAN-2003 (first entry)
XX DE
XX DE Human leukocyte gene expression profiling probe SEQ ID NO 6576.
XX T7; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX OS Homo sapiens.
XX FN WO200257414-A2.
XX PD 25-JUL-2002.
XX PF 22-OCT-2001; 2001WO-US047856.
XX PR 20-OCT-2000; 2000US-0241994P.
XX PR 08-JUN-2001; 2001US-0296764P.
XX PA (BIOC-) BIOCARDIA INC.
XX PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quettermous T, Johnson F;
XX WPI; 2002-636525/68.
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.

PS Claim 1; Page 54; Opp; English.

XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual.

XX The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX Sequence 50 BP; 16 A; 1 C; 23 G; 10 T; 0 U; 0 Other;

Query Match 60.0%; Score 15; DB 6; Length 50;
Best Local Similarity 78.3%; Pred. No. 9.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY      2  AACTCATCACCACCTCTCTCCAT 24
      ||||| | | | | | | | |
Db      27  AACTCATCTCGAATCTCTCAT 5
      ||||| | | | | | | |

RESULT 20
AD117836
ID  AD117836 standard; DNA; 22 BP.
XX
AC  AD117836;
XX
XX
DT  15-APR-2004 (first entry)
XX
XX  Forward PCR primer used to amplify human NOVX DNA SeqID1372.
XX
XX  PCR; ss; NOVX; metabolic disorder; diabetes; anorexia; cancer;
XX  cardiovascular; infectious; neurodegenerative; immune;
XX  haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;
XX  antiinflammatory; neuroprotective; antilipemic; anabolic; cardiant;
XX  neurogenesis; wound healing; angiogenesis; chromosome mapping;
XX  tissue typing; preventive medicine; pharmacogenomic; primer; human.
XX
OS  Homo sapiens.
XX
XX  WO200268649-A2.
XX
XX  06-SEP-2002.
XX
XX  31-JAN-2002; 2002WO-US002785.
XX
XX  31-JAN-2001; 2001US-02653395P.
XX  31-JAN-2001; 2001US-0265412P.
XX  31-JAN-2001; 2001US-0265514P.
XX  31-JAN-2001; 2001US-0265517P.
XX  02-FEB-2001; 2001US-0266406P.
XX  05-FEB-2001; 2001US-0266767P.
XX  07-FEB-2001; 2001US-0266975P.
XX  07-FEB-2001; 2001US-0267057P.
XX  08-FEB-2001; 2001US-0267459P.
XX  09-FEB-2001; 2001US-0267823P.
XX  15-FEB-2001; 2001US-0268974P.
XX  26-FEB-2001; 2001US-0271664P.
XX  27-FEB-2001; 2001US-0271839P.
XX  27-FEB-2001; 2001US-0271855P.
XX  02-MAR-2001; 2001US-0272788P.
XX  02-MAR-2001; 2001US-0273046P.
XX  14-MAR-2001; 2001US-0275925P.
XX  14-MAR-2001; 2001US-0275947P.
XX  14-MAR-2001; 2001US-0275950P.
XX  14-MAR-2001; 2001US-0275989P.
XX  15-MAR-2001; 2001US-0276448P.
XX  16-MAR-2001; 2001US-0276450P.
XX  16-MAR-2001; 2001US-0276397P.
XX  16-MAR-2001; 2001US-0276768P.
XX  20-MAR-2001; 2001US-0278652P.
XX  26-MAR-2001; 2001US-0278675P.
XX  26-MAR-2001; 2001US-0278775P.
XX  26-MAR-2001; 2001US-0278778P.
XX  29-MAR-2001; 2001US-0279882P.
XX  29-MAR-2001; 2001US-0279884P.
XX  30-MAR-2001; 2001US-0280147P.
XX  11-APR-2001; 2001US-0282992P.
XX  11-APR-2001; 2001US-0283083P.
XX  20-APR-2001; 2001US-0285133P.
XX  23-APR-2001; 2001US-0285749P.
XX  03-MAY-2001; 2001US-0288327P.
XX  03-MAY-2001; 2001US-0288504P.
XX  29-MAY-2001; 2001US-0284047P.
XX  30-MAY-2001; 2001US-0294473P.
XX  08-JUN-2001; 2001US-0296964P.
XX  18-JUN-2001; 2001US-0298959P.
XX  19-JUN-2001; 2001US-0299324P.
XX  13-AUG-2001; 2001US-0312020P.

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PR  16-AUG-2001; 2001US-0312889P.
PR  16-AUG-2001; 2001US-0312908P.
PR  21-AUG-2001; 2001US-0313390P.
PR  28-AUG-2001; 2001US-0315470P.
PR  31-AUG-2001; 2001US-0316447P.
PR  07-SEP-2001; 2001US-0318115P.
PR  07-SEP-2001; 2001US-0318118P.
PR  12-SEP-2001; 2001US-0318740P.
PR  19-SEP-2001; 2001US-0323379P.
PR  18-OCT-2001; 2001US-0330245P.
PR  18-OCT-2001; 2001US-0330308P.
PR  14-NOV-2001; 2001US-0332701P.
XX
XX  (CURA-) CURAGEN CORP.
XX
XX  Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkets RA;
XX  Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CB;
XX  Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
XX  Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX  WPI; 2002-706998/76.
XX
XX  New NOVX polypeptides and nucleic acids, useful for preventing or
XX  treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX  atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
XX  pharmacogenomics.
XX
XX  Example 2; SEQ ID NO 1372; 1498pp; English.
XX
XX  This invention relates to a novel nucleic acids, and encoded polypeptides
XX  thereof, which have properties related to the stimulation of biochemical
XX  or physiological responses in a cell, tissue, organ or organism.
XX  Specifically, it refers to the use of biologically active fragments for
XX  diagnostic and prognostic assays and furthermore in the treatment of
XX  diverse pathological conditions. The present invention describes novel
XX  human and murine NOVX proteins, as well as methods to modulate their
XX  expression using antisense oligos, ribozymes and peptide nucleic acids.
XX  The polypeptides, nucleic acid molecules and antibodies are useful in the
XX  manufacture of a medicament for treating metabolic disorders, diabetes,
XX  anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune
XX  and haematopoietic diseases as well as various dyslipidaemias.
XX  Accordingly, these molecules have many activities including anorectic,
XX  virucide, nootropic, antiinflammatory, neuroprotective, antilipemic,
XX  anabolic and cardiant. Furthermore, they are useful in screening assays
XX  to identify small molecules that modulate or inhibit, for example,
XX  neurogenesis, wound healing and angiogenesis. The nucleic acids are also
XX  used as in chromosome mapping, tissue typing, preventive medicine and
XX  pharmacogenomics. This oligonucleotide is a PCR primer used to amplify
XX  human NOVX DNA of the invention.
XX
XX  Sequence 22 BP; 4 A; 11 C; 0 G; 7 T; 0 U; 0 Other;
XX
XX  Query Match 59.2%; Score 14.8; DB 6; Length 22;
XX  Best Local Similarity 88.9%; Pred. No. 1e+04;
XX  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy  8 TCACCACCTCTCTTCCATC 25
   ||||| | | | | | | | |
Db  3 TCACCTCTCTCTTCCATC 20
   ||||| | | | | | | | |

RESULT 21
ADN42918
ID  ADN42918 standard; DNA; 22 BP.
XX
XX  ADN42918;
XX
XX  17-JUN-2004 (first entry)
XX
XX  Human NOV96a/b/c RTQ-PCR forward primer #1.
XX  Human; ss; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis; PCR;
XX  primer; RTQ PCR; real time quantitative PCR.

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```
XX OS Homo sapiens.
XX PN US2004033493-A1.
XX PD 19-FEB-2004.
XX PF 31-JAN-2002; 2002US-00072012.
XX PR 31-JAN-2001; 2001US-0265395P.
XX PR 31-JAN-2001; 2001US-0265412P.
XX PR 31-JAN-2001; 2001US-0265514P.
XX PR 31-JAN-2001; 2001US-0265517P.
XX PR 02-FEB-2001; 2001US-0266406P.
XX PR 05-FEB-2001; 2001US-0266767P.
XX PR 07-FEB-2001; 2001US-0266975P.
XX PR 07-FEB-2001; 2001US-0267057P.
XX PR 08-FEB-2001; 2001US-0267459P.
XX PR 09-FEB-2001; 2001US-0267823P.
XX PR 15-FEB-2001; 2001US-0268974P.
XX PR 26-FEB-2001; 2001US-0271664P.
XX PR 27-FEB-2001; 2001US-0271839P.
XX PR 27-FEB-2001; 2001US-0271855P.
XX PR 02-MAR-2001; 2001US-0272789P.
XX PR 02-MAR-2001; 2001US-0273046P.
XX PR 14-MAR-2001; 2001US-0275925P.
XX PR 14-MAR-2001; 2001US-0275947P.
XX PR 14-MAR-2001; 2001US-0275950P.
XX PR 14-MAR-2001; 2001US-0275989P.
XX PR 15-MAR-2001; 2001US-0276448P.
XX PR 15-MAR-2001; 2001US-0276450P.
XX PR 16-MAR-2001; 2001US-0276397P.
XX PR 16-MAR-2001; 2001US-0276768P.
XX PR 20-MAR-2001; 2001US-0278652P.
XX PR 26-MAR-2001; 2001US-0278775P.
XX PR 26-MAR-2001; 2001US-0278778P.
XX PR 29-MAR-2001; 2001US-0279882P.
XX PR 29-MAR-2001; 2001US-0279884P.
XX PR 30-MAR-2001; 2001US-0280147P.
XX PR 11-APR-2001; 2001US-0282992P.
XX PR 11-APR-2001; 2001US-0283083P.
XX PR 20-APR-2001; 2001US-0285133P.
XX PR 23-APR-2001; 2001US-0285749P.
XX PR 03-MAY-2001; 2001US-0288327P.
XX PR 03-MAY-2001; 2001US-0288504P.
XX PR 29-MAY-2001; 2001US-0294047P.
XX PR 30-MAY-2001; 2001US-0294473P.
XX PR 08-JUN-2001; 2001US-0296964P.
XX PR 18-JUN-2001; 2001US-0298959P.
XX PR 19-JUN-2001; 2001US-0299324P.
XX PR 13-AUG-2001; 2001US-0312020P.
XX PR 16-AUG-2001; 2001US-0312889P.
XX PR 16-AUG-2001; 2001US-0312908P.
XX PR 21-AUG-2001; 2001US-0313930P.
XX PR 28-AUG-2001; 2001US-0315470P.
XX PR 31-AUG-2001; 2001US-0316447P.
XX PR 07-SEP-2001; 2001US-0318115P.
XX PR 07-SEP-2001; 2001US-0318118P.
XX PR 12-SEP-2001; 2001US-0318740P.
XX PR 19-SEP-2001; 2001US-0323379P.
XX PR 18-OCT-2001; 2001US-0330245P.
XX PR 18-OCT-2001; 2001US-0330308P.
XX PR 14-NOV-2001; 2001US-0332701P.
XX PR (TCHE/) TCHERNEV V T.
XX PA (SPYT/) SPYTEK K A.
XX PA (ZERH/) ZERHUSEN B D.
XX PA (PATT/) PATTURAJAN M.
XX PA (SHIM/) SHIMKETS R A.
XX PA (LILL/) LI L.
XX PA (GANG/) GANGOLLI E A.
XX PA (PADI/) PADIGARU M.
XX PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENNA/) PENNA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEFLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
XX Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
PI Li L, Gangolli EA, Padigar M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grosse WM, Alsbrook JP, Lepley DW, Rieger DK, Burgess CE;
XX WPI; 2004-180039/17.
XX Isolated NOVX polypeptides and polynucleotides, useful for preventing
PT diagnosing and/or treating cancer, diabetes, cardiomyopathy and
PT atherosclerosis.
XX Example 2; SEQ ID NO 1372; 1309pp; English.
XX The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99,
CC including splice variants) and the nucleic acids (NA) that encode them.
CC Also included are the mature NOVX proteins (and their encoding
CC polynucleotides), a vector comprising NOVX NA, a cell comprising the
CC vector, an antibody that binds immunospecifically to NOVX, determining
CC the presence or amount of NOVX in a sample, determining the presence or
CC amount of NOVX NA in a sample, identifying an agent that binds to NOVX,
CC modulating the activity of NOVX, treating or preventing a disease
CC disorder, determining the presence of or predisposition to a disease
CC associated with altered levels of NOVX and treating a pathological state
CC in a mammal comprising administering a polypeptide which is at least 95%
CC identical to NOVX (or fragment). NOVX and NA may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,
CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and
CC antagonists may also be used to down regulate expression and activity of
CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for
CC detecting the presence of NOVX in samples (e.g. by enzyme linked
CC immunosorbent assay (ELISA)). The agents and methods may be used in this
CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
CC and/or atherosclerosis. The present sequence is a real time quantitative
CC PCR (RTQ PCR) primer for tissue specific expression studies for a NOVX
CC gene.
XX Sequence 22 BP; 4 A; 11 C; 0 G; 7 T; 0 U; 0 Other;
SQ Query Match 59.2%; Score 14.8; DB 12; Length 22;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TCACACATCTCTTCATC 25
Db 3 TCACCTCTCTCTTCATC 20
RESULT 22
AAZ34011/c
ID AAZ34011 standard; DNA; 24 BP.
XX AC AAZ34011;
XX DT 07-DEC-1999 (first entry)
XX DE Human PRO352 PCR reverse primer 2.
XX XX
```

KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein; ss.

OS Synthetic.
OS Homo sapiens.

PN WO9946281-A2.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.

PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-00404220.

PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078910P.

PR 20-MAR-1998; 98US-0078936P.

PR 20-MAR-1998; 98US-0078939P.

PR 25-MAR-1998; 98US-0079294P.

PR 26-MAR-1998; 98US-0079656P.

PR 27-MAR-1998; 98US-0079663P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079689P.

PR 27-MAR-1998; 98US-0079728P.

PR 27-MAR-1998; 98US-0079786P.

PR 30-MAR-1998; 98US-0079920P.

PR 30-MAR-1998; 98US-0079923P.

PR 31-MAR-1998; 98US-0080105P.

PR 31-MAR-1998; 98US-0080107P.

PR 31-MAR-1998; 98US-0080165P.

PR 31-MAR-1998; 98US-0080172P.

PR 01-APR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

PR 01-APR-1998; 98US-0080328P.

PR 01-APR-1998; 98US-0080333P.

PR 01-APR-1998; 98US-0080334P.

PR 08-APR-1998; 98US-0081049P.

PR 08-APR-1998; 98US-0081070P.

PR 08-APR-1998; 98US-0081071P.

PR 09-APR-1998; 98US-0081195P.

PR 09-APR-1998; 98US-0081203P.

PR 09-APR-1998; 98US-0081229P.

PR 15-APR-1998; 98US-0081817P.

PR 15-APR-1998; 98US-0081838P.

PR 15-APR-1998; 98US-0081952P.

PR 15-APR-1998; 98US-0081955P.

PR 21-APR-1998; 98US-0082568P.

PR 21-APR-1998; 98US-0082569P.

PR 22-APR-1998; 98US-0082700P.

PR 22-APR-1998; 98US-0082704P.

PR 22-APR-1998; 98US-0082804P.

PR 23-APR-1998; 98US-0082767P.

PR 23-APR-1998; 98US-0082766P.

PR 27-APR-1998; 98US-0083336P.

PR 28-APR-1998; 98US-0083322P.

PR 29-APR-1998; 98US-0083392P.

PR 29-APR-1998; 98US-0083495P.

PR 29-APR-1998; 98US-0083499P.

PR 29-APR-1998; 98US-0083500P.

PR 29-APR-1998; 98US-0083545P.

PR 29-APR-1998; 98US-0083554P.

PR 29-APR-1998; 98US-0083558P.

PR 29-APR-1998; 98US-0083559P.

PR 30-APR-1998; 98US-0083742P.

PR 05-MAY-1998; 98US-0084366P.

PR 06-MAY-1998; 98US-0084414P.

PR 06-MAY-1998; 98US-0084441P.

PR 07-MAY-1998; 98US-0084598P.

PR 07-MAY-1998; 98US-0084600P.

PR 07-MAY-1998; 98US-0084627P.

PR 07-MAY-1998; 98US-0084637P.

PR 07-MAY-1998; 98US-0084639P.

PR 07-MAY-1998; 98US-0084640P.

PR 07-MAY-1998; 98US-0084643P.

PR 13-MAY-1998; 98US-0085323P.

PR 13-MAY-1998; 98US-0085338P.

PR 13-MAY-1998; 98US-0085339P.

PR 15-MAY-1998; 98US-0085573P.

PR 15-MAY-1998; 98US-0085579P.

PR 15-MAY-1998; 98US-0085580P.

PR 15-MAY-1998; 98US-0085582P.

PR 15-MAY-1998; 98US-0085689P.

PR 15-MAY-1998; 98US-0085697P.

PR 15-MAY-1998; 98US-0085700P.

PR 15-MAY-1998; 98US-0085704P.

PR 18-MAY-1998; 98US-0086023P.

PR 22-MAY-1998; 98US-0086392P.

PR 22-MAY-1998; 98US-0086414P.

PR 22-MAY-1998; 98US-0086430P.

PR 22-MAY-1998; 98US-0086486P.

PR 28-MAY-1998; 98US-0087098P.

PR 28-MAY-1998; 98US-0087106P.

PR 28-MAY-1998; 98US-0087208P.

PR 30-JUL-1998; 98US-0094651P.

PR 11-SEP-1998; 98US-0100038P.

XX (GETH) GENENTECH INC.

XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI; 1999-551358/46.

XX New secreted and transmembrane polypeptides and their polynucleotides,

PT useful for treating blood coagulation disorders, cancers and cellular

PT adhesion disorders.

XX Example 23; Page 200; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides

CC and their polynucleotides. The nucleotide sequences are useful as sources

CC of probes, primers, for chromosome mapping, and for generation of

CC antisense sequences. They can also be used to create transgenic animals.

CC The proteins can be used to treat a variety of diseases and disorders.

CC depending on their function. Diseases that may be treated include blood

CC coagulation disorders, cancers and cellular adhesion disorders. They may

CC also be used to raise antibodies. AAZ33891 to AAZ4338, and AAY41685 to

CC AAY41774 represent polynucleotide and polypeptide sequence given in the

CC exemplification of the present invention

XX SQ Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.8; DB 2; Length 24;

Best Local Similarity 88.9%; Pred. No. 1e+04;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTC 21

Db 23 CACATCACCACCTCTCTTC 6

RESULT 23

AAC78692/c

ID AAC78692 standard; DNA; 24 BP.

XX AAC78692;

AC AAC78692;

DT 08-FEB-2001 (first entry)

XX Human PRO352 reverse PCR primer SEQ ID NO.142.

DE Human PRO352 reverse PCR primer SEQ ID NO.142.

XX

KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
KW expressed sequence tag; detection; cancer; PCR primer; probe; ss.
OS Homo sapiens.
XX WO200053756-A2.
XX 14-SEP-2000.
XX 18-FEB-2000; 2000WO-US004341.
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 29-MAR-1999; 99US-0126773P.
XX 21-APR-1999; 99US-0130232P.
XX 28-APR-1999; 99US-0131445P.
XX 14-MAY-1999; 99US-0134287P.
XX 23-JUN-1999; 99US-0141037P.
XX 26-JUL-1999; 99US-0145698P.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 16-DEC-1999; 99WO-US030095.
XX 30-DEC-1999; 99WO-US031243.
XX 05-JAN-2000; 2000WO-US031274.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fillvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart JA, Tumas D, Williams PW, Wood WI;
XX WPI; 2000-611443/58.
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX Example 23; Page 253; 636pp; English.
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytosstatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;
SQ Query Match 59.2%; Score 14.8; DB 3; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CTCATCACACCTCTTC 21
Db 23 CACATCACACCTCTTC 6
RESULT 24
ACA63579/c
ID ACA63579 standard; DNA; 24 BP.
XX

AC ACA63579;
XX 16-JUN-2003 (first entry)
DE Novel human secreted and transmembrane protein related primer #71.
XX Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing; PCR; primer; ss.
OS Homo sapiens.
XX US2002192706-A1.
XX 19-DEC-2002.
XX 24-OCT-2001; 2001US-00999832.
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066364P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-00040220.
XX 20-MAR-1998; 98US-0078888P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079689P.
XX 27-MAR-1998; 98US-0079728P.
XX 27-MAR-1998; 98US-0079786P.
XX 30-MAR-1998; 98US-0079920P.
XX 30-MAR-1998; 98US-0079923P.
XX 31-MAR-1998; 98US-0080105P.
XX 31-MAR-1998; 98US-0080107P.
XX 31-MAR-1998; 98US-0080165P.
XX 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080327P.
XX 01-APR-1998; 98US-0080328P.
XX 01-APR-1998; 98US-0080333P.
XX 01-APR-1998; 98US-0080334P.
XX 08-APR-1998; 98US-0081049P.
XX 08-APR-1998; 98US-0081070P.
XX 08-APR-1998; 98US-0081071P.
XX 09-APR-1998; 98US-0081195P.
XX 09-APR-1998; 98US-0081203P.
XX 15-APR-1998; 98US-0081229P.
XX 15-APR-1998; 98US-0081817P.
XX 15-APR-1998; 98US-0081819P.
XX 15-APR-1998; 98US-0081838P.
XX 15-APR-1998; 98US-0081952P.
XX 21-APR-1998; 98US-0081955P.
XX 21-APR-1998; 98US-0082568P.
XX 21-APR-1998; 98US-0082569P.
XX 22-APR-1998; 98US-0082700P.
XX 22-APR-1998; 98US-0082704P.
XX 22-APR-1998; 98US-0082797P.
XX 22-APR-1998; 98US-0082804P.
XX 23-APR-1998; 98US-0082796P.
XX 07-OCT-1998; 98WO-US021141.

PR 12-APR-1999; 99US-00284291.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380142.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000US-00709238.
 PR 27-NOV-2000; 2000US-00723749.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-0074259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 22-MAR-2001; 2001US-00816920.
 PR 22-MAR-2001; 2001WO-US009552.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00870792.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 30-JUL-2001; 2001US-00918585.
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Klijavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2003-328499/31.
 XX
 XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
 PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
 PT modulators of receptor-ligand interactions.
 XX
 XX Disclosure; SEQ ID NO 142; 55pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane
 CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
 CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
 CC linking a bioactive molecule to a cell. The PRO polypeptide or an
 CC antibody against it is useful for modulating a biological activity of a
 CC cell. The PRO polypeptide is useful in industrial applications including

CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
 CC polypeptide is also useful as a thrombolytic agent, interferon,
 CC interleukin, erythropoietin, colony stimulating factor and other
 CC cytokines. The PRO polypeptide is useful for treating disease such as
 CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
 CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
 CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
 CC Parkinson's disease; cardiovascular disease e.g. hypertension and
 CC myocardial ischaemia; kidney disease e.g. renal failure and
 CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
 CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
 CC bowel disease; reproductive disorders e.g. premature labour and
 CC preclampsia; carcinogenesis. The present sequence represents a PRO
 CC polypeptide associated oligonucleotide of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=20020177553
 XX
 SQ Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;
 Query Match 59.2%; Score 14.8; DB 8; Length 24;
 Best Local Similarity 88.9%; Pred. No. 1e+04; Mismatches 2; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CTCATCACCACCTCTCTTC 21
 Db 23 CACATCACCACCTCTTC 6
 RESULT 26
 ABX92383/c
 ID ABX92383 standard; DNA; 24 BP.
 XX
 AC ABX92383;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 XX Human PRO DNA PCR primer SEQ ID NO 142.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW immune disorder; diabetes; hyperinsulinaemia; hypo-insulinaemia;
 KW cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
 KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;
 XX cardiant; PCR; primer; ss.
 OS Homo sapiens.
 XX
 XX US2002169284-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 16-OCT-2001; 2001US-00978697.
 XX
 PR 26-MAY-1981; 81US-00267213.
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0084249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0065364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.


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PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-0021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-00204855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99US-0000106.
PR 05-JAN-1999; 99US-00254465.
PR 08-MAR-1999; 99US-0005028.
PR 10-MAR-1999; 99US-00285686.
PR 10-MAR-1999; 99US-000505190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-00310733.
PR 02-JUN-1999; 99US-00102252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99US-00283113.
PR 02-DEC-1999; 99US-0028551.
PR 02-DEC-1999; 99US-00285565.
PR 16-DEC-1999; 99US-0030095.
PR 30-DEC-1999; 99US-0031274.
PR 05-JAN-2000; 2000US-0000219.
PR 06-JAN-2000; 2000US-0000277.
PR 06-JAN-2000; 2000US-0000376.
PR 11-FEB-2000; 2000US-0003565.
PR 18-FEB-2000; 2000US-0004341.
PR 24-FEB-2000; 2000US-0005004.
PR 01-MAR-2000; 2000US-0005601.
PR 02-MAR-2000; 2000US-0005841.
PR 10-MAR-2000; 2000US-0006319.
PR 21-MAR-2000; 2000US-0007532.
PR 30-MAR-2000; 2000US-0008439.
PR 17-MAY-2000; 2000US-0013705.
PR 22-MAY-2000; 2000US-0014042.
PR 30-MAY-2000; 2000US-0014941.
PR 02-JUN-2000; 2000US-0015264.
PR 28-JUL-2000; 2000US-0020710.
PR 24-AUG-2000; 2000US-0023328.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000US-0030873.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000US-0032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.

PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001US-00816920.
PR 10-MAY-2001; 2001US-00854552.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-00886342.
PR 29-JUN-2001; 2001US-00886342.
PR 09-JUL-2001; 2001US-00886342.
PR 30-JUL-2001; 2001US-00886342.
PR 30-JUL-2001; 2001US-00886342.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-341189/32.
XX New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
XX PRO1559), useful for treating or diagnosing e.g. cancers,
XX atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
XX sclerosis in mammals.
XX Example 23; Page 135; 460pp; English.
XX The invention relates to a new isolated nucleic acid molecule comprising a
XX sequence with at least 80% identity to: (a) a nucleotide encoding any of
XX 94 PRO polypeptides whose sequences are fully defined in the
XX specification; or (b) any of 94 nucleotide sequences fully defined in the
XX specification; or the full length coding sequence of any these 94
XX nucleotide sequences. Also included are an isolated PRO polypeptide
XX scoring at least 80% positives when compared to any of the PRO
XX polypeptide sequences cited above (or an isolated PRO polypeptide having
XX at least 80% amino acid sequence identity to: (a) an amino acid sequence
XX encoded by the nucleotide deposited with ATCC numbers listed in the
XX specification; (b) the PRO polypeptide, lacking its associated signal
XX peptide; or (c) an extracellular domain of the PRO polypeptide, with or
XX lacking its associated signal peptide), a vector comprising the nucleic
XX acid molecule, a host cell comprising the vector (and producing a PRO
XX polypeptide), a chimeric molecule comprising the PRO polypeptide fused
XX to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
XX polypeptides or polynucleotides are useful as pharmaceuticals,
XX diagnostics, biosensors or bioeffectors. These are particularly useful for
XX detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
XX colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
XX neurosis, atherosclerosis, infertility, premature aging, psoriasis,
XX inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
XX stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
XX PRO polypeptides are useful in drug screening, particularly as targets
XX for therapeutic intervention in these diseases, and in the diagnostic
XX determination of the presence of these diseases. The PRO polypeptides are
XX also useful as molecular weight markers, or for chromosome
XX identification. The PRO genes are useful as hybridisation probes, or for
XX screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
XX also be used in gene therapy, particularly for replacing a defective
XX gene. The present sequence is a PCR primer used in the isolation of a
XX cDNA encoding a PRO polypeptide
XX Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;
SQ Query Match 59.2%; Score 14.8; DB 8; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 4 CTCATCACCACCTCTCTTC 21
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Db      23 CACATCACCACCTCTTC 6
RESULT 28
ADA24681/c
ID ADA24681 standard; DNA; 24 BP.
XX
AC ADA24681;
XX
XX
DT 20-NOV-2003 (first entry)
XX
DE Secreted and transmembrane PRO protein associated primer #73.
XX
KW Human; secreted and transmembrane protein; PRO; tissue typing;
KW chromosome identification; vaccine; cancer; retinal disorder;
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW wound healing; obesity; diabetes; hearing loss;
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW haemoglobin associated disorder; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003050241-A1.
XX
PD 13-MAR-2003.
XX
XX
PF 16-OCT-2001; 2001US-00978564.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0085311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081839P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083352P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 28-MAY-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 26-JUN-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0094651P.
PR 30-JUL-1998; 98US-0100038P.
PR 11-SEP-1998; 98WO-US021141.
PR 07-OCT-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 20-NOV-1998; 98US-0113296P.
PR 22-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
PR 12-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 28-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 29-OCT-1999; 99US-0162506P.
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PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-521814/49.
XX
XX New isolated PRO polypeptides for example extracellular, secreted and
PT membrane bound proteins, useful for modulating the biological activities
PT of cells and for treating, for example diabetes, cancer, rheumatoid
PT arthritis, and hearing loss.
XX
XX Example 23; Page 143; 461pp; English.
XX
XX The invention describes an isolated secreted and transmembrane (PRO)
CC polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
CC polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
CC useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
CC useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
CC useful for linking a bioactive molecule to a cell expressing a PRO337
CC polypeptide, and PRO337 is useful for linking a bioactive molecule to a
CC cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
CC bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739
CC polypeptide, and PRO735, PRO700 and PRO739 polypeptides are useful for
Query Match 59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 CTCATCACCACTCTCTTC 21
Db 23 CACATCACCACTCTCTTC 6
RESULT 29
ACD29725/c
ID ACD29725 standard; DNA; 24 BP.
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KW primer; ss; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; tissue typing; human; PCR.

OS Homo sapiens.

XX US200305216-A1.

PN

PD

XX 20-MAR-2003.

XX 17-OCT-2001; 2001US-00978824.

XX 21-MAY-1996; 96US-0018049P.

PR 17-OCT-1997; 97US-0062250P.

PR 03-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0068364P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.

PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-0004022O.

PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078910P.

PR 20-MAR-1998; 98US-0078936P.

PR 20-MAR-1998; 98US-0078939P.

PR 25-MAR-1998; 98US-0079294P.

PR 26-MAR-1998; 98US-0079656P.

PR 27-MAR-1998; 98US-0079663P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079689P.

PR 27-MAR-1998; 98US-0079728P.

PR 27-MAR-1998; 98US-0079786P.

PR 30-MAR-1998; 98US-0079920P.

PR 30-MAR-1998; 98US-0079923P.

PR 31-MAR-1998; 98US-0080105P.

PR 31-MAR-1998; 98US-0080107P.

PR 31-MAR-1998; 98US-0080163P.

PR 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

PR 01-APR-1998; 98US-0080328P.

PR 01-APR-1998; 98US-0080333P.

PR 01-APR-1998; 98US-0080334P.

PR 08-APR-1998; 98US-0081070P.

PR 09-APR-1998; 98US-0081195P.

PR 09-APR-1998; 98US-0081203P.

PR 09-APR-1998; 98US-0081223P.

PR 15-APR-1998; 98US-0081817P.

PR 15-APR-1998; 98US-0081819P.

PR 15-APR-1998; 98US-0081838P.

PR 15-APR-1998; 98US-0081952P.

PR 21-APR-1998; 98US-0081955P.

PR 21-APR-1998; 98US-0082568P.

PR 22-APR-1998; 98US-0082569P.

PR 22-APR-1998; 98US-0082700P.

PR 22-APR-1998; 98US-0082704P.

PR 22-APR-1998; 98US-0082797P.

PR 23-APR-1998; 98US-0082804P.

PR 27-APR-1998; 98US-0082796P.

PR 28-APR-1998; 98US-0083336P.

PR 29-APR-1998; 98US-0083322P.

PR 29-APR-1998; 98US-0083392P.

PR 29-APR-1998; 98US-0083495P.

PR 29-APR-1998; 98US-0083496P.

PR 29-APR-1998; 98US-0083499P.

PR 29-APR-1998; 98US-0083500P.

PR 29-APR-1998; 98US-0083545P.

PR 29-APR-1998; 98US-0083554P.

PR 29-APR-1998; 98US-0083558P.

PR 29-APR-1998; 98US-0083559P.

PR 30-APR-1998; 98US-0083742P.

PR 05-MAY-1998; 98US-0084366P.

PR 06-MAY-1998; 98US-0084414P.

PR 06-MAY-1998; 98US-0084441P.

PR 07-MAY-1998; 98US-0084598P.

PR 07-MAY-1998; 98US-0084600P.

PR 07-MAY-1998; 98US-0084627P.

PR 07-MAY-1998; 98US-0084637P.

PR 07-MAY-1998; 98US-0084639P.

PR 07-MAY-1998; 98US-0084640P.

PR 07-MAY-1998; 98US-0084643P.

PR 13-MAY-1998; 98US-0085323P.

PR 13-MAY-1998; 98US-0085338P.

PR 15-MAY-1998; 98US-0085339P.

PR 15-MAY-1998; 98US-0085573P.

PR 15-MAY-1998; 98US-0085579P.

PR 15-MAY-1998; 98US-0085580P.

PR 15-MAY-1998; 98US-0085582P.

PR 15-MAY-1998; 98US-0085689P.

PR 15-MAY-1998; 98US-0085697P.

PR 15-MAY-1998; 98US-0085700P.

PR 15-MAY-1998; 98US-0085704P.

PR 18-MAY-1998; 98US-0086023P.

PR 22-MAY-1998; 98US-0086392P.

PR 22-MAY-1998; 98US-0086414P.

PR 22-MAY-1998; 98US-0086430P.

PR 22-MAY-1998; 98US-0086486P.

PR 28-MAY-1998; 98US-0087098P.

PR 28-MAY-1998; 98US-0087106P.

PR 26-JUN-1998; 98US-00105413.

PR 26-JUN-1998; 98US-0090863P.

PR 26-JUN-1998; 98US-0091010P.

PR 01-JUL-1998; 98US-0091359P.

PR 30-JUL-1998; 98US-0094651P.

PR 11-SEP-1998; 98US-0100038P.

PR 07-OCT-1998; 98US-00168978.

PR 07-OCT-1998; 98US-001842141.

PR 02-NOV-1998; 98US-00184216.

PR 06-NOV-1998; 98US-00187368.

PR 20-NOV-1998; 98US-0109304P.

PR 20-NOV-1998; 98US-0109304P.

PR 07-DEC-1998; 98US-00202054.

PR 22-DEC-1998; 98US-00218517.

PR 22-DEC-1998; 98US-0113296P.

PR 23-DEC-1998; 98US-0113621P.

PR 05-JAN-1999; 99US-0000106.

PR 05-MAR-1999; 99US-00254465.

PR 08-MAR-1999; 99US-0005028.

PR 10-MAR-1999; 99US-00265686.

PR 10-MAR-1999; 99US-0005190.

PR 12-MAR-1999; 99US-00267213.

PR 12-MAR-1999; 99US-0123957P.

PR 29-MAR-1999; 99US-0126773P.

PR 12-APR-1999; 99US-00284291.

PR 21-APR-1999; 99US-0130232P.

PR 26-APR-1999; 99US-0131022P.

PR 28-APR-1999; 99US-0131445P.

PR 14-MAY-1999; 99US-00311832.

PR 14-MAY-1999; 99US-0134287P.

PR 02-JUN-1999; 99US-0010733.

PR 16-JUN-1999; 99US-0012252.

PR 23-JUN-1999; 99US-0139557P.

PR 07-JUL-1999; 99US-0141037P.

PR 26-JUL-1999; 99US-0142680P.

PR 28-JUL-1999; 99US-0145698P.

PR 25-AUG-1999; 99US-0146222P.

PR 25-AUG-1999; 99US-00380137.

PR 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380142.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99US-0028313.

PR 02-DEC-1999; 99US-0028551.

```
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000227.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 21-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
Query Match 59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred.No.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CTCATCACCACCTCTTTC 21
Db 23 CACATCACCACCTCTTTC 6
RESULT 31
ACD29140/c
ID ACD29140 standard; DNA; 24 BP.
XX
XX ACD29140;
XX
XX 27-AUG-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein related primer #71.
XX
XX Human; secreted and transmembrane protein; PRO; viral infection;
KW tumour growth; retinal disorder; injury; sight loss;
KW retinitis pigmentosa; age-related macular degeneration;
KW sport-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;
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KW cardiac- insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW Refsum's disease; PCR; primer; ss.
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XX US2003049633-A1.
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cell death; neuropathy; neuropathy related disease;
Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
chromosome mapping; gene mapping; genetic disorder; septic shock;
antibacterial; immunosuppressive; neuroprotective; PCR; primer; ss.
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PF 16-OCT-2001; 2001US-00978608.
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PR
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Db 23 CACATCACCACCTCTTC 6

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XX
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KW cell death; neuropathy; neuropathy related disease;

KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;

KW chromosome mapping; gene mapping; genetic disorder; septic shock;

KW antibacterial; immunosuppressive; neuroprotective; PCR; primer; ss.

XX
XX Homo sapiens.

OS

XX

PN US2003083248-A1.

XX

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PR 06-JAN-2000; 2000WO-US000376.
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PR 21-MAR-2000; 2000WO-US007532.
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PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
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PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
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( GETH ) GENENTECH INC.
XX
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XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrata N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
Godard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2003-755118/71.
XX
XX New PRO polypeptides useful for treating peripheral neuropathy,
XX or AIDS-associated syndrome.
XX
XX Example 23; Page 137; 425pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for linking
XX bioactive molecules to cells expressing PRO polypeptides, for modulating
XX biological activities of cells expressing PRO polypeptides, and for
XX identifying agonists or antagonists. The bioactive molecule may be a
XX toxin, radiolabel or antibody, and cause cell death. The PRO polypeptides
XX are useful for treating neuropathy and neuropathy related diseases such
XX as Charcot-Marie-Tooth disorder, Refsum's disease, and Krabbe's disease.
XX The polynucleotide sequences encoding PRO polypeptides are useful as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, in the preparation of PRO polypeptides, for
Query Match 59.2%; Score 14.6; DB 10; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
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XX 18-DEC-2003 (first entry)
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XX
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XX ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnary;
XX auditory; tumour growth; retinal disorder; sports-related joint problem;
XX articular cartilage defects; osteoarthritis; rheumatoid arthritis;
XX wound healing; hearing loss; primer.
XX
XX Homo sapiens.
XX
XX US2003054986-A1.
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XX 20-MAR-2003.
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XX 16-OCT-2001; 2001US-00981915.
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XX 12-MAR-1998; 98US-0077791P.
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XX (GETH ) GENENTECH INC.
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Query Match 59.2%; Score 14.8; DB 10; Length 24;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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wound healing; hearing loss; primer.
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PR	18-FEB-2000;	2000WO-US004341.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	21-MAR-2000;	2000WO-US007532.
PR	30-MAR-2000;	2000WO-US008439.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	28-JUL-2000;	2000WO-US020710.
PR	24-AUG-2000;	2000WO-US023328.
PR	08-NOV-2000;	2000US-00709238.
PR	27-NOV-2000;	2000US-00723749.
PR	01-DEC-2000;	2000WO-US032678.
PR	20-DEC-2000;	2000US-00747259.
PR	28-DEC-2000;	2000WO-US034956.
PR	28-FEB-2001;	2001WO-US006520.
PR	22-MAR-2001;	2001US-00816744.
PR	22-MAR-2001;	2001US-00816920.
PR	22-MAR-2001;	2001WO-US009552.
PR	10-MAY-2001;	2001US-00854208.
PR	10-MAY-2001;	2001US-00854280.
PR	25-MAY-2001;	2001WO-US017092.
PR	01-JUN-2001;	2001US-00872035.
PR	05-JUN-2001;	2001WO-US017800.
PR	14-JUN-2001;	2001US-00882636.
PR	19-JUN-2001;	2001US-00886342.
PR	20-JUN-2001;	2001WO-US019692.
PR	29-JUN-2001;	2001WO-US021066.
PR	09-JUL-2001;	2001WO-US021735.

PR 30-JUL-2001; 2001US-00918585.
XX (GETH) GENENTECH INC.
PA
XX

Query Match 59.2%; Score 14.8; DB 10; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTCATCACACCTCTCTC 21
Db 23 CACATCACACCTCTCTC 6

RESULT 37
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ID ADC66614 standard; DNA; 24 BP.
XX
AC ADC66614;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRO 352 PCR primer #5.

XX
KW vulnary; virucide; neuroprotective; cytostatic; gene therapy;
KW tumour cell proliferation inhibitor;
KW secreted and transmembrane protein; PRO; viral infection; wound healing;
KW tissue growth; muscle generation; muscle regeneration;
KW amytrophic lateral sclerosis; neuropathy; AIDS-associated neuropathy;
KW diabetic peripheral neuropathy; chromosome identification; antagonist;
KW tissue typing; immunohistochemical staining; primer; ss.

XX Homo sapiens.

XX US2003060406-A1.

XX 27-MAR-2003.

XX 30-JUL-2001; 2001US-00918585.

XX 17-OCT-1997; 97US-0062250P.

PR 03-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066364P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.

PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-00040220.

PR 20-MAR-1998; 98US-0078888P.

PR 20-MAR-1998; 98US-0078910P.

PR 20-MAR-1998; 98US-0078936P.

PR 20-MAR-1998; 98US-0078939P.

PR 25-MAR-1998; 98US-0079294P.

PR 26-MAR-1998; 98US-0079656P.

PR 27-MAR-1998; 98US-0079663P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079689P.

PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265886.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
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PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
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PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-596568/56.

XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them, useful for treating wound healing, tissue growth and
XX muscle generation and regeneration, amyotrophic lateral sclerosis or
XX neuropathy.

XX Example 23; SEQ ID NO 142; 472pp; English.

CC The invention describes an isolated secreted and transmembrane PRO
CC polypeptide (I). PRO polypeptide such as PRO213, PRO700, PRO320 or PRO615
CC is useful in biotechnological and medical research, as well as in various
CC industrial applications. PRO polypeptide such as PRO300, PRO866, PRO703,
CC PRO708, PRO320, PRO351, PRO352, PRO381, PRO615, PRO618, PRO772, PRO853,
CC PRO860 or PRO846 is useful for therapeutic purposes. PRO363 is useful
CC therapeutically in vivo for lessening the effects of viral infection.
CC PRO200 is useful for the treatment of wound healing, tissue growth and
CC muscle generation and regeneration. PRO337 is useful for treating
CC amyotrophic lateral sclerosis, neuropathy, AIDS-associated neuropathy or
CC diabetic peripheral neuropathy. A polynucleotide (II) encoding (I) is
CC useful for generating transgenic animals or knockout animals which are
CC useful in the development and screening of therapeutically useful
CC reagents, as probes for generating a pool of sequences for identifying
CC related PRO coding sequences, and to construct hybridisation probes for
CC mapping the gene which encodes the PRO and for the genetic analysis of
CC individuals with genetic disorders, for recombinantly expressing (I) and
CC for chromosome identification. (I) is useful as molecular marker for
CC protein electrophoresis purposes, and as therapeutic agents. (I) is also
CC useful for screening compounds to identify those that mimic the PRO
CC polypeptide (agonists) or prevent the effect of the PRO polypeptide
CC (antagonists). (I) and (II) are useful for tissue typing. PRO antibodies
CC are useful for immunohistochemical staining and/or assay of sample
CC fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g.
CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. This sequence represents a human secreted and transmembrane PRO
CC protein associated primer.
XX
SQ Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.8; DB 10; Length 24;
Best Local Similarity 88.9%; Pred. No. le+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qv 4 CTCATCACCACTCTCTTC 21
| | | | | | | | | | | | | | | | | | | | | |
Db 23 CACATCACCACTCTCTTC 6

RESULT 38

ADC68738/c

ID ADC68738 standard; DNA; 24 BP.

XX ADC68738;

XX 18-DEC-2003 (first entry)

XX Human PRO 352 PCR primer #5.

XX Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytostatic;
KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
XX wound healing; hearing loss; primer.

XX Homo sapiens.

XX US2003064407-A1.

XX 03-APR-2003.

XX 24-OCT-2001; 2001US-00999834.

XX 17-OCT-1997; 97US-0062250P.

XX 03-NOV-1997; 97US-0064249P.

XX 13-NOV-1997; 97US-0065311P.

XX 21-NOV-1997; 97US-0066364P.

XX 10-MAR-1998; 98US-0077450P.

XX 11-MAR-1998; 98US-0077632P.

XX 11-MAR-1998; 98US-0077641P.

XX 11-MAR-1998; 98US-0077649P.

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PR 08-MAR-1999; 99US-00005028.
PR 10-MAR-1999; 99US-00285686.
PR 10-MAR-1999; 99US-00005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
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PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
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PR 27-NOV-2000; 2000US-00723749.

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PR 20-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
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PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH ) GENENTECH INC.
XX
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Query Match 59.2%; Score 14.8; DB 10; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CTCATCACCACCTCTCTTC 21
Db 23 CACATCACCACCTCTTC 6

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AC ADC62798;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRO 352 PCR primer #5.
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KW Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosstatic;
KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulneryary;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW wound healing; hearing loss; primer.
XX
OS Homo sapiens.
XX
FN US2003068648-A1.
XX
PD 10-APR-2003.
XX
PF 25-OCT-2001; 2001US-00013921.
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PR 14-MAY-1999; 99WO-US010733.
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PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
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PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2000WO-US034956.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
FA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini IA, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TJ, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-695924/66.
DR
XX
XX New isolated secreted and transmembrane PRO polypeptides, useful in the
PT Preparation of a medicament for treating a condition responsive to the
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS Example 23; SEQ ID NO 142; 467pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity

CC to an amino acid sequence chosen from 94 fully defined sequences as given
CC in the specification (including PRO lacking its associated signal
CC peptide, a PRO extracellular domain with or without its associated signal
CC peptide). Also included are nucleic acids encoding the PRO proteins
CC mentioned above, a vector comprising a PRO nucleic acid), a host cell
CC comprising the vector and producing PRO, a chimeric molecule comprising
CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
CC antibody. PRO337 polypeptide is useful for detecting a PRO4993
CC polypeptide in a sample suspected of containing PRO4993 polypeptide.
CC Similarly, PRO4993 polypeptide is useful for detecting PRO337
CC polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
CC PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting
CC PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a
CC bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive
CC molecule is the toxin, radiolabel, or an antibody. The bioactive molecule
CC causes death of the cell. PRO337 polypeptide is useful for linking a

Query Match 59.2%; Score 14.8; DB 10; Length 24;

Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACTCTCTTC 21

Db 23 CACATCACCACTCTCTTC 6

RESULT 40

ID ADC67863/c

AD ADC67863 standard; DNA; 24 BP.

XX AC ADC67863;

XX 18-DEC-2003 (first entry)

DE Human PRO 352 PCR primer #5.

XX Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytostatic;
KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW wound healing; hearing loss; primer.

XX Homo sapiens.

XX US2003069178-A1.

XX 10-APR-2003.

XX 16-OCT-2001; 2001US-00978423.

XX 17-OCT-1997; 97US-0062250P.

PR 03-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066364P.

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PR 11-MAR-1998; 98US-0077632P.

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PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.

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PR 20-MAR-1998; 98US-0078936P.

PR 20-MAR-1998; 98US-0078939P.

PR 25-MAR-1998; 98US-0079294P.

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PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1195.82 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-9

Perfect score: 25

Sequence: 1 CAACATCATCACCACTCTCTTCCATC 25

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_hic:*

4: gb_est3:*

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6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	14.2	56.8	29	TA133D12P	AL465919 T. brucei
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6	14	56.0	44	AZ9833982	AZ9833982 2M0265013
7	13.8	55.2	44	AZ340483	AZ340483 1M0072N19
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	31	12.8	51.2	37	1	AI188273	AI188273
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	33	12.8	51.2	39	9	TA110A12Q	TA110A12Q
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	36	12.8	51.2	42	7	CF920754	CF920754
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ALIGNMENTS

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ACCESSION BH627451
VERSION BH627451.1 GI:18440702
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 48)
Walbot, V.
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007071 column: 20
Class: transposon-tagged.
Location/Qualifiers
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/lab_host="DH10B"
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmmb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using

BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 62.4%; Score 15.6; DB 8; Length 48;
 Best Local Similarity 81.8%; Pred. No. 3.2e+04;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 Db 2 CTCCTCTCCCTCTCTTCAC 23

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ACCESSION AZ641286
 VERSION AZ641286.1 GI:11765116
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0503 row: C column: 14
 Seq primer: CACACAGGAACACTATGACC
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers

FEATURES

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 /mol_type="genomic DNA"
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 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 60.0%; Score 15; DB 8; Length 32;
 Best Local Similarity 78.3%; Pred. No. 5.4e+04;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ACTCATCACCACCTCTCTTCATC 25
 ||||| ||||| ||||| ||||| |||||
 Db 7 ACTCATCACCACCTCTCTAC 29

RESULT 3
 AA576280/c
 LOCUS
 DEFINITION nm060G01.s1 NCI CGAP Br3 Homo sapiens cDNA clone IMAGE:1072656 3', similar to gb:X63563 DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE (HUMAN);, mRNA sequence.

ACCESSION AA576280
 VERSION AA576280.1 GI:2350795
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 48)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-i@mail.nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Stratagene, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1214 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1. .48
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1072656"
 /sex="female"
 /tissue_type="breast tumor"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="NCI CGAP Br3"
 /notes="Organ: breast; Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Ductal breast tumor. 5' adaptor sequence: 5' GAATTCGGCAGCAG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 0.9 kb."

ORIGIN

Query Match 58.4%; Score 14.6; DB 1; Length 48;
 Best Local Similarity 81.0%; Pred. No. 8.6e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ACTCATCACCACCTCTCTTCCA 23
 ||||| ||||| ||||| ||||| |||||
 Db 47 ACACATCACCACCTCTCTACAA 27

```

RESULT 4
TA133D12P/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 133d12, forward sequence,
genomic survey sequence.
ACCESSION
AL465919
VERSION
AL465919.1 GI:11835041
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 29)
HALL, N., BOWMAN, S., LENNARD, N.J., DOGGETT, J., ATKIN, R.,
CHILLINGWORTH, C., ORMOND, D., HARRIS, B., EL-SAYED, N., HOU, L.,
MELVILLE, S.E., RAJANDREAM, M.A. and BARRELL, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhi@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
FEATURES
source
1..29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="133d12"

Query Match 56.8%; Score 14.2; DB 9; Length 29;
Best Local Similarity 84.2%; Pred. No. 1.2e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATCACCACTCTCTCCAT 24
Db 28 CTTACCCCTCCCTCCAT 10

RESULT 5
W69493/c
LOCUS
DEFINITION
W69493 z47g08.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
IMAGE:343838 3' similar to PIR:S24168 S24168 hypothetical protein -
human ;, mRNA sequence.
ACCESSION
W69493
VERSION
W69493.1 GI:1378774
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 34)
HILLIER, L., CLARK, N., DUBUQUE, T., ELLISTON, K., HAWKINS, M.,
HOLMAN, M., HULTMAN, M., KUCABA, T., LE, M., LENNON, G., MARRA, M.,
PARSONS, J., RIFKIN, L., ROHLFING, T., SOARES, M., TAN, F.,
TREVAISKIS, E., WATERSTON, R., WILLIAMSON, A., WOHLDMANN, P. and
WILSON, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK

TITLE
JOURNAL
COMMENT

```

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyt not found
Insert Length: 983 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 1.

Location/Qualifiers

FEATURES
source

```

1..34
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1269213"
/db_xref="taxon:9606"
/clone="IMAGE:343838"
/sex="unknown"
/dev_stages="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCCGACATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."

```

ORIGIN

```

Query Match 56.0%; Score 14; DB 7; Length 34;
Best Local Similarity 77.3%; Pred. No. 1.5e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

Qy 4 CTCATCACCACTCTCTCCATC 25

Db 25 CTCACACCACTCTCCACATC 4

RESULT 6

AZ983982/c

LOCUS

DEFINITION

2M0265013F Mouse 10kb plasmid UUC2M library Mus musculus genomic

clone UUC2M0265013 F, genomic survey sequence.

ACCESSION

AZ983982

VERSION

AZ983982.1 GI:13855209

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 44)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0265 row: 0 column: 13
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 44.

FEATURES

Location/Qualifiers
 1. .44
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0265013"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [GI4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 56.0%; Score 14; DB 8; Length 44;
 Best Local Similarity 77.3%; Pred. No. 1.5e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTCATCACCCTCTTCCATC 25
 |||||
 Db 42 CTCCTTTACCTCTTCCATC 21

RESULT 7

AZ340483
 LOCUS AZ340483 44 bp DNA linear GSS 29-SEP-2000
 DEFINITION lM0072N19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0072N19 F, genomic survey sequence.

ACCESSION AZ340483
 VERSION AZ340483.1 GI:10415782

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 44)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

Unpublished(2000)

JOURNAL

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0072 row: N column: 19
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 44.

FEATURES

Location/Qualifiers
 1. .44
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0072N19"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [GI4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.2%; Score 13.8; DB 8; Length 44;
 Best Local Similarity 88.2%; Pred. No. 1.9e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACATCATCACCCTCT 17
 |||||
 Db 23 CAACAGATCACCCTCT 39

RESULT 8

AG188152/c
 LOCUS AG188152 33 bp DNA linear GSS 06-MAR-2004
 DEFINITION Pan troglodytes DNA, clone: RP43-061L05.T7, genomic survey sequence.

ACCESSION AG188152
 VERSION AG188152.1 GI:45220321

KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes
 Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Pan.
 1 (bases 1 to 33)

REFERENCE

AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
 BAC end sequences of Library RP-43
 Unpublished

TITLE

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail:redstone@mail.krribb.re.kr, URL:http://pns.grc.krribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)

COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

LIBRARY

Sequencing: T7

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1..33

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-061L05.T7"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

FEATURES

Source

ORIGIN

Query Match 54.4%; Score 13.6; DB 9; Length 33;
Best Local Similarity 80.0%; Pred. No. 2.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTCATCACCACCTCTCTC 21

Db 28 ACCTCATCACCACCTCTC 9

RESULT 9

BZ377820

LOCUS

DEFINITION SALK_106264.42.05.x Arabidopsis thaliana DNA linear GSS 26-NOV-2002
Arabidopsis thaliana genomic clone SALK_106264.42.05.x, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

CONTACT: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..46

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_106264.42.05.x"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

ORIGIN

Query Match 54.4%; Score 13.6; DB 8; Length 46;
Best Local Similarity 80.0%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAATCATCACCACCTCTCTT 20

Db 16 CTACTAATCTCACTAATCTT 35

RESULT 10

BH866288

LOCUS

DEFINITION SALK_101113 Arabidopsis thaliana TDNA linear GSS 05-AUG-2002
thaliana genomic clone SALK_101113, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

CONTACT: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of Atlg59520.

Class: TDNA tagged.

Location/Qualifiers

1..48

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_101113"

/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 54.4%; Score 13.6; DB 8; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CATCACCACCTCTCTTCATC 25

Db 11 CATCTGGCTCTCTTCATC 30

RESULT 11

AI201105

LOCUS

DEFINITION qf69g04.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1755318
3' similar to gb:X68285 GLYCEROL KINASE (HUMAN);, mRNA sequence.

ACCESSION AI201105
 VERSION AI201105.1 GI:3753711
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 49)
 REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES
 source

1..49
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1755318"
 /sex="male"
 /lab_host="DH10B"
 /clone_lib="Soares testis NHT"

/note="Vector: p77T3p-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech
 Laboratories, Inc., and primed with a Not I - oligo(dT)
 primer [5',
 TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p77T3 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 54.4%; Score 13.6; DB 1; Length 49;
 Best Local Similarity 80.0%; Pred. No. 2.3e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TCATCACACTCTCTTCCAT 24
 ||||| ||||| ||||| |||||
 Db 16 TCATTACTGCTTCTTCCAT 35

RESULT 12
 AZ590062/c
 LOCUS
 DEFINITION 1M0399M23F Mouse 10kb plasmid UGCLM library Mus musculus genomic
 clone UUGCLM0399M23 F, genomic survey sequence.

ACCESSION AZ590062
 VERSION AZ590062.1 GI:11712252
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 42)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 JOURNAL
 COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0399 row: M column: 23
 Seq primer: CGTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 42.

FEATURES
 source

1..42
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0399M23"
 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 Kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 53.6%; Score 13.4; DB 8; Length 42;
 Best Local Similarity 73.3%; Pred. No. 2.8e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACTCTCTTCCATC 25
 ||||| ||||| ||||| |||||
 Db 40 AATCATTAATACACTCTTCTTC 18

RESULT 13
 AZ635993/c

LOCUS
 DEFINITION 1M0493E20R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGCLM0493E20 R, genomic survey sequence.

ACCESSION AZ635993
 VERSION AZ635993.1 GI:11758183
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0493 row: E column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0493E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
source
1. .25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0493E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 52.8%; Score 13.2; DB 8; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 CTCATCACACTCTCTTC 21
|||||
Db 20 CTCCTCTCTCTCTCTTC 3

RESULT 14
LOCUS AZ576137
DEFINITION AST-T33E0033 Genetrapp T47D Human Breast Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.
ACCESSION AZ576137
VERSION AZ576137.1 GI:11562448
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 39)
AUTHORS Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M., Bernardino,A., Durick,K. and Pollok,B.
TITLE Exon-trap tags from a T47D GenomeScreen(TM) Library
JOURNAL Unpublished (2000)

CONTACT Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The tagging element consisting of: 1) A promoterless beta-lactamase preceded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pamp-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.
Class: exon-trapped.
Location/Qualifiers
1. .39
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Carcinoma"
/cell_type="Epithelial"
/cell_line="T47D"
/clone_lib="Genetrapp T47D Human Breast Carcinoma Library"
/note="Organ: Breast; Vector: pamp-1; 3' RACE of total RNA from genetrapp pools; shotgun clone in pamp-1 and used to transform DH5-alpha competent bacteria."

ORIGIN
Query Match 52.8%; Score 13.2; DB 8; Length 39;
Best Local Similarity 83.3%; Pred. No. 3.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 ACTCATCACACTCTCTTC 20
|||||
Db 35 ACTCTTACCTCTCTCTTC 18

RESULT 15
LOCUS A1192173
DEFINITION A1192173.1 GI:3743382
ACCESSION A1192173
VERSION A1192173.1 GI:3743382
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: ccgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1730 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1722037"

oligo(dT) primer 5' ACTGGAGAAATTCGCGCGCCCTTTT TTTT TTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

RESULT 17	BH903423/c	BH903423	47 bp	DNA	linear	GSS	04-SEP-2002
LOCUS	BH903423/c	BH903423					
DEFINITION		SALK_102585.22.30.x Arabidopsis thaliana			TDNA insertion lines		
		Arabidopsis thaliana genomic clone SALK_102585.22.30.x, genomic			survey sequence.		
ACCESSION		BH903423					
VERSION		BH903423.1			GI:22714608		
KEYWORDS		GSS.					
SOURCE		Arabidopsis thaliana (thale cress)					
ORGANISM		Arabidopsis thaliana					

REFERENCE	1 (bases 1 to 47)
AUTHORS	Alonso, J.M., Jeske, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab, C., Leske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL	Unpublished (2001)
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g23970. Class: TDNA tagged.

```

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecot_type="Col-0"
/db_xref="taxon:3702"
/clone="SALK_102585.23.30.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

ORIGIN

Query Match          52.8%;   Score 13.2;   DB 8;   Length 47;
Best Local Similarity 83.3%;   Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CAACTCATCACCACCTTC 18
        ||||| ||||| |||||
Db      19  CAACTCTTCATCAGTCTC 2

RESULT 18
BZ766487
LOCUS
DEFINITION
SALK_137474.23.60.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_137474.23.60.x, genomic
survey sequence.
47 bp DNA linear GSS 13-MAR-2003

```

ACCESSION BZ766487
 VERSION BZ766487.1 GI:28939040
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 47)
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmerman, J., and Ecker, J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 5' end of
 At1g20200 and 300 bases of the 5' end of At1g20210.
 Class: TDNA tagged.
 FEATURES Location/Qualifiers
 source 1..47
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
 Query Match 52.8%; Score 13.2; DB 8; Length 47;
 Best Local Similarity 83.3%; Pred. No. 3.4e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 5 TCATCACCACTCTCTTCC 22
 ||||| ||||| |||||
 Db 22 TCATCATCACTTTCTCCC 39

RESULT 19
 ACZ308699
 LOCUS
 DEFINITION IM0011N24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0011N24 R, genomic survey sequence.
 ACCESSION ACZ308699
 VERSION ACZ308699.1 GI:10348959
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center

University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0011 row: N column: 24
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 33.
 Location/Qualifiers
 source 1..33
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0011N24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gil4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 52.0%; Score 13; DB 8; Length 33;
 Best Local Similarity 76.2%; Pred. No. 3.9e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 CAACTCATCACTCTCTTC 21
 ||||| ||||| |||||
 Db 4 CATCTCTCATCACCTCATC 24

RESULT 20
 BX534557
 LOCUS
 DEFINITION BX534557 33 bp DNA linear GSS 04-APR-2004
 Arabidopsis thaliana T-DNA flanking sequence GK-510D07-019532,
 genomic survey sequence.
 ACCESSION BX534557
 VERSION BX534557.1 GI:31411687
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1
 AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
 TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 MEDLINE 22755829
 PUBMED 12874060
 REFERENCE 2

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 33)
AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T19G15. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source
 1. 33
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-510D07-019532"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 52.0%; Score 13; DB 9; Length 33;
 Best Local Similarity 76.2%; Pred. No. 3.9e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTCCATC 25
 |||||
 Db 1 TCATCACCACACATTTTCC 21

RESULT 21
AZ938244
LOCUS AZ938244
DEFINITION 2M0196E13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0196E13 R, genomic survey sequence.
ACCESSION AZ938244
VERSION AZ938244.1 GI:13797754
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 36)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0196 row: E column: 13
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 36.

FEATURES

source
 1. 36
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0196E13"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: pWD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 13; DB 8; Length 36;
 Best Local Similarity 76.2%; Pred. No. 4e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTGATCACCACCTCTCTCCAT 24
 |||||
 Db 11 CCCACCCCCACCTCTTTCAT 31

RESULT

AZ938244
LOCUS AZ938244
DEFINITION 09P20 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA 3', mRNA sequence.
ACCESSION CD531219
VERSION CD531219.1 GI:40451231
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 43)
AUTHORS Guo, Y., Cai, Z. and Gan, S.
TITLE Transcriptome of Arabidopsis leaf senescence
JOURNAL Plant Cell Environ. 27 (5), 521-549 (2004)
COMMENT Contact: Susheng Gan
 Department of Horticulture

Query Match 52.0%; Score 13; DB 1; Length 50;
 Best Local Similarity 76.2%; Pred. No. 4.2e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTTTCAT 24
 |||||
 Db 3 CTGACCACCCCTCTTTCAT 23

RESULT 28
 AI441968 31 bp mRNA linear EST 23-JUL-2004
 LOCUS sa83dl1.y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-cl004-5902 5' similar to TR:024099 024099 MTN12 ;, mRNA
 sequence.

ACCESSION AI441968.1 GI:4292882
 VERSION AI441968.1
 KEYWORDS EST.
 SOURCE Glycine max (soybean)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE 1 (bases 1 to 31)
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,
 Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
 Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
 Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
 Schurk,R., Ritter,S., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterston,R. and Wilson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. Trace
 considered overall poor quality possible reversed clone: similarity
 on wrong strand This clone is available through: Biogenetic
 Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
 4163; email: info@biogeneticservices.com)
 Insert Length: 969 Std Error: 0.00
 Seq primer: -40RP from Gibco
 High quality sequence stop: 1
 POLYA=No.

FEATURES source
 1..31
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl004-5902"
 /tissue_type="root"
 /lab_host="XL10-Gold"
 /clone_lib="Gm-cl004"
 /note="Vector: pBluescript II Xr; Site 1: EcoRI; Site 2:
 XhoI; Root cDNA. The mRNA was isolated from entire roots
 of 8 day old 'Williams' seedlings which were propagated on
 paper towels with distilled water. Stragene's cDNA
 Synthesis Kit (catalog #200401) was used to synthesize the
 cDNA. First- strand synthesis was performed with 5-methyl
 dCTP, hence the ligated cDNA is hemimethylated.
 Stragene's first-strand synthesis primer was used
 [GAGAGAGAGAGAGAGAACTAGTCGAG(T)-18]. After
 second-strand synthesis, the cDNA ends were 'polished'
 with clone Pfu DNA polymerase, ligated to EcoRI adaptors,
 and phosphorylated. The XhoI site within the first-strand
 synthesis primer was restricted by digestion with XhoI;

all XhoI sites in the cDNA would be protected by their
 hemimethylated status. The cDNA constructs were
 size-fractionated with a 500bp cutoff, using GibcoBRL Life
 Technologies' cDNA size fractionation column. The column
 eluent was then ligated into Stragene's pBluescript II
 XR predigested vector (pBluescript II SK(+)) that had been
 digested with EcoRI and XhoI, and phosphorylated. Both
 the white and blue colonies appear to contain recombinant
 plasmids with cDNA inserts. Blue colonies (n=15) have been
 sequenced, and possess putative cDNA inserts. This library
 was constructed by Dr. Paul Keim & Virginia H. Coryell,
 Department of Biology, Box5640, Northern Arizona
 University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
 Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
 520-523-7500, email: paul.keim@nau.edu,
 virginia.coryell@nau.edu"

ORIGIN

Query Match 51.2%; Score 12.8; DB 1; Length 31;
 Best Local Similarity 87.5%; Pred. No. 4.7e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 ACCACTCTCTTCCATC 25
 |||||
 Db 12 ACCACTCTCTCCACC 27

RESULT 29
 TA021E12Q/c

LOCUS T. brucei sheared genomic DNA clone 221e12, reverse sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL480383
 VERSION AL480383.1 GI:11846152
 KEYWORDS GSS.

SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE 1 (bases 1 to 32)

AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (
 4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).

FEATURES source
 1..32
 Location/Qualifiers
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="221e12"

ORIGIN

Query Match 51.2%; Score 12.8; DB 9; Length 32;
 Best Local Similarity 70.8%; Pred. No. 4.8e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

Qy 1 CAACTCATCACCACCTCTCTCCAT 24
   ||| ||||| ||| ||| ||| |||
Db 25 CAATACATCATCATCCGCTTCAT 2

RESULT 30
BH909685          36 bp   DNA      linear   GSS 04-SEP-2002
LOCUS             SALK_055402.24.05.x Arabidopsis thaliana TDNA insertion lines
DEFINITION        Arabidopsis thaliana genomic clone SALK_055402.24.05.x, genomic
                  survey sequence.
ACCESSION         BH909685
VERSION           BH909685.1 GI:22722618
KEYWORDS          GSS.
SOURCE            Arabidopsis thaliana (thale cress)
ORGANISM          Arabidopsis thaliana
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
                  Shinn,P., Zimmermann,J. and Ecker,J.R.
TITLE             A Sequence-Indexed Library of Insertion Mutations in the
                  Arabidopsis Genome
JOURNAL           Unpublished (2001)
COMMENT           Contact: Joseph R. Ecker
                  Salk Institute Genomic Analysis Laboratory (SIGnAL)
                  The Salk Institute for Biological Studies
                  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                  Tel: 858 453 4100 x1752
                  Fax: 858 558 6379
                  Email: ecker@salk.edu
                  This is single pass sequence recovered from the left border of
                  TDNA.
FEATURES
  source
    Location/Qualifiers
      1..36
        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /ecotype="Col-0"
        /db_xref="taxon:3702"
        /clone="SALK_055402.24.05.x"
        /clone_lib="Arabidopsis thaliana TDNA insertion lines"
        /note="PCR was performed on Arabidopsis thaliana lines
        each of which contains one or more TDNA insertion
        elements. The resultant fragment for each line was
        directly sequenced to determine the genomic sequence at
        the site of insertion. Details of the protocols used can
        be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          51.2%; Score 12.8; DB 8; Length 36;
Best Local Similarity 87.5%; Pred. No. 4.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CACCACCTCTCTTCAT 24
   ||| ||||| ||| ||| ||| |||
Db 18 CTCAACTCTCTTCAT 33

RESULT 31
AL188273          37 bp   mRNA      linear   EST 28-OCT-1998
LOCUS             qd1g10.x1 Soares placenta 8tc9weeks 2NbHP8tc9w Homo sapiens cDNA
DEFINITION        clone IMAGE:1723458 3' similar to TR:O42204 O42204 PUTATIVE
                  TRANSMEMBRANE PROTEIN E3-16. ;, mRNA sequence.
ACCESSION         AL188273
VERSION           AL188273.1 GI:3739482
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 37)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1920 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
  source
    Location/Qualifiers
      1..37
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:1723458"
        /db_stge="two placentae: one from 8 weeks and another
        from 9 weeks post conception"
        /lab_host="DH10B (ampicillin resistant)"
        /clone_lib="Soares placenta 8tc9weeks 2NbHP8tc9w"
        /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
        modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
        strand cDNA was primed with a Not I - oligo(dT) primer [5'
        TGTTCACATCTGAGTGGGCGCGCGATTTTTTTTTTTT 3'],
        double-stranded cDNA was size selected, ligated to Eco RI
        adapters (Pharmacia), digested with Not I and cloned into
        the Not I and Eco RI sites of a modified pT7T3 vector
        (Pharmacia). Library constructed by Bento Soares and
        M.Fatima Bonaldo."

ORIGIN
Query Match          51.2%; Score 12.8; DB 1; Length 37;
Best Local Similarity 87.5%; Pred. No. 4.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CATCACCACTCTCTTC 21
   ||| ||||| ||| ||| ||| |||
Db 15 CAACACCACTCTCTTC 30

RESULT 32
BH903343/c        39 bp   DNA      linear   GSS 04-SEP-2002
LOCUS             SALK_102465.31.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION        Arabidopsis thaliana genomic clone SALK_102465.31.50.x, genomic
                  survey sequence.
ACCESSION         BH903343
VERSION           BH903343.1 GI:22714519
KEYWORDS          GSS.
SOURCE            Arabidopsis thaliana (thale cress)
ORGANISM          Arabidopsis thaliana
                  Arabidopsis thaliana
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
                  Shinn,P., Zimmermann,J. and Ecker,J.R.
TITLE             A Sequence-Indexed Library of Insertion Mutations in the
                  Arabidopsis Genome
JOURNAL           Unpublished (2001)
COMMENT           Contact: Joseph R. Ecker
                  Salk Institute Genomic Analysis Laboratory (SIGnAL)
                  The Salk Institute for Biological Studies
                  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                  Tel: 858 453 4100 x1752
                  Fax: 858 558 6379
                  Email: ecker@salk.edu
                  This is single pass sequence recovered from the left border of

```

```

TDNA.
Class: TDNA tagged.
FEATURES
    source
        1..39
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /ecotype="Col-0"
            /db_xref="taxon:3702"
            /clone="SALK_102465.31.50.x"
            /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can
            be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
    Query Match      51.2%; Score 12.8; DB 8; Length 39;
    Best Local Similarity 70.8%; Pred. No. 4.9e+05;
    Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTCCATC 25
    ||||| ||||| ||||| |||||
Db 39 AATTCTACACTACTTAACCCATC 16
    ||||| ||||| ||||| |||||

RESULT 33
LOCUS TAIL10A120/c
DEFINITION T. brucei sheared genomic DNA clone 110a12, reverse sequence,
genomic survey sequence.
ACCESSION AL461172
VERSION AL461172.1 GI:11832134
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 39)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhi@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
        1..39
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="110a12"

ORIGIN
    Query Match      51.2%; Score 12.8; DB 9; Length 39;
    Best Local Similarity 70.8%; Pred. No. 4.9e+05;
    Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy 1 CAACTCATCACCACCTCTCTCCAT 24
    ||||| ||||| ||||| |||||
Db 36 CAGTCAGCATCACTCTCTCGCAT 13
    ||||| ||||| ||||| |||||

RESULT 34
LOCUS AJ595714/c
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
422E10, genomic survey sequence.
ACCESSION AJ595714
VERSION AJ595714.1 GI:37945342
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
JOURNAL 22363535
MEDLINE 12446565
PUBMED 12446565
REFERENCE 2 (bases 1 to 40)
AUTHORS Balzergue,S.
Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
    source
        1..40
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassillewskija"
            /db_xref="taxon:3702"
            /clone="422E10"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            /note="T-DNA flanking sequence
            left border"
        misc_feature
            1..40
                /note="T-DNA flanking sequence
                left border"
    ORIGIN
        Query Match      51.2%; Score 12.8; DB 9; Length 40;
        Best Local Similarity 87.5%; Pred. No. 5e+05;
        Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTCTC 18
    ||||| ||||| |||||
Db 32 ACTCGTCACCACTCAC 17
    ||||| ||||| |||||

RESULT 35
LOCUS BZ381485/c
DEFINITION SALK_116783.20.40.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_116783.20.40.x, genomic
survey sequence.
ACCESSION BZ381485
VERSION BZ381485.1 GI:25475482

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KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1 (bases 1 to 41)
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmermann,J. and Ecker,J.R.
TITLE
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL
Unpublished (2001)
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g30852.
Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..41
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_116783.20.40.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
Query Match 51.2%; Score 12.8; DB 8; Length 41;
Best Local Similarity 70.8%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 2 AACTCATCACCACCTCTCTCCATC 25
Db 41 AATTCACACTACTCTAACCCATC 18
RESULT 36
CF920754
LOCUS
CF920754 42 bp mRNA linear EST 05-NOV-2003
DEFINITION
gmhRw3-01_C02_1_012 Soybean root hair subtracted cDNA library
gmhRw3 Glycine max cDNA, mRNA sequence.
ACCESSION
CF920754
VERSION
CF920754.1 GI:38191548
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 42)
AUTHORS
Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
TITLE
Expressed sequence tags from soybean root hair subtractive cDNA
library
JOURNAL
Unpublished (2003)
COMMENT
Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
Seq primer: F7.
Location/Qualifiers
1..42
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmhRw3"
/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."
ORIGIN
Query Match 51.2%; Score 12.8; DB 7; Length 42;
Best Local Similarity 70.8%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCACCTCTCTCCAT 24
Db 1 CAAGACCTCGTCATCTCTTCAAT 24
RESULT 37
AZ828302/c
LOCUS
AZ828302 42 bp DNA linear GSS 20-FEB-2001
DEFINITION
2M0105011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0105011 F, genomic survey sequence.
ACCESSION
AZ828302
VERSION
AZ828302.1 GI:12998210
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 42)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: 0 column: 11
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0105011"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.2%; Score 12.8; DB 8; Length 42;
Best Local Similarity 70.8%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCATC 25

Db 39 ACCACCTCATCACTCACTCCAGC 16

RESULT 38

BH903344/c

LOCUS BH903344 43 bp DNA linear GSS 04-SEP-2002
DEFINITION SALK_102466.48.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_102466.48.25.x, genomic survey sequence.

ACCESSION BH903344

VERSION BH903344.1 GI:22714520

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 43)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

CONTACT: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

FEATURES

source

Location/Qualifiers

1..43

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_102466.48.25.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.2%; Score 12.8; DB 8; Length 43;

Best Local Similarity 70.8%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCATC 25

Db 43 AATTCTACTACTCTTAACCCATC 20

RESULT 39

BH861884

LOCUS BH861884

DEFINITION

Arabidopsis thaliana

Accession

Version

Keywords

Source

Organism

Arabidopsis thaliana

Arabidopsis thaliana

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 44)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of

Class: TDNA tagged.

Location/Qualifiers

1..44

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_088239"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.2%; Score 12.8; DB 8; Length 44;

Best Local Similarity 70.8%; Pred. No. 5e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCATC 25

Db 12 ACCACATCACTCTTCTCCAC 35

RESULT 40

BH901162

LOCUS BH901162

DEFINITION

Arabidopsis thaliana

Accession

Version

Keywords

GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 45)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Arabidopsis Genome
COMMENT Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At1g76170.
Class: TDNA tagged.
FEATURES
 Location/Qualifiers
 1..45
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_073346.39.40.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
 Query Match 51.2%; Score 12.8; DB 8; Length 45;
 Best Local Similarity 70.8%; Pred. No. 5.1e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy 1 CAACTCATCACCACCTCTCTTCAT 24
Db 19 CAGCTAATCAACAAACATTCAT 42

Search completed: November 18, 2005, 21:12:57
Job time : 1198.82 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 48.5741 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-9

Perfect score: 25

Sequence: 1 CAACCTCATCCACTCTCTTCATC 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	1	US-07-989-160-9
2	18.2	72.8	47	4	US-09-422-978-3589
3	16.2	64.8	46	1	US-07-977-434-38
4	16.2	64.8	46	1	US-08-458-819-38
5	15.2	60.8	46	5	PCT-US91-07035-38
6	15.4	61.6	25	4	US-09-888-413-147
7	15.4	61.6	47	3	US-09-641-638-1288
8	15.4	61.6	47	4	US-10-170-097-1288
9	15.2	60.8	20	1	US-08-469-802B-23
10	15.2	60.8	20	2	US-08-267-803B-41
11	15.2	60.8	42	2	US-09-133-774-24
12	15.2	60.8	42	3	US-09-303-862-24
13	15	60.0	25	4	US-09-396-196G-7617
14	14.8	59.2	25	3	US-08-943-731-312
15	14.6	58.4	25	4	US-09-396-196G-75841
16	14.6	58.4	25	4	US-09-396-196G-75842
17	14.6	58.4	25	4	US-09-396-196G-100658
18	14.4	57.6	47	4	US-09-422-978-1201
19	14.2	56.8	24	1	US-07-977-284A-208
20	14.2	56.8	24	2	US-08-256-426B-208
21	14.2	56.8	22	4	US-09-396-196G-75840
22	14	56.0	22	2	US-08-810-599-22
23	14	56.0	22	3	US-08-757-438-2
24	14	56.0	25	4	US-09-396-196G-22970
25	14	56.0	25	4	US-09-396-196G-52198
26	14	56.0	25	4	US-09-396-196G-52200
27	14	56.0	25	4	US-09-396-196G-83551

Sequence 20, Appl
Sequence 20, Appl
Sequence 144, App
Sequence 145, App
Sequence 13, Appl
Sequence 19, Appl
Sequence 21, Appl
Sequence 13, Appl
Sequence 19, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 107, App
Sequence 1287, Ap
Sequence 1287, Ap
Sequence 22971, A
Sequence 41212, A
Sequence 80104, A
Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-07-989-160-9
; Sequence 9, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-07-989-160-9

Query Match 100.0%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. NO. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACCTCATCCACTCTCTTCATC 25
|||||

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Db      1 CAACTCATCACCACCTCTCTTCCATC 25
US-09-422-978-3589/c
; Sequence 3589, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3589
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-6834-307 : polymorphic base G or A
US-09-422-978-3589

Query Match      72.8%; Score 18.2; DB 4; Length 47;
Best Local Similarity 80.0%; Pred. No. 71;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACCTCTCTTCCATC 25
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Db

RESULT 3
US-07-977-434-38
; Sequence 38, Application US/07977434
; Patent No. 5466591
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: Wordperfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,434
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA: WO PCT/US90/07641
; APPLICATION NUMBER: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cseri
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2972
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA primer TAFR01
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-977-434-38

Query Match      64.8%; Score 16.2; DB 1; Length 46;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 CTCATCACCACCTCTCTTCCAT 24
      17 CTCATCCCACTCTTTTCCAT 37
Db

RESULT 4
US-08-458-819-38
; Sequence 38, Application US/08458819
; Patent No. 5795762
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
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;; ZIP: 07110-1199
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Macintosh
;; OPERATING SYSTEM: 7
;; SOFTWARE: WordPerfect 2.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US 08/458,819
;; FILING DATE: 02-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/977,434
;; FILING DATE: 23-FEB-1993
;; APPLICATION NUMBER: US 590,490
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 590,466
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 590,213
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 523,394
;; FILING DATE: 15-MAY-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 143,441
;; FILING DATE: 12-JAN-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 063,509
;; FILING DATE: 17-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 899,241
;; FILING DATE: 22-AUG-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 746,121
;; FILING DATE: 15-AUG-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US90/07641
;; FILING DATE: 21-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 585,471
;; FILING DATE: 20-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 455,611
;; FILING DATE: 22-DEC-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 609,157
;; FILING DATE: 02-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 557,517
;; FILING DATE: 24-JUL-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Luann Cserr
;; REGISTRATION NUMBER: 31,822
;; REFERENCE/DOCKET NUMBER: Case No. 5795762 8753
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 814-2972
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 46 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; MOLECULE TYPE: DNA primer TAFR01
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; US-08-458-819-38

Query Match 64.8%; Score 16.2; DB 1; Length 46;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 4 CTCATCACCACCTCTTTCAT 24

Db 17 CTCATCACCACCTCTTTCAT 37

RESULT 5
PCT-US91-07035-38
; Sequence 38, Application PC/TUS9107035
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-third Street
; CITY: Emeryville
; STATE: California
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07035
; FILING DATE: 19910930
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D, Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: Case No. 2580
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-420-3300

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; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA primer TAFR01
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US91-07035-38

Query Match 64.8%; Score 16.2; DB 5; Length 46;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCAT 24
Db 17 CTCATTCCTCCACTCTTTCAT 37

RESULT 6
US-09-888-413-147/c
; Sequence 147, Application US/09888413
; Patent No. 6759198
; GENERAL INFORMATION:
; APPLICANT: KRIS, RICHARD M.
; APPLICANT: FELDER, STEPHEN
; TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
; FILE REFERENCE: NEOGEN-1 P4
; CURRENT APPLICATION NUMBER: US/09/888,413
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/337,325
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/218,166
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/109,076
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/068,291
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: attenuation factor oligonucleotide
US-09-888-413-147

Query Match 61.6%; Score 15.4; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAATCATCACCACTCTCTTCATC 25
Db 25 CACCTCATAGCACTCTCAACACC 1

RESULT 7
US-09-641-638-1288
; Sequence 1288, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16

; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA primer TAFR01
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US91-07035-39

Query Match 61.6%; Score 15.4; DB 3; Length 47;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCC 22
Db 11 CTCATCAGCCTCTCTTCC 29

RESULT 8
US-10-170-097-1288
; Sequence 1288, Application US/10170097
; Patent No. 6794143
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GEN-T14XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1288
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-507-364 : polymorphic base C or T
US-10-170-097-1288

Query Match 61.6%; Score 15.4; DB 4; Length 47;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCC 22
Db 11 CTCATCAGCCTCTCTTCC 29

RESULT 9
US-10-170-097-1288
; Sequence 1288, Application US/10170097
; Patent No. 6794143
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GEN-T14XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1288
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-507-364 : polymorphic base C or T
US-10-170-097-1288

Query Match 61.6%; Score 15.4; DB 4; Length 47;
Best Local Similarity 84.2%; Pred. No. 1.2e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCC 22
Db 11 CTCATCAGCCTCTCTTCC 29
```

RESULT 9
US-08-469-802B-23/c
; Sequence 23, Application US/08469802B
; Patent No. 5741645
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5741645
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueiting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: 119 No. 5741645th Fourth Street, Suite 203
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,802B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueiting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00030101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1225
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-469-802B-23
Query Match 60.8%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CAACTCATCACACTCTCTT 20
Db 20 CAACTCATGACCCCTCTCT 1
RESULT 10
US-08-267-803B-41/c
; Sequence 41, Application US/08267803B
; Patent No. 5834183
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5834183
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueiting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN

COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-41
Query Match 60.8%; Score 15.2; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CAACTCATCACACTCTCTT 20
Db 20 CAACTCATGACCCCTCTCT 1
RESULT 11
US-09-133-774-24
; Sequence 24, Application US/09133774B
; Patent No. 5962636
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Heart
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/133,774B
; CURRENT FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Human
US-09-133-774-24
Query Match 60.8%; Score 15.2; DB 2; Length 42;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 AACTCATCACACTCTCTTC 21
Db 8 AGCTCATGGCCTCTCTTC 27
RESULT 12
US-09-303-862-24
; Sequence 24, Application US/09303862
; Patent No. 6034230
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt

```
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 6034230e1 Peptides Capable of Modulating Inflammatory Heart
; TITLE OF INVENTION: Disease
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/303,862
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: 09/133,774
; EARLIER FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Human
US-09-303-862-24

Query Match          60.8%; Score 15.2; DB 3; Length 42;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AACATCATCACCACTCTCTTC 21
    ||||| ||||| |||||
Db  8 AGCTCATGGCCACTCTCTTC 27

RESULT 13
US-09-396-196G-7617
; Sequence 7617, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7617
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-7617

Query Match          60.0%; Score 15; DB 4; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 AACATCATCACCACTCTCTTCAT 24
    ||||| ||||| ||||| |||||
Db  3 AACATCATCTGACTCTCACCAT 25

RESULT 14
US-08-943-731-312/c
; Sequence 312, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA W.
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
```

```
; APPLICANT: ALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLR.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-312

Query Match          59.2%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  8 TCACCACTCTCTTCCATC 25
    ||||| ||||| ||||| |||||
Db  25 TCCCACTCTCTTCCCTC 8

RESULT 15
US-09-396-196G-75841
; Sequence 75841, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75841
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: mus musculus
US-09-396-196G-75841

Query Match      58.4%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTCTCTTCCA 23
Db 4 ACTCATGGCTACTCTCTTCAA 24

RESULT 16
US-09-396-196G-75842
; Sequence 75842, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75842
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-75842

Query Match      58.4%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTCTCTTCCA 23
Db 1 ACTCATGGCTACTCTCTTCAA 21

RESULT 17
US-09-396-196G-100658
; Sequence 100658, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100658
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-100658

Query Match      58.4%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTTCAATC 25
Db 1 ACTCATGGCTACTCTCTTCAA 21

; ORGANISM: mus musculus
US-09-422-978-1201
; Sequence 1201, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1201
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-21370-87 : polymorphic base C or T
US-09-422-978-1201

Query Match      57.6%; Score 14.4; DB 4; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTTC 21
Db 25 CTCCTCATCCTCTCTTTC 42

RESULT 19
US-07-977-284A-208/c
; Sequence 208, Application US/07977284A
; Patent No. 5558988
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
; FILE REFERENCE: 261
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA: US/07/977,284A
; APPLICATION NUMBER: 13-NOV-1992
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-07-977-284A-208

Query Match 56.8%; Score 14.2; DB 1; Length 24;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATCACCACTCTCTTCCAT 24
Db 24 CATCACCCCTCTTCCCAT 6

RESULT 20
US-08-256-426B-208/c
; Sequence 208, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; NUMBER OF SEQUENCES: 293
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,426B
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10964
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,284
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
```

```
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-256-426B-208

Query Match 56.8%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATCACCACTCTCTTCCAT 24
Db 24 CATCACCCCTCTTCCCAT 6

RESULT 21
US-09-396-196G-75840
; Sequence 75840, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-75840

Query Match 56.8%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACTCTCTTC 21
Db 7 ACTCATGGCTACTCTCTTC 25

RESULT 22
US-08-810-599-22/c
; Sequence 22, Application US/08810599
; Patent No. 5976798
; GENERAL INFORMATION:
; APPLICANT: PARKER, W. Davis
; APPLICANT: HERNSTADT, Corinna
; APPLICANT: GHOSH, Soumitra S.
; APPLICANT: FAHY, Bojin
; TITLE OF INVENTION: Methods for Detecting Mitochondrial Mutations
; TITLE OF INVENTION: Diagnostic for Alzheimer's Disease and Methods for Determining
; TITLE OF INVENTION: of Mitochondrial Nucleic Acid
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/810,599
FILING DATE: Concurrent Herewith
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,438
FILING DATE: 27 NO. 5976798 1996
APPLICATION NUMBER: US 08/614,072
FILING DATE: 12 Mar 1996
APPLICATION NUMBER: US 08/536,036
FILING DATE: 29 Sep 1995
APPLICATION NUMBER: US 08/414,969
FILING DATE: 31 Mar 1995
APPLICATION NUMBER: US 08/413,740
FILING DATE: 30 Mar 1995
APPLICATION NUMBER: US 08/410,658
FILING DATE: 24 MARCH 1995
APPLICATION NUMBER: US 08/397,808
FILING DATE: 3 Mar 1995
APPLICATION NUMBER: US 08/219,842
FILING DATE: 30 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2105/17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: No
ANTI-SENSE: No
US-08-810-599-22

Query Match 56.0%; Score 14; DB 2; Length 22;
Best Local Similarity 77.3%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTTCCATC 25
|||||
DB 22 CTCACACCACTTCTTCGACC 1

RESULT 23
US-08-757-438-2/c
Sequence 2, Application US/08757438
Patent No. 6027883
GENERAL INFORMATION:
APPLICANT: Hernstadt, Corinna
APPLICANT: Ghosh, Soumitra
APPLICANT: Fahy, Eoin D.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: OPTIMAL PROCEDURE FOR ISOLATION OF
TITLE OF INVENTION: MUTANT MITOCHONDRIAL ALLELES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,438

FILING DATE: 27-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenman, Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.407C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-438-2

Query Match 56.0%; Score 14; DB 3; Length 22;
Best Local Similarity 77.3%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTTCCATC 25
|||||
DB 22 CTCACACCACTTCTTCGACC 1

RESULT 24
US-09-396-196G-22970
Sequence 22970, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22970
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-22970

Query Match 56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 77.3%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTTCCATC 25
|||||
DB 2 CCCATCAGCATCTTGTCCATC 23

RESULT 25
US-09-396-196G-52198/c
Sequence 52198, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678

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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52198
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-52198

Query Match      56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTC 16
    |||||
Db 24 ACTCATCACCACCTC 11

RESULT 26
US-09-396-196G-52200/c
; Sequence 52200, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52200
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-52200

Query Match      56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTC 16
    |||||
Db 22 ACTCATCACCACCTC 9

RESULT 27
US-09-396-196G-83551
; Sequence 83551, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83551
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-83551

Query Match      56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTC 16
    |||||
Db 22 ACTCATCACCACCTC 9

RESULT 28
US-08-646-538-20/c
; Sequence 20, Application US/08646538
; Patent No. 6027881
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Gaitanaris, George A.
; APPLICANT: Stauber, Roland H.
; APPLICANT: Vournakis, John N.
; TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
; TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,538
; FILING DATE: No. 6027881 yet assigned
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-249000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..40
; OTHER INFORMATION: /note="oligonucleotide #bio25"
US-08-646-538-20

Query Match      56.0%; Score 14; DB 3; Length 40;
Best Local Similarity 77.3%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTCTCTTCAT 24
    ||| |||||
Db 33 ACTAGTCACCTACTCTCTCTCAT 12

RESULT 29
US-09-503-222-20/c
; Sequence 20, Application US/09503222
; Patent No. 6265548
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Gaitanaris, George A.
```



```

; APPLICANT: Stauber, Roland H.
; APPLICANT: Vournakis, John N.
; TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
; TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503.222
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646.538
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-249000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..40
; OTHER INFORMATION: /note= "oligonucleotide #bic25"
;
US-09-503-222-20
Query Match 56.0%; Score 14; DB 3; Length 40;
Best Local Similarity 77.3%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACTCTCTTCCAT 24
   ||| |||| ||||| |||
Db 33 ACTACTCACTACTCTCTCTCAT 12

RESULT 30
PCT-US91-03680-144
; Sequence 144. Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; APPLICANT: Krawczyk, Steven
; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
; TITLE OF INVENTION: DUPLEX DNA
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03680
; FILING DATE: 19910524
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4610-0011.40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1..4
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 6
; OTHER INFORMATION: /mod_base= OTHER
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 7
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 9
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 11
; OTHER INFORMATION: /mod_base= OTHER
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 12
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 14
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 18
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 21
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 23
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; OTHER INFORMATION: /mod_base= OTHER
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 7
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 9
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 11
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 12
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 14
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod_base= OTHER
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 18
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 21
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 23
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 24
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 26
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N4,N4-ethanocytosine"
; PCT-US91-03680-145

Query Match 55.2%; Score 13.8; DB 5; Length 26;
Best Local Similarity 57.1%; Pred. No. 5.3e+03;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAACTCATCACCACTCTCTTC 21
Db 1 MWWWMTCTCTMCTCTCTCTTC 21

RESULT 31
PCT-US91-03680-145
; Sequence 145, Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; APPLICANT: Krawczyk, Steven
; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
; TITLE OF INVENTION: DUPLEX DNA
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03680
; FILING DATE: 19910524
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4610-0011.40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1..4
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 6
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
```

; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009,893A
; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
; ORGANISM: primer
US-09-009-893A-13

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 33
US-09-009-893A-19/c
; Sequence 19, Application US/09009893A
; Patent No. 6623938
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009,893A
; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-009-893A-19

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 34
US-09-009-893A-21/c
; Sequence 21, Application US/09009893A
; Patent No. 6623938
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.

; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Rec
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009,893A
; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
; ORGANISM: primer
US-09-009-893A-21

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 35
US-09-489-155-13/c
; Sequence 13, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-489-155-13

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 36
US-09-489-155-19/c
; Sequence 19, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.

```
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
; FILE REFERENCE: CD-95 Induced Apoptosis
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-489-155-19

Query Match      55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TCACCACTCTCTTCAT 24
        ||||| ||||| |||||
Db      32 TCACCAATCTCTGCAT 16

RESULT 37
US-09-489-155-21/c
; Sequence 21, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
; FILE REFERENCE: CD-95 Induced Apoptosis
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-489-155-21

Query Match      55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TCACCACTCTCTTCAT 24
        ||||| ||||| |||||
Db      32 TCACCAATCTCTGCAT 16

RESULT 38
US-07-744-282C-64
; Sequence 64, Application US/07744282C
; Patent No. 5521300
; GENERAL INFORMATION:
; APPLICANT: Shah, Jyotsna S.
; APPLICANT: Nietupski, Raymond M.
; APPLICANT: Liu, Jing
; TITLE OF INVENTION: Oligonucleotides Complementary to
; Mismatched Nucleic Acids
```

```
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,282C
; FILING DATE: August 13, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kevin M. Farrell
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: GTR90-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-744-282C-64

Query Match      55.2%; Score 13.8; DB 1; Length 39;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 CATCACCACTCTCTTCC 22
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Db      2 CATCACCACTCTCTTCC 18

RESULT 39
PCT-US92-06821A-107
; Sequence 107, Application PC/TUS9206821A
; GENERAL INFORMATION:
; APPLICANT: Shah, Jyotsna S.
; APPLICANT: Nietupski, Raymond M.
; APPLICANT: Liu, Jing
; TITLE OF INVENTION: Oligonucleotides Complementary to
; TITLE OF INVENTION: Mycobacterial Nucleic Acids
; NUMBER OF SEQUENCES: 133
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corporation
; STREET: 200 East Randolph Drive, P.O. Box 87703
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06821A
; PRIOR APPLICATION DATA: US 07/744,282
; FILING DATE: 13-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, Norval B.
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: CN 5851
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-856-7180
TELEFAX: 312-856-4972
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US92-06821A-107

Query Match 55.2%; Score 13.8; DB 5; Length 39;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CATCACCACCTCTCTTCC 22
||| ||| ||| ||| |||
DB 2 CATCACCACCTCTCTTCC 18

RESULT 40
US-09-641-638-1287
; Sequence 1287, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET 051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1287
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-507-353 : polymorphic base C or T
US-09-641-638-1287

Query Match 55.2%; Score 13.8; DB 3; Length 47;
Best Local Similarity 78.9%; Pred. No. 5.8e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTCTTCC 22
||| ||| ||| ||| |||
DB 22 CTATCAGCGCTCTCTTCC 40

Search completed: November 18, 2005, 11:22:03
Job time : 49.5741 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 336.027 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-9

Perfect score: 25

Sequence: 1 CAACCTCATCACCACCTCTCTCCATC 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
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23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
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28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	25	100.0	25	US-08-469-172-9	Sequence 9, Appli
2	25	100.0	25	US-10-788-779-9	Sequence 9, Appli
C 3	18.2	72.8	47	US-10-349-143-3589	Sequence 3589, Ap
C 4	17.6	70.4	25	US-11-036-317-879180	Sequence 879180,
C 5	17.6	70.4	25	US-11-036-317-961186	Sequence 961186,

C 6	17.2	68.8	25	26	US-11-036-317-979596	Sequence 979596,
C 7	16.2	64.8	25	22	US-10-719-900-264364	Sequence 264364,
C 8	16.2	64.8	25	22	US-10-719-900-381320	Sequence 381320,
C 9	16.2	64.8	25	22	US-10-719-900-754829	Sequence 754829,
C 10	16	64.0	25	26	US-11-036-317-879179	Sequence 879179,
C 11	16	64.0	25	26	US-11-036-317-961185	Sequence 961185,
C 12	16	64.0	42	16	US-10-326-844-14	Sequence 14, Appl
C 13	15.8	63.2	25	22	US-10-719-900-224994	Sequence 224994,
C 14	15.6	62.4	25	24	US-10-681-773-71822	Sequence 71822, A
C 15	15.6	62.4	25	24	US-10-681-773-105909	Sequence 105909,
C 16	15.6	62.4	25	26	US-11-036-317-853737	Sequence 853737,
C 17	15.6	62.4	25	26	US-11-036-317-979595	Sequence 979595,
C 18	15.4	61.6	25	10	US-09-888-413-147	Sequence 147, App
C 19	15.4	61.6	25	22	US-10-865-853-147	Sequence 147, App
C 20	15.4	61.6	47	18	US-10-170-097-1288	Sequence 1288, Ap
C 21	15.4	61.6	47	22	US-10-326-884-1288	Sequence 1288, Ap
C 22	15.2	60.8	25	24	US-10-719-956-5098	Sequence 5098, Ap
C 23	15.2	60.8	25	24	US-10-719-956-666093	Sequence 666093,
C 24	15.2	60.8	25	24	US-10-719-956-691491	Sequence 691491,
C 25	15.2	60.8	25	26	US-11-036-317-768601	Sequence 768601,
C 26	15.2	60.8	25	26	US-11-060-756-294238	Sequence 294238,
C 27	15.2	60.8	33	24	US-10-891-260-7937	Sequence 7937, Ap
C 28	15	60.0	25	22	US-10-809-189-7617	Sequence 7617, Ap
C 29	15	60.0	25	22	US-10-956-157-53604	Sequence 53604, A
C 30	15	60.0	25	22	US-10-956-157-53604	Sequence 53604, A
C 31	15	60.0	25	22	US-10-956-157-53605	Sequence 53605, A
C 32	15	60.0	25	24	US-10-719-956-602018	Sequence 602018,
C 33	15	60.0	50	18	US-10-131-827-6576	Sequence 6576, Ap
C 34	15	60.0	50	18	US-10-131-827-6966	Sequence 6966, Ap
C 35	14.8	59.2	21	22	US-10-861-304-1	Sequence 1, Appli
C 36	14.8	59.2	22	19	US-10-072-012-1372	Sequence 1372, Ap
C 37	14.8	59.2	24	9	US-09-978-295A-142	Sequence 142, App
C 38	14.8	59.2	24	9	US-09-978-697-142	Sequence 142, App
C 39	14.8	59.2	24	9	US-09-978-192A-142	Sequence 142, App
C 40	14.8	59.2	24	10	US-09-978-189-142	Sequence 142, App
C 41	14.8	59.2	24	10	US-09-978-608A-142	Sequence 142, App
C 42	14.8	59.2	24	10	US-09-978-585A-142	Sequence 142, App
C 43	14.8	59.2	24	10	US-09-978-191A-142	Sequence 142, App
C 44	14.8	59.2	24	10	US-09-978-403A-142	Sequence 142, App
C 45	14.8	59.2	24	10	US-09-978-403A-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-08-469-172-9
; Sequence 9, Application US/08469172
; Publication No. US200300543A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-469-172-9

Query Match 100.0%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACATCATCACACTCTCTTCCATC 25
Db 1 CAACATCATCACACTCTCTTCCATC 25

RESULT 2
US-10-788-779-9
; Sequence 9, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-788-779-9

Query Match 100.0%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACATCATCACACTCTCTTCCATC 25
Db 1 CAACATCATCACACTCTCTTCCATC 25

RESULT 3
US-10-349-143-3589/c
; Sequence 3589, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET-020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3589
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-6834-307 : polymorphic base G or A
US-10-349-143-3589

Query Match 72.8%; Score 18.2; DB 18; Length 47;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAACATCATCACACTCTCTTCCATC 25
Db 32 CACCTCATYAGCACGTGTCTTCTTC 8

RESULT 4
US-11-036-317-879180/c
; Sequence 879180, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 879180
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
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US-11-036-317-879180

Query Match 70.4%; Score 17.6; DB 26; Length 25;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTTCCATC 25
|||||
Db 25 AACTCATCACCACCTGATTTCAC 2

RESULT 5

US-11-036-317-961186/c
; Sequence 961186, Application US/11036317
; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036.317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536.639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 961186

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-961186

Query Match 70.4%; Score 17.6; DB 26; Length 25;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTTCCATC 25
|||||
Db 24 AACTCATCACCACCTGATTTCAC 1

RESULT 6

US-11-036-317-979596/c

; Sequence 979596, Application US/11036317

; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036.317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536.639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 979596

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-979596

Query Match 68.8%; Score 17.2; DB 26; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTTCCA 23
|||||
Db 22 AACTCATCACCACCTGATTCCA 1

RESULT 7

US-10-719-900-264364/c

; Sequence 264364, Application US/10719900
; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719.900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 264364

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-264364

Query Match 64.8%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTTCCAT 24
|||||
Db 21 CTCATCACCACCTTCTGCCAT 1

RESULT 8

US-10-719-900-381320/c

; Sequence 381320, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719.900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 381320

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-381320

Query Match 64.8%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTTCC 22
|||||
Db 25 AACTGATGACCACTGTCTTC 5

RESULT 9

US-10-719-900-754829

; Sequence 754829, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719.900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 754829

; LENGTH: 25

; TYPE: DNA

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; ORGANISM: Mus musculus
US-10-719-900-754829

Query Match      64.8%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTTCCATC 25
   ||| ||||| ||||| |||
Db 1 TAATAACCACTCTCTTCCCTC 21

RESULT 10
US-11-036-317-879179/c
; Sequence 879179, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 879179
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-879179

Query Match      64.0%; Score 16; DB 26; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.8e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACTCTCTTCCATC 25
   ||| ||||| ||||| |||
Db 25 AACTCATCACCACTGATTTCCAAAC 2

RESULT 11
US-11-036-317-961185/c
; Sequence 961185, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 961185
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-961185

Query Match      64.0%; Score 16; DB 26; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.8e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACTCTCTTCCATC 25
   ||| ||||| ||||| |||
Db 24 AACTCATCACCTGATTTCCAAAC 1

RESULT 12
```

```
US-10-226-844-14
; Sequence 14, Application US/10226844
; Publication No. US20030113764A1
; GENERAL INFORMATION:
; APPLICANT: Bodary, Sarah C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: P1773R1
; CURRENT APPLICATION NUMBER: US/10/226,844
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US/09/627,202
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/146,217
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 14
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-226-844-14

Query Match      64.0%; Score 16; DB 16; Length 42;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACTCTCTTCCATC 25
   ||| ||||| ||||| |||
Db 6 AATGCATCAAGACTCTCTGCCATC 29

RESULT 13
US-10-719-900-224994
; Sequence 224994, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 224994
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-224994

Query Match      63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ATCACCACCTCTCTTCCATC 25
   ||| ||||| ||||| |||
Db 1 ATAACCACTCTCTTCCCTC 19

RESULT 14
US-10-681-773-71822
; Sequence 71822, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Mateuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
```

```
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 71822
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-71822
```

```
Query Match 62.4%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 7e+03;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;
```

```
QY 1 CAATCATCACCACTCTCTTCC 22
    ||||| ||||| ||||| |||||
DB 3 CAATCATTAGCTCTCTTCC 24
```

```
RESULT 15
US-10-681-773-105909
; Sequence 105909, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-105909
```

```
Query Match 62.4%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 7e+03;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;
```

```
QY 1 CAATCATCACCACTCTCTTCC 22
    ||||| ||||| ||||| |||||
DB 4 CAATCATTAGCTCTCTTCC 25
```

```
RESULT 16
US-11-036-317-853737/c
; Sequence 853737, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 853737
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-853737
```

```
Query Match 62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 4 CTCATCACCACTCTCTTCCATC 25
    ||||| ||||| ||||| |||||
DB 25 CTCATCACCACTGATTCCAAAC 4
```

```
RESULT 17
US-11-036-317-979595/c
; Sequence 979595, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 979595
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-979595
```

```
Query Match 62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 AACTCATCACCACTCTCTTCCA 23
    ||||| ||||| ||||| |||||
DB 22 AACTCATCACCTCTGATTCCA 1
```

```
RESULT 18
US-09-888-413-147/c
; Sequence 147, Application US/09888413
; Publication No. US20030096232A1
; GENERAL INFORMATION:
; APPLICANT: KRIS, RICHARD M.
; APPLICANT: FEJDER, STEPHEN
; TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
; FILE REFERENCE: NEOGEN-1 P4
; CURRENT APPLICATION NUMBER: US/09/888,413
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/337,325
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/218,166
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/109,076
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/068,291
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: attenuation factor oligonucleotide
US-09-888-413-147
```


Publication No. US20040146910A1
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 5098
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-5098

Query Match 60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTCCAT 24
||||| ||||||| |||||
Db 24 TCATCAGCACTCTCAGCCAT 5

RESULT 23

US-10-719-956-666093
Sequence 666093, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 666093
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-666093

Query Match 60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTCCAT 24
||||| ||||||| |||||
Db 2 TCATCATGACTCTCTTCCTT 21

RESULT 24

US-10-719-956-691491
Sequence 691491, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 691491
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus

US-10-719-956-691491

Query Match 60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCA 23
||||| ||||||| |||||
Db 4 CTCATGACTACTTCTTCCA 23

RESULT 25

US-11-036-317-768601
Sequence 768601, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:

APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 768601
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-768601

Query Match 60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTTCCAT 24
||||| ||||||| |||||
Db 1 TCATCAACTCTCTCTTCAAT 20

RESULT 26

US-11-060-756-294238
Sequence 294238, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 294238
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-294238

Query Match 60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTC 21
||| ||||||| |||||
Db 5 AAGTAATCACCACCTTCTTTC 24

RESULT 27

US-10-891-260-7937
Sequence 7937, Application US/10891260

```
; Publication No. US20050227244A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms
; FILE REFERENCE: 3522.3
; CURRENT APPLICATION NUMBER: US/10/891,260
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: 10/681,773
; PRIOR FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 10244
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7937
; LENGTH: 33
; TYPE: DNA
; ORGANISM: homo sapien
US-10-891-260-7937

Query Match      60.0%; Score 15.2; DB 24; Length 33;
Best Local Similarity 77.3%; Pred. No. 1.2e+04;
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACTCTCTTCC 22
      ||||| ||||| ||||| |||||
Db      11 CAAATCTTAGCTCTCTCTTCC 32

RESULT 28
US-10-809-189-7617
; Sequence 7617, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7617
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-7617

Query Match      60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AACTCATCACCACTCTCTTCCAT 24
      ||||| ||||| ||||| |||||
Db      3 AACTCATCTGACTCTCACCCAT 25

RESULT 29
US-10-956-157-53600/c
; Sequence 53600, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7617
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-7617
```

```
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53600
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-53600

Query Match      60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACTCTCTTCCA 23
      ||||| ||||| ||||| |||||
Db      23 CATCTATTAAACACTCTGGTCCA 1

RESULT 30
US-10-956-157-53604/c
; Sequence 53604, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53604
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-53604

Query Match      60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACTCTCTTCCA 23
      ||||| ||||| ||||| |||||
Db      24 CATCTATTAAACACTCTGGTCCA 2

RESULT 31
US-10-956-157-53605/c
; Sequence 53605, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53605
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-53605

Query Match      60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACTCTCTTCCA 23
      ||||| ||||| ||||| |||||
```



```
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Mastelli, Luca
; APPLICANT: Rastler, Charles E.
; APPLICANT: Kellach, Valerie
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1372
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ag4532 Forward
US-10-072-012-1372
Query Match 59.2%; Score 14.8; DB 19; Length 22;
Best Local Similarity 88.9%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 TCACACTCTCTTCATC 25
Db 3 TCACCTCTCTCTCCATC 20
RESULT 37
US-09-978-295A-142/c
; Sequence 142, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
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; PRIOR APPLICATION NUMBER: 60/079920
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTC 21
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Db 23 CACATCACCACCTCTCTTC 6

RESULT 38
US-09-978-697-142/c
; Sequence 142, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/378,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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RESULT 39

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; Sequence 142, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Eaton, Dan
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.

;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas P.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
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Query Match      59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      4 CTCATCACCACCTCTCTTC 21
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Db      23 CACATCACCACCTCTTC 6

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US-09-999-832A-142/c
; Sequence 142, Application US/09999832A
; Publication No US20020192706A1
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR FILING DATE: 1997-10-17
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Query Match 59.2%; Score 14.8; DB 9; Length 24;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	4	CTCATCACCACTCTCTTC	21
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OM nucleic - nucleic search, using sw model

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Perfect score: 25
Sequence: 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	14.6	58.4	29	6	AR526910	AR526910 Sequence
C 4	14.2	56.8	22	6	AX703317	AX703317 Sequence
5	14.2	56.8	25	6	A83424	A83424 Sequence 10
6	14.2	56.8	39	6	AR481983	AR481983 Sequence
7	14.2	56.8	41	6	A18467	A18467 light chain
8	14.2	56.8	41	6	A24273	A24273 Oligonucleo
9	14.2	56.8	41	6	AR028581	AR028581 Sequence
10	14.2	56.8	41	6	AR085792	AR085792 Sequence
11	14.2	56.8	41	6	AR474145	AR474145 Sequence
12	14.2	56.8	48	6	I03017	I03017 Sequence 7
13	14.2	56.8	49	6	A08605	A08605 Oligonucleo
14	14.2	56.8	49	6	AR337938	AR337938 Sequence
C 15	14.2	56.8	50	6	CQ009070	CQ009070 Sequence
C 16	14	56.0	50	6	CQ003048	CQ003048 Sequence
17	13.8	55.2	21	6	BD134567	BD134567 Method fo
C 18	13.8	55.2	33	6	AX787200	AX787200 Sequence
C 19	13.8	55.2	33	6	AX787202	AX787202 Sequence

C 20	13.8	55.2	33	6	AX787209	AX787209 Sequence
C 21	13.8	55.2	33	6	AX787211	AX787211 Sequence
C 22	13.8	55.2	49	6	CQ848579	CQ848579 Sequence
23	13.8	55.2	50	6	CQ003302	CQ003302 Sequence
24	13.8	55.2	50	6	CQ848580	CQ848580 Sequence
C 25	13.6	54.4	20	6	AX294559	AX294559 Sequence
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C 28	13.6	54.4	25	6	CQ620789	CQ620789 Sequence
C 29	13.6	54.4	25	6	CQ620790	CQ620790 Sequence
C 30	13.6	54.4	25	6	CQ620791	CQ620791 Sequence
C 31	13.6	54.4	25	6	CQ620792	CQ620792 Sequence
C 32	13.6	54.4	25	6	CQ620793	CQ620793 Sequence
C 33	13.6	54.4	25	6	CQ620794	CQ620794 Sequence
C 34	13.6	54.4	25	6	AR461852	AR461852 Sequence
C 35	13.6	54.4	25	6	AR461853	AR461853 Sequence
C 36	13.6	54.4	25	6	AR461854	AR461854 Sequence
C 37	13.6	54.4	25	6	AR461855	AR461855 Sequence
C 38	13.6	54.4	25	6	AR461856	AR461856 Sequence
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ALIGNMENTS

RESULT 1	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
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DEFINITION	I12903	Sequence 10 from patent US 5429923.				
ACCESSION	I12903	Sequence 10 from patent US 5429923.				
VERSION	I12903.1	GI:910880				
KEYWORDS						
SOURCE		Unknown.				
ORGANISM		Unknown.				
REFERENCE		Unclassified.				
AUTHORS		1 (bases 1 to 25)				
TITLE		Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.				
JOURNAL		Method for detecting hypertrophic cardiomyopathy associated				
FEATURES		mutations				
source		Patent: US 5429923-A 10 04-JUL-1995;				
		Location/Qualifiers				
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LOCUS	CQ774405	Sequence 10 from Patent WO2004013169.	25 bp	DNA	linear	PAT 06-MAR-2004
DEFINITION	CQ774405	Sequence 10 from Patent WO2004013169.				
ACCESSION	CQ774405	Sequence 10 from Patent WO2004013169.				
VERSION	CQ774405.1	GI:45237639				
KEYWORDS						
SOURCE		synthetic construct				
ORGANISM		synthetic construct				
REFERENCE		other sequences; artificial sequences.				
AUTHORS		1 Vanderkimpfen,G., van Eldik,G. and Meulewaeter,F.				

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TITLE      Corn root preferential promoters and uses thereof
JOURNAL    Patent: WO 2004013169-A 10 12-FEB-2004;
           Bayer BioScience N.V. (BE)
FEATURES   source
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Qy 4 GAGCCTAGCAGATTCATGGCA 24
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Db 23 GAGCATAGTCGATCCATGGCA 3

RESULT 3
LOCUS      AR526910
DEFINITION Sequence 24 from patent US 6723520.
ACCESSION  AR526910
VERSION     AR526910.1 GI:53913800
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 29)
AUTHORS     Wang, W., Gish, K.C., Schall, T.J., Vicari, A. and Zlotnik, A.
TITLE       Antibodies that bind chemokine teck
JOURNAL     Patent: US 6723520-A 24 20-APR-2004;
           Location/Qualifiers
FEATURES    source
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ORIGIN
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Best Local Similarity 81.0%; Pred. No. 1.8e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCAC 25
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Db 8 AGCAGAGCAGAGTGATGGCAC 28

RESULT 4
LOCUS      AX703317/c
DEFINITION Sequence 546 from Patent WO02059313.
ACCESSION  AX703317
VERSION     AX703317.1 GI:29538363
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Li, L., Ballinger, R.A., Padigar, M., Kekuda, R., Colman, S.D.,
           Spytek, K.A., Casman, S.J., Vernet, C.A., Shenoy, S.G., Gusev, V.,
           Malyankar, U.M., Edinger, S., Gerlach, V., Smithson, G., Stone, D.J.,
           Sciore, P., Macdougall, J.R., Gunther, E., Peyman, J.A., Ellerman, K.,
           Gangolli, E.A. and Milliet, I.
TITLE       G-protein coupled receptors and nucleic acids encoding same
JOURNAL     Patent: WO 02059313-A 546 01-AUG-2002;
           Curagen Corporation (US)
           Location/Qualifiers
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TITLE      Corn root preferential promoters and uses thereof
JOURNAL    Patent: WO 2004013169-A 10 12-FEB-2004;
           Bayer BioScience N.V. (BE)
FEATURES   source
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ACCESSION  AR526910
VERSION     AR526910.1 GI:53913800
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 29)
AUTHORS     Wang, W., Gish, K.C., Schall, T.J., Vicari, A. and Zlotnik, A.
TITLE       Antibodies that bind chemokine teck
JOURNAL     Patent: US 6723520-A 24 20-APR-2004;
           Location/Qualifiers
FEATURES    source
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Best Local Similarity 81.0%; Pred. No. 1.8e+04;
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Qy 5 AGCCTAGCAGATTCATGGCAC 25
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Db 8 AGCAGAGCAGAGTGATGGCAC 28

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LOCUS      AX703317/c
DEFINITION Sequence 546 from Patent WO02059313.
ACCESSION  AX703317
VERSION     AX703317.1 GI:29538363
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Li, L., Ballinger, R.A., Padigar, M., Kekuda, R., Colman, S.D.,
           Spytek, K.A., Casman, S.J., Vernet, C.A., Shenoy, S.G., Gusev, V.,
           Malyankar, U.M., Edinger, S., Gerlach, V., Smithson, G., Stone, D.J.,
           Sciore, P., Macdougall, J.R., Gunther, E., Peyman, J.A., Ellerman, K.,
           Gangolli, E.A. and Milliet, I.
TITLE       G-protein coupled receptors and nucleic acids encoding same
JOURNAL     Patent: WO 02059313-A 546 01-AUG-2002;
           Curagen Corporation (US)
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FEATURES    source
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TITLE      Corn root preferential promoters and uses thereof
JOURNAL    Patent: WO 2004013169-A 10 12-FEB-2004;
           Bayer BioScience N.V. (BE)
FEATURES   source
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 21 TGGTCTTACCAGATTCATG 3

RESULT 5
LOCUS      A83424
DEFINITION Sequence 10 from Patent WO9850067.
ACCESSION  A83424
VERSION     A83424.1 GI:6732762
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 25)
AUTHORS     Goebel, W. and Demuth, A.
TITLE       USE OR A SECRETION VECTOR FOR FERTILITY CONTROL BY ORAL VACCINATION
JOURNAL     Patent: WO 9850067-A 10 12-NOV-1998;
           GOEBEL WERNER (DE); SCHERING AG (DE)
           Location/Qualifiers
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Best Local Similarity 84.2%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCA 24
|||||
Db 1 GCCTAGAGGATGCATGGCA 19

RESULT 6
LOCUS      AR481983
DEFINITION Sequence 50 from patent US 6699974.
ACCESSION  AR481983
VERSION     AR481983.1 GI:47243890
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 39)
AUTHORS     Ono, K., Ohtomo, T., Tsuchiya, M., Yoshimura, Y., Koishihara, Y. and
           Kosaka, M.
TITLE       Reshaped human anti-HM 1.24 antibody
JOURNAL     Patent: US 6699974-A 50 02-MAR-2004;
           Location/Qualifiers
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           /organism="unknown"
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Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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REFERENCE	1 (bases 1 to 41)	Score	DB	Length	DB	Length	DB	Length
AUTHORS	Crowe, J. Scott. and Lewis, A. Peter.	56.8%;	14.2;	41;	6;	41;	6;	41;
TITLE	Preparation of chimaeric antibodies using the recombinant PCR strategy	84.2%;	3.1e+04;	3;	0;	3;	0;	3;
JOURNAL	Patent: US 5858725-A 17 12-JAN-1999;							
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Db	22 GGTGTGCCAAGCAGATTCA 40							
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DEFINITION	Sequence 22 from patent US 5985279.							
ACCESSION	AR085792							
VERSION	AR085792.1 GI:10012558							
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1 (bases 1 to 41)							
AUTHORS	Waldmann, H., Sims, M. and Crowe, S.							
TITLE	Humanized antibody against CD18							
JOURNAL	Patent: US 5985279-A 22 16-NOV-1999;							
FEATURES	Location/Qualifiers							
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DEFINITION	Sequence 22 from patent US 6689869.							
ACCESSION	AR474145							
VERSION	AR474145.1 GI:42712951							
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1 (bases 1 to 41)							
AUTHORS	Waldmann, H., Sims, M.J. and Crowe, J.S.							
TITLE	Labeled humanized anti-CD18 antibodies and fragments and kits comprising same							
JOURNAL	Patent: US 6689869-A 22 10-FEB-2004;							
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Db      22 GGTGTGCCAAGCAGATTCA 40

RESULT 12
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DEFINITION   Sequence 7 from Patent US 4618578.
ACCESSION   I03017
VERSION     I03017.1 GI:268476
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 48)
AUTHORS    Burke,R.L., Urdea,M.S. and Valenzuela,P.D.T.
TITLE      Expression of glycoprotein D of herpes simplex virus
JOURNAL    Patent: US 4618578-A 7 21-OCT-1986;
           Chiron Corporation; Emeryville, CA
FEATURES   source
           1..48
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 48;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
Db      13 GCTGACCCAAACAGATTCA 31

RESULT 13
LOCUS   A08605               49 bp      DNA          linear      PAT 10-SEP-1993
DEFINITION   Oligonucleotide KK2.
ACCESSION   A08605
VERSION     A08605.1 GI:411672
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
           other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 49)
AUTHORS    .
JOURNAL    Patent: WO 8907452-A 7 24-AUG-1989;
           Location/Qualifiers
           1..49
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 49;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
Db      12 GGTGTGCCAAGCAGATTCA 30

RESULT 14
LOCUS   AR337938             49 bp      DNA          linear      PAT 17-AUG-2003
DEFINITION   Sequence 41 from patent US 6569430.
ACCESSION   AR337938
VERSION     AR337938.1 GI:33724583
KEYWORDS    .
SOURCE      Unknown.

ORGANISM    Unknown.
REFERENCE   1
AUTHORS    Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
           methods of use thereof
JOURNAL    Patent: WO 0147944-A 1688 05-JUL-2001;

ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 49)
AUTHORS    Waldmann,H., Clark,M.R., Winter,G.P. and Riechmann,L.
TITLE      Antibodies to the antigen Campath-1
JOURNAL    Patent: US 6569430-A 41 27-MAY-2003;
           Location/Qualifiers
           1..49
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 49;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
Db      12 GGTGTGCCAAGCAGATTCA 30

RESULT 15
LOCUS   CQ009070/c           50 bp      DNA          linear      PAT 16-JAN-2004
DEFINITION   Sequence 7710 from Patent WO0147944.
ACCESSION   CQ009070
VERSION     CQ009070.1 GI:41015796
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
           methods of use thereof
JOURNAL    Patent: WO 0147944-A 7710 05-JUL-2001;
           Curagen Corporation (US)
           Location/Qualifiers
           1..50
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

misc_feature
           25..26
           /note="Nucleotide deleted between bases 25 and 26
           Accession number cg43950029"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 50;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
Db      25 GCAGAGCCTAGCAGACACA 7

RESULT 16
LOCUS   CQ003048/c           50 bp      DNA          linear      PAT 16-JAN-2004
DEFINITION   Sequence 1688 from Patent WO0147944.
ACCESSION   CQ003048
VERSION     CQ003048.1 GI:41009680
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
           methods of use thereof
JOURNAL    Patent: WO 0147944-A 1688 05-JUL-2001;

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FEATURES
  source
    Curagen Corporation (US)
    Location/Qualifiers
      1..50
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
      25..26
      /note="Nucleotide deleted between bases 25 and 26"
      Accession number CG44019290"

ORIGIN
Query Match      56.0%; Score 14; DB 6; Length 50;
Best Local Similarity 77.3%; Pred. No. 4e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGG 22
    ||||| ||||| ||||| |||||
Db 26 GCTGGCCTAGCAGCGACATGG 5

RESULT 17
BD134567
LOCUS BD134567 21 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for assaying an enzyme participating in conjugation with
sulfuric acid in human beings, and probe and kit therefor.
ACCESSION BD134567
VERSION BD134567.1 GI:23229512
KEYWORDS JP 2002085067-A/17.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.
TITLE Method for assaying an enzyme participating in conjugation with
sulfuric acid in human beings, and probe and kit therefor
JOURNAL Patent: JP 2002085067-A 17 26-MAR-2002;
OTSUKA PHARMACEUTICAL FACTORY INC
COMMENT OS Human CHST4 gene
PN JP 2002085067-A/17
PD 26-MAR-2002
PF 07-SEP-2000 JP 2000272229
PI MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,ISAO HIRAOKA
PC C12N15/09,C12Q1/25,C12Q1/68,G01N21/78,G01N33/53,PC
G01N33/566,
PC C12N15/00
CC Method for assaying an enzyme participating in conjugation CC
with sulfuric
CC acid in human beings, and probe and kit therefor FH Key
Location/Qualifiers
FT source 1..21
FT Location/Qualifiers
  source
    Location/Qualifiers
      1..21
      /organism="unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644"

ORIGIN
Query Match      55.2%; Score 13.8; DB 6; Length 21;
Best Local Similarity 88.2%; Pred. No. 4.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATG 21
    ||||| ||||| ||||| |||||
Db 5 AGCCAGCAAAATTCATG 21

RESULT 18
AX787200/c
LOCUS AX787200 33 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 7 from Patent WO03031469.
ACCESSION AX787200
VERSION AX787200.1 GI:32954380
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KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Lopez,S.M. and Jimenez,M.T.
TITLE Means for improving immune response
JOURNAL Patent: WO 03031469-A 7 17-APR-2003;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ; Lopez,
Sonia Moreno (ES) ; Jimenez, Marcos Timon (ES)
FEATURES
  source
    Location/Qualifiers
      1..33
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="1. PCR: Primer left"

ORIGIN
Query Match      55.2%; Score 13.8; DB 6; Length 33;
Best Local Similarity 72.0%; Pred. No. 4.9e+04;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 32 GGTGACCCTCGATGTTTCATGGTAC 8

RESULT 19
AX787202/c
LOCUS AX787202 33 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 9 from Patent WO03031469.
ACCESSION AX787202
VERSION AX787202.1 GI:32954382
KEYWORDS synthetic construct
SOURCE synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Lopez,S.M. and Jimenez,M.T.
TITLE Means for improving immune response
JOURNAL Patent: WO 03031469-A 9 17-APR-2003;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ; Lopez,
Sonia Moreno (ES) ; Jimenez, Marcos Timon (ES)
FEATURES
  source
    Location/Qualifiers
      1..33
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="2. PCR: Primer left"

ORIGIN
Query Match      55.2%; Score 13.8; DB 6; Length 33;
Best Local Similarity 72.0%; Pred. No. 4.9e+04;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 32 GGTGACCCTCGATGTTTCATGGTAC 8

RESULT 20
AX787209/c
LOCUS AX787209 33 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 6 from Patent WO03031470.
ACCESSION AX787209
VERSION AX787209.1 GI:32954387
KEYWORDS synthetic construct
SOURCE synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fuentes,L. and Jimenez,M.T.
TITLE Dna-expression construct for treatment of infections with
```


Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGG 22
Db 29 GACTAGCAGATTCACGG 45

RESULT 25
AX294559/c
LOCUS AX294559
DEFINITION Sequence 6321 from Patent WO0179548.
ACCESSION AX294559
VERSION AX294559.1 GI:17056242
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 6321 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 20 GTCCCGCAGATTCAGGCAC 1

RESULT 26
AR148747/c
LOCUS AR148747
DEFINITION Sequence 104 from patent US 6225451.
ACCESSION AR148747
VERSION AR148747.1 GI:15112837
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Ballinger,D.G., Ding,W., Wagner,S. and Hess,M.A.
TITLE Chromosome 11-linked coronary heart disease susceptibility gene
JOURNAL CHD1
PATENT: US 6225451-A 104 01-MAY-2001;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 21;
Best Local Similarity 80.0%; Pred. No. 6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 21 GCTTAGAAGAGTGATGGCAC 2

RESULT 27
AX289926/c
LOCUS AX289926
DEFINITION Sequence 5530 from Patent WO0192524.
ACCESSION CO620790
VERSION CO620790.1 GI:41671008
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DEFINITION Sequence 1688 from Patent WO0179548.
ACCESSION AX289926
VERSION AX289926.1 GI:17051609
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 1688 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 24;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 24 GTCCCGCAGATTCAGGCAC 5

RESULT 28
CO620789/c
LOCUS CO620789
DEFINITION Sequence 5529 from Patent WO0192524.
ACCESSION CO620789
VERSION CO620789.1 GI:41671007
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5529 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 25 GCCCAGCATCTCCATGGCAC 6

RESULT 29
CO620790/c
LOCUS CO620790
DEFINITION Sequence 5530 from Patent WO0192524.
ACCESSION CO620790
VERSION CO620790.1 GI:41671008
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5530 06-DEC-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 24 GCCCAGCATCTCCATGGCAC 5
RESULT 30
CO620791/c
LOCUS CO620791 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5531 from Patent WO0192524.
ACCESSION CO620791
VERSION CO620791.1 GI:41671009
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5531 06-DEC-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 23 GCCCAGCATCTCCATGGCAC 4
RESULT 31
CO620792/c
LOCUS CO620792 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5532 from Patent WO0192524.
ACCESSION CO620792
VERSION CO620792.1 GI:41671010
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5532 06-DEC-2001;
Acemica, Inc. (US)

FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 22 GCCCAGCATCTCCATGGCAC 3
RESULT 32
CO620793/c
LOCUS CO620793 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5533 from Patent WO0192524.
ACCESSION CO620793
VERSION CO620793.1 GI:41671011
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5533 06-DEC-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 21 GCCCAGCATCTCCATGGCAC 2
RESULT 33
CO620794/c
LOCUS CO620794 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5534 from Patent WO0192524.
ACCESSION CO620794
VERSION CO620794.1 GI:41671012
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5534 06-DEC-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

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Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      20 GCCCAGCATCTCCATGGCAC 1

RESULT 34
AR461852/c
LOCUS      AR461852      25 bp      DNA
DEFINITION Sequence 5529 from patent US 6686188.
ACCESSION  AR461852
VERSION     AR461852.1 GI:42696909
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL     Patent: US 6686188-A 5529 03-FEB-2004;
FEATURES    Location/Qualifiers
            source
            1..25
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      23 GCCCAGCATCTCCATGGCAC 4

RESULT 37
AR461855/c
LOCUS      AR461855      25 bp      DNA
DEFINITION Sequence 5532 from patent US 6686188.
ACCESSION  AR461855
VERSION     AR461855.1 GI:42696912
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL     Patent: US 6686188-A 5532 03-FEB-2004;
FEATURES    Location/Qualifiers
            source
            1..25
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      22 GCCCAGCATCTCCATGGCAC 3

RESULT 38
AR461856/c
LOCUS      AR461856      25 bp      DNA
DEFINITION Sequence 5533 from patent US 6686188.
ACCESSION  AR461856
VERSION     AR461856.1 GI:42696913
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
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Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      20 GCCCAGCATCTCCATGGCAC 1

RESULT 34
AR461852/c
LOCUS      AR461852      25 bp      DNA
DEFINITION Sequence 5529 from patent US 6686188.
ACCESSION  AR461852
VERSION     AR461852.1 GI:42696909
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL     Patent: US 6686188-A 5529 03-FEB-2004;
FEATURES    Location/Qualifiers
            source
            1..25
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      25 GCCCAGCATCTCCATGGCAC 6

RESULT 35
AR461853/c
LOCUS      AR461853      25 bp      DNA
DEFINITION Sequence 5530 from patent US 6686188.
ACCESSION  AR461853
VERSION     AR461853.1 GI:42696910
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL     Patent: US 6686188-A 5530 03-FEB-2004;
FEATURES    Location/Qualifiers
            source
            1..25
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      24 GCCCAGCATCTCCATGGCAC 5

RESULT 36
AR461854/c
```

TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 5533 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25
||| ||||| ||||| |||||
Db 21 GCCCAGCATCTCCATGGCAC 2

RESULT 39
AR461857/c
LOCUS AR461857 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 5534 from patent US 6686188.
ACCESSION AR461857
VERSION AR461857.1 GI:42696914
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu.Y., Ji.Y., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 5534 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25
||| ||||| ||||| |||||
Db 20 GCCCAGCATCTCCATGGCAC 1

RESULT 40
AX427664
LOCUS AX427664 43 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from Patent WO0233106.
ACCESSION AX427664
VERSION AX427664.1 GI:21537783
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233106-A 5 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES Location/Qualifiers
source 1..43
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ProRIPR primer"
misc_feature 1..19
/note="Introduced restriction sites"

ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 43;
Best Local Similarity 80.0%; Pred. No. 6.3e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTCATGGC 23
||| ||||| ||||| |||||
Db 5 GAGTCTAGAGGATCCATGGC 24

Search completed: November 18, 2005, 17:43:03
Job time : 694.731 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 172.148 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-10

Perfect score: 25

Sequence: 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
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4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	2	AAQ911130
2	25	100.0	25	9	ACA63120
3	25	100.0	25	13	ADRO5306
4	15	60.0	50	6	AB201194
C 5	14.8	59.2	37	12	ADOS3185
C 6	14.6	58.4	25	12	ADK70978
7	14.6	58.4	29	10	ABX95944
8	14.6	58.4	29	12	ADQ67857
C 9	14.4	57.6	29	6	ABQ76852
C 10	14.4	57.6	33	6	AD31605
C 11	14.2	56.8	22	6	AB559198
C 12	14.2	56.8	25	2	AAV65080
C 13	14.2	56.8	28	10	ADB67035
C 14	14.2	56.8	29	4	AAH47313
C 15	14.2	56.8	38	2	AAQ94493
16	14.2	56.8	38	2	AAI38608
17	14.2	56.8	39	2	AAQ12689
18	14.2	56.8	39	2	AAV39382
19	14.2	56.8	39	2	AAQ59432
20	14.2	56.8	41	2	AAQ24659

21	14.2	56.8	41	2	AAQ35184	AAQ35184 Light cha
C 22	14.2	56.8	50	4	AAI34502	AAI34502 Human SNP
23	14	56.0	41	12	ADH05434	ADH05434 Gene poly
24	14	56.0	41	12	ADH91221	ADH91221 1-beta-me
25	14	56.0	47	2	AAZ52556	AAZ52556 Human gen
26	14	56.0	47	3	AAZ68752	AAZ68752 Human map
C 27	14	56.0	50	4	AAI28480	AAI28480 Human SNP
28	14	56.0	50	6	ABZ05333	ABZ05333 Human leu
29	13.8	55.2	51	6	ABK70835	ABK70835 PCR prime
30	13.8	55.2	25	9	ACK02180	ACK02180 Human mic
C 31	13.8	55.2	33	10	ADC21315	ADC21315 Plasmid p
C 32	13.8	55.2	33	10	ADC21313	ADC21313 Plasmid p
C 33	13.8	55.2	33	10	ADC21307	ADC21307 Plasmid p
C 34	13.8	55.2	33	10	ADC21305	ADC21305 Plasmid p
35	13.8	55.2	49	13	ADQ31581	ADQ31581 Multiplex
36	13.8	55.2	50	4	AAI28734	AAI28734 Human SNP
37	13.8	55.2	50	13	ADQ31582	ADQ31582 Multiplex
C 38	13.6	54.4	20	6	ABI94601	ABI94601 Capture o
C 39	13.6	54.4	21	2	AAZ26929	AAZ26929 Human chr
C 40	13.6	54.4	21	4	AAF95928	AAF95928 Human chr
C 41	13.6	54.4	24	6	ABI85772	ABI85772 Capture o
C 42	13.6	54.4	24	6	ABI85773	ABI85773 Capture o
C 43	13.6	54.4	25	6	ABN05537	ABN05537 Human GDM
C 44	13.6	54.4	25	6	ABN05540	ABN05540 Human GDM
C 45	13.6	54.4	25	6	ABN05539	ABN05539 Human GDM

ALIGNMENTS

RESULT 1
AAQ911130
ID AAQ911130 standard; cDNA; 25 BP.
XX
AC AAQ911130;
XX
DT 19-FEB-1996 (first entry)
XX
DE Beta-cardiac myosin heavy chain PCR primer B9.1R.
XX
KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
diagnosis; primer; mutation; detection; ss.
XX
OS Synthetic.
XX
FN US429923-A.
XX
PD 04-JUL-1995.
XX
PF 11-DEC-1992; 92US-00989160.
XX
PR 11-DEC-1992; 92US-00989160.
XX
(HARD) HARVARD COLLEGE.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
(GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.
PI Seidman J, Seidman C, Watkins H, Rosenzweig A;
XX WPI; 1995-245715/32.
PT Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
XX useful for testing asymptomatic individual(s).
XX
Example 1; Col 10; 22pp; English.
XX
AAQ91121-091130 are nested PCR primers used for the amplification and
CC identification of beta-cardiac myosin heavy-chain RNA. They are used in a
CC new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
CC the method involves detecting the presence or absence of specific HC-
CC associated mutations in the beta-cardiac myosin heavy-chain obtained from
CC a blood sample. The method may be used to diagnose familial or sporadic
CC HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
CC a broad applicability and may be used to detect mutations responsible for
CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Db 1 GCTGAGCCTAGCAGATTCATGGCAC 25

RESULT 2

ACA63120
ID ACA63120 standard; DNA; 25 BP.

XX ACA63120;

DT 28-AUG-2003 (first entry)

DE Human beta cardiac myosin heavy chain PCR primer B9.1R.

XX Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

OS US2003054343-A1.

XX 20-MAR-2003.

XX 06-JUN-1995; 95US-00469172.

XX 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.
XX (SEID/) SEIDMAN J.
XX (WATK/) WATKINS H.
XX (ROSE/) ROSENZWEIG A.

PI Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with
XX hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
XX hemophilia, by detecting a mutation in an amplified product of a beta
XX cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
XX associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
XX and FHC) comprises detecting a mutation associated with hypertrophic
XX cardiomyopathy in an amplified product of a beta cardiac myosin heavy
XX chain DNA. The mutations associated with SHC/FHC are detected in the
XX myosin gene isolated from blood, by detecting mis-matched areas in RNA-
XX DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
XX sample). FHC associated point mutation can be classified and used to
XX determine life expectancy in affected individuals e.g. using a Kaplan-
XX Meier curve for the classified type of FHC causing point mutation. Also
XX included are an RNA probe comprising ribonucleotides arranged in a
XX sequence which is complementary to at least a portion of beta-cardiac
XX myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
XX amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
CC DNA. The method is useful for detecting the presence or absence of a
CC mutation associated with hypertrophic cardiomyopathy. This method is
CC especially useful for diagnosing SHC and FHC, as well as for determining
CC the estimated life expectancy of a person with familial hypertrophic
CC cardiomyopathy. In particular, the method is useful for determining an
CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
CC chain gene containing an FHC-associated mutation

XX Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Db 1 GCTGAGCCTAGCAGATTCATGGCAC 25

RESULT 3

ADR05306
ID ADR05306 standard; DNA; 25 BP.

XX ADR05306;

XX 21-OCT-2004 (first entry)

DE Human beta cardiac myosin heavy chain mutation detection primer B9.1R.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;

KW familial hypertrophic cardiomyopathy;
KW sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

XX US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.
XX (SEID/) SEIDMAN J.
XX (WATK/) WATKINS H.
XX (ROSE/) ROSENZWEIG A.

PI Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to
XX diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
XX myosin heavy-chain DNA and detecting the mutation in the amplified
XX product.

XX Claim 18; SEQ ID NO 10; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
XX associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
XX SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
XX comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
XX amplified product, and detecting the presence or absence of a mutation
XX associated with hypertrophic cardiomyopathy in the amplified product,
XX thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
XX included are a set of DNA oligonucleotide primers for amplifying beta-
XX cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

XX Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCATGGCAC 25
|||||
DB 1 GCTGAGCCTAGCAGATTCATGGCAC 25

RESULT 4

ID ABZ01194
ABZ01194 standard; DNA; 50 BP.

XX AC ABZ01194;

XX 09-JAN-2003 (first entry)

XX Human leukocyte gene expression profiling probe SEQ ID NO 1185.

XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.

XX Homo sapiens.

XX WO200257414-A2.

XX 25-JUL-2002.

XX 22-OCT-2001; 2001WO-US047856.

XX 20-OCT-2000; 2000US-0241994P.

XX 08-JUN-2001; 2001US-0296764P.

XX (BIOTEC) BIOMEDICAL INC.

XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

XX Ly N, Woodward R, Quettermous T, Johnson F;

XX WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 362; Opp; English.

XX The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX Sequence 50 BP; 21 A; 9 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 15; DB 6; Length 50;
Best Local Similarity 78.3%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGAGCCTAGCAGATTCATGGCAC 25
|||||
DB 14 TGAGCCTAGCAGATTCATGGCAC 36

RESULT 5

ADO59185/c
ID ADO59185 standard; DNA; 37 BP.

XX AC ADO59185;

XX 26-AUG-2004 (first entry)

XX PCR primer used to amplify human SLC-1 DNA SeqID 7.

XX human; SLC-1; primer; ss; melanin-concentrating hormone receptor;
KW antagonist; heterocyclic ring; anorectic; obesity; PCR.

XX Homo sapiens.

XX WO2004046110-A1.

XX 03-JUN-2004.

XX 14-NOV-2003; 2003WO-JP014534.

XX 15-NOV-2002; 2002JP-00332950.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX Kaku H, Kondoh Y, Hayashibe S, Kamikubo T, Iwasaki F;

XX Matsumoto S, Kimura Y, Kurama T;

XX WPI; 2004-440938/41.

XX Melanin concentrating hormone receptor antagonist useful in
PT pharmaceuticals for preventing obesity, contains heterocyclic ring
PT derivative or its salt as active ingredient.

XX Example 359; SEQ ID NO 7; 155pp; Japanese.

XX This invention relates to a novel melanin-concentrating hormone receptor
CC protein antagonist, a heterocyclic ring derivative or a salt thereof.
CC Specifically, it refers to the development of a drug that contains this
CC nitrogen-containing heterocyclic ring as the main skeleton of the
CC antagonist compound, that works as the active ingredient. The present
CC invention describes this antagonist as a melanin-concentrating hormone
CC receptor inhibitor that exhibits anorectic activities and as such can be
CC used to treat and/or prevent obesity. This oligonucleotide sequence is a
CC PCR primer used in an exemplification of the invention.

DE Human CRAM RT-PCR primer for exon 3.
 XX Human; ss; PCR; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
 KW chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR;
 KW Monocyte/dendritic cell receptor for chemokine; abnormal physiology;
 KW development; inflammatory condition; asthma; RT-PCR;
 KW reverse transcriptase PCR; primer; CRAM.
 XX
 OS Mus sp.
 XX
 PN US2004137578-A1.
 XX
 PD 15-JUL-2004.
 XX
 PF 09-JAN-2004; 2004US-00754071.
 XX
 PR 05-JUL-1996; 96US-0021664P.
 PR 11-OCT-1996; 96US-0028329P.
 PR 04-JUN-1997; 97US-0048593P.
 PR 03-JUL-1997; 97US-0088797P.
 PR 03-JAN-2002; 2002US-00039659.
 XX
 PA (WANG/) WANG W.
 PA (GISH/) GISH K C.
 PA (SCHA/) SCHALL T J.
 PA (VICA/) VICARI A.
 PA (ZLOT/) ZLOTNIK A.
 XX
 PI Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;
 XX WPI; 2004-533376/51.
 DR
 XX
 XX New substantially pure or isolated Thymus Expressed Chemokine (TECK),
 PT useful for treating conditions associated with abnormal physiology or
 PT development, including inflammatory conditions, e.g. asthma.
 XX
 PS Example 6; SEQ ID NO 24; 54pp; English.
 XX
 CC The invention relates to a substantially pure or isolated polypeptide
 CC comprises the mature protein of human TECK (thymus expressed chemokine)
 CC whose full length sequence appears as ADQ67837. Also included are an
 CC isolated or recombinant nucleic acid encoding mature TECK, an expression
 CC vector comprising the nucleic acid, a host cell comprising the expression
 CC vector and a method for producing the polypeptide. Also disclosed are the
 CC mouse TECK cDNA and protein, human chemokines MIP-3alpha and MIP-3beta
 CC (and their encoding cDNAs), and the cDNAs and encoded proteins
 CC corresponding to human chemokine receptors DCCR (dendritic cell receptor
 CC for chemokine) and M/DCCR (Monocyte/dendritic cell receptor for
 CC chemokine). The polypeptide is useful for treating conditions associated
 CC with abnormal physiology or development, including inflammatory
 CC conditions, e.g. asthma. An experiment was performed analysing the
 CC expression of human CRAM (not defined, unclear what its relation to TECK
 CC is). The present sequence is a reverse transcriptase (RT)-PCR primer used
 CC in the above analysis.
 XX
 SQ Sequence 29 BP; 11 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 58.4%; Score 14.6; DB 12; Length 29;
 Best Local Similarity 81.0%; Pred. No. 3.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 AGCCTAGCAGATTCATGGCAC 25
 ||| ||||| ||||| |||||
 DB 8 AGCAGACGACGATGATGGCAC 28
 ||| ||||| ||||| |||||
 RESULT 9
 ABQ76852
 ID ABQ76852 standard; DNA; 29 BP.
 XX
 AC ABQ76852;
 XX
 DT 25-MAR-2003 (first entry)

XX DE DC3 promoter associated oligonucleotide DC3a #4.
 XX Promoter; expression cassette; structural gene; plant; transgenic;
 KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
 KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
 KW heart disease; seed-specific; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN DE10102338-A1.
 XX
 PD 25-JUL-2002.
 XX
 PF 19-JAN-2001; 2001DE-01002338.
 XX
 PR 19-JAN-2001; 2001DE-01002338.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
 XX WPI; 2002-675961/73.
 DR
 XX
 XX New expression cassette for plant genes, useful for preparing transgenic
 PT plants that have increased production of polyunsaturated fatty acids.
 PT
 XX
 PS Example 13; Page 40; 188pp; German.
 XX
 CC This invention describes novel expression cassette (EC) containing at
 CC least one each of plant promoter (P) and structural gene (SG) expressed
 CC in plants, flanked by specific restriction enzyme (RE) recognition sites.
 CC The EC has the structure (L1-P-SG-L2) n where L1 is a polylinker
 CC (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
 CC sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing
 CC sequences and n = 1-3. The invention discloses a vector containing this
 CC EC, an organism containing the EC or the vector and a transgenic plant
 CC containing a (non-)functional nucleic acid in the vector. Transgenic
 CC plants e.g. linseed can be prepared with improved production of fatty acid
 CC esters with an increased content of polyunsaturated fatty acids (PUFA),
 CC useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
 CC PUFA are known to reduce levels of cholesterol in the blood and to
 CC protect against heart disease. The expression cassettes of the invention
 CC provide increased and more efficient production of fine chemicals
 CC (especially PUFA), including seed-specific production. This sequence
 CC represents a PCR primer used to illustrate the method of the invention
 XX
 SQ Sequence 29 BP; 4 A; 7 C; 8 G; 10 T; 0 U; 0 Other;
 Query Match 57.6%; Score 14.4; DB 6; Length 29;
 Best Local Similarity 75.0%; Pred. No. 4.2e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GCTGAGCCTAGCAGATTCATGGCA 24
 ||| ||||| ||||| |||||
 DB 2 GCGGATCCTAGCTTTTCTTGGCA 25
 ||| ||||| ||||| |||||
 RESULT 10
 AAD31605/C
 ID AAD31605 standard; DNA; 33 BP.
 XX
 AC AAD31605;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human reaper (hRpr) ORF amplifying primer, Fwd13.
 XX
 KW Human; reaper protein; Rpr; detection; purification; screening; therapy;
 KW tumour; cytostatic; open reading frame; ORF; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX

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PN WO200212540-A2.
XX
PD 14-FEB-2002.
XX
XX
PF 08-AUG-2001; 2001WO-US024765.
XX
XX
PR 08-AUG-2000; 2000US-0223699P.
XX
XX
PA (UYDU-) UNIV DUKE.
XX
XX
PI Kornbluth SA, Holley C;
XX
XX
PI WPT; 2002-241769/29.
XX
XX
PT New human homologue of Drosophila melanogaster reaper protein (hrpr),
PT useful for generating antibodies and for screening compounds, which can
PT inhibit or enhance hrpr activity.
XX
XX
PS Example 1; Page 24; 45pp; English.
XX
XX
CC The invention relates to human homologue of Drosophila melanogaster
CC Reaper protein (hrpr) and its corresponding nucleic acid. The hrpr
CC polypeptides are useful for generating antibodies, which can be used in
CC detection or purification protocols designed to detect or purify the
CC polypeptide to which the antibody is directed. These sequences are also
CC used for screening compounds, which can enhance or inhibit hrpr and for
CC treating tumours. The hrpr polynucleotides are useful as a probe or
CC primer. The present sequence is a PCR primer used to amplify human hrpr
CC open reading frame (ORF)
XX
XX
SQ Sequence 33 BP; 4 A; 12 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 57.6%; Score 14.4; DB 6; Length 33;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCTGAGCTAGCAGATTCATGGCA 24
    ||||| ||| |||| |||||
Db 32 GCTGGGCCACGACGACCATGGCA 9

RESULT 11
ABS55198/c
ID ABS55198 standard; DNA; 22 BP.
XX
XX
AC ABS55198;
XX
XX
DT 05-NOV-2002 (first entry)
XX
DE Human G-protein coupled receptor, forward primer #116.
XX
XX
KW Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;
KW diabetes; cell signal processing; metabolic pathway modulation; cancer;
KW adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;
KW immune response; neurodegenerative disorder; inflammatory disorder;
KW Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;
KW primer; PCR; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200259313-A2.
XX
XX
PD 01-AUG-2002.
XX
XX
PF 18-DEC-2001; 2001WO-US049394.
XX
XX
PR 18-DEC-2000; 2000US-0256635P.
PR 21-DEC-2000; 2000US-0257876P.
PR 04-JAN-2001; 2001US-0259743P.
PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.

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PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.
XX
XX
PA (CURA-) CURAGEN CORP.
XX
XX
PI Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;
PI Casman SJ, Vernet CAM, Shenoy SG, Gusev V, Malyankar UM, Edinger S;
PI Gerlach V, Smithson G, Stone DJ, Sciore P, Macdougall JR, Gunther E;
PI Peyman JA, Ellerman K, Gangolli EA, Millet I;
XX
XX
DR WPI; 2002-599789/64.
XX
XX
PT New G protein coupled receptor polypeptides and polynucleotides, useful
PT in gene therapy, particularly for treating or preventing cardiomyopathy,
PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
PT in humans.
XX
XX
PS Claim 1; Page 617; 685pp; English.
XX
XX
CC The invention relates to novel isolated G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
CC and antibody are useful for treating, preventing or alleviating a GPCR-
CC associated disorder or a pathological state in a subject, particularly a
CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
CC diabetes, or a disorder related to cell signal processing and metabolic
CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
CC for diagnosing the presence of or predisposition to a disease associated
CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
CC and polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant GPCR expression or
CC activity. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. Furthermore, the nucleic acids and
CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
CC cancer, uterus cancer, immune response, neurodegenerative disorders,
CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
CC Albritght hereditary osteodystrophy. These are also useful in developing a
CC powerful assay system for functional analysis of various human disorders,
CC as well as in diagnostic applications. ABS58747-ABS59231 represent human
CC GPCR coding sequences, primers and probes of the invention
XX
XX
SQ Sequence 22 BP; 7 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 56.8%; Score 14.2; DB 6; Length 22;
Best Local Similarity 84.2%; Pred. No. 5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGAGCCTAGCAGATTCATG 21
    ||||| ||||| |||||
Db 21 TGGTCTCTACCAGATTCATG 3

RESULT 12
AAV65080
ID AAV65080 standard; DNA; 25 BP.
XX
XX
AC AAV65080;
XX
XX
DT 05-FEB-1999 (first entry)
XX
XX
DE Human ZPA PCR primer huZPA5 #2.
XX
XX
KW ZPA; human; vector; expression; secretion; fertility control antigen;
KW attenuated Salmonella; Gram-negative; oral vaccine; haemolysin operon;
KW hly specific promoter; hlyR enhancer-like regulator; contraception;
KW PCR primer; ss.
XX
XX
OS Synthetic.
OS Homo sapiens.

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XX DE19720761-A1.
XX 12-NOV-1998.
XX
XX 07-MAY-1997; 97DE-01020761.
XX
XX 07-MAY-1997; 97DE-01020761.
XX (SCHD ) SCHERING AG.
XX
XX Donner P, Goebel W, Demuth A, Gentschev I, Hess J, Kaufmann S;
XX WPI; 1998-596140/51.
XX
XX Oral contraceptive vaccine containing recombinant salmonella -
XX transformed with vector containing gene for fertility control antigen.
XX
XX Disclosure; Page 6; 17pp; German.
XX
XX AAV65071-V65104 are PCR primers used in the construction of a novel
XX vector for expression and secretion of a fertility control antigen in
XX attenuated salmonella or other attenuated Gram-negative vaccine strains
XX to produce an oral vaccine. The vector comprises a gene encoding the
XX fertility control antigen under the control of a complete haemolysin
XX operon, including the hly specific promoter and the hlyR enhancer-like
XX regulator but excluding most of the hlyA gene. The vector is used for
XX immunological contraception by oral administration
XX
XX Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 56.8%; Score 14.2; DB 2; Length 25;
XX Best Local Similarity 84.2%; Pred. No. 5, 1e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 6 GCCTAGCAGATTCATGGCA 24
XX ||||| ||| |||||
XX Db 1 GCCTAGAGGATGCATGGCA 19
XX
XX RESULT 13
XX ADB67035/c
XX ID ADB67035 standard; DNA; 28 BP.
XX
XX AC ADB67035;
XX
XX DT 04-DEC-2003 (first entry)
XX
XX DE Mouse Galanin-like Peptide, GALP, primer mG-300R, SEQ ID 3.
XX
XX KW Cystostatic; Anorectic; Antidiabetic; Nootropic; Neuroprotective;
XX Gynaecological; mouse; Galanin-like Peptide; GALP; prostate cancer;
XX ovarian cancer; gynaecological disorder; diabetes; dementia;
XX eating disorder; primer; ss.
XX
XX OS Mus sp.
XX
XX PN WO2003070950-A1.
XX
XX PD 28-AUG-2003.
XX
XX PF 20-FEB-2003; 2003WO-JP001856.
XX
XX PR 22-FEB-2002; 2002JP-00047006.
XX
XX PR 24-APR-2002; 2002JP-00123170.
XX
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX
XX PI Kumano S, Kobayashi H, Ohtaki T;
XX
XX DR WPI; 2003-671814/63.
XX
XX PT Novel DNA for constructing knockout animals applicable in clarifying
XX
XX PT physiological function of the galactose membrane transporter and in
XX screening preventives or remedies for diseases, e.g. cancer.
XX
XX Example 1; Page 36; 118pp; Japanese.
XX
XX The present invention relates to mouse Galanin-like Peptide (GALP)
XX sequences (ADB67033-ADB67032). The sequences are useful for constructing
XX knockout animals which are useful in clarifying the physiological
XX function of GALP and in screening preventives or remedies for diseases
XX due to hypo- or hypersecretion of LH, e.g. prostate cancer, ovarian
XX cancer, gynaecological disorders, diabetes, dementia and eating
XX disorders, e.g. obesity and other disorders. The present sequence is a
XX primer for mouse GALP, which was used in an example from the invention.
XX
XX Sequence 28 BP; 5 A; 7 C; 9 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 56.8%; Score 14.2; DB 10; Length 28;
XX Best Local Similarity 84.2%; Pred. No. 5, 2e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 GCTGAGCCTAGCAGATTCA 19
XX ||||| ||| ||||| ||
XX Db 22 GCTGAGCCTGGCAGAAACA 4
XX
XX RESULT 14
XX AAH47313/c
XX ID AAH47313 standard; DNA; 29 BP.
XX
XX AC AAH47313;
XX
XX DT 30-NOV-2001 (first entry)
XX
XX DE Mouse MCHIR cDNA amplifying primer MCHIR (Eco RI).
XX
XX KW Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;
XX fluorescent polypeptide; orexigenic; anabolic; food intake; MCHIR;
XX green fluorescent protein; GFP; PCR primer; ss.
XX
XX OS Mus sp.
XX
XX PN WO200168706-A1.
XX
XX PD 20-SEP-2001.
XX
XX PF 14-MAR-2001; 2001WO-US008071.
XX
XX PR 15-MAR-2000; 2000US-0189698P.
XX
XX PA (MERI ) MERCK & CO INC.
XX
XX PI Marsh DJ;
XX
XX DR WPI; 2001-565791/63.
XX
XX PT Fusion proteins comprising melanin concentrating hormone receptor
XX peptides and fluorescent proteins, useful for identifying appetite
XX stimulants.
XX
XX Example 2; Page 33; 71pp; English.
XX
XX The invention provides melanin concentrating hormone (MCH) receptor
XX (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
XX MCHR polypeptide regions from different species. The MCHR fusion protein
XX comprise MCHR polypeptide region and a fluorescent polypeptide region
XX joined directly, or via a linker, to the carboxy side of the MCHR
XX polypeptide region. The MCHR fusion proteins can be expressed by standard
XX recombinant methodology. MCH action promotes feeding (orexigenic) and up
XX regulation of MCH activity stimulates food intake. Sequences AAH7313-14
XX represent PCR primers for amplifying mouse MCHIR cDNA, used in the
XX construction of mouse MCHIR-linker-green fluorescent protein (GFP)
XX variant fusion constructs
XX

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XX (MERI) MERCK & CO INC.
 XX Law MF, Mark GE, Williamson AR;
 XX WPI; 1991-216983/30.
 XX Prodn. of humanised recombinant immunoglobulin - including polymerase
 PT chain reaction amplification of murine antibody light and heavy chain
 PT variable portions.
 XX Disclosure; Fig 4; 78pp; English.
 XX The sequences in AAQ12685-Q12692 are primers for PCR mutagenesis and
 CC amplification of the Rei light chain variable region template so as to
 CC graft the CDRs of murine 1B4 into the Rei light chain variable region.
 CC See also EP-438312
 XX Sequence 39 BP; 11 A; 11 C; 9 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 56.8%; Score 14.2; DB 2; Length 39;
 Best Local Similarity 84.2%; Pred. No. 5.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCA 19
 DB 19 GGTGTGCCAAGCAGATTCA 37

RESULT 18
 ID AAV39382
 XX AAV39382 standard; DNA; 39 BP.
 XX AC
 XX AAV39382;
 XX DT 21-SEP-1998 (first entry)
 XX DE Humanised anti-HM1.24 antibody PCR primer SEQ ID NO:50.
 XX KW Mouse; human; humanised; anti-HM1.24 antibody; myeloma; FR; CDR;
 KW framework region; complementarity determining region; antigenicity;
 KW PCR primer; ss.
 XX OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX WO9814580-A1.
 XX PD 09-APR-1998.
 XX PF 03-OCT-1997; 97WO-JP003553.
 XX PR 04-OCT-1996; 96JP-00264756.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Ono K, Ontomo T, Tsuchiya M, Yoshimura Y, Koishihara Y, Kosaka M;
 WPI; 1998-286421/25.
 XX Humanised anti-HM1.24 antibody - for treatment of myeloma.
 XX Example 9; Page 134; 210pp; Japanese.
 XX A humanised anti-HM1.24 antibody has been developed which comprises human
 CC L and H chain C regions, and L and/or H chain V regions containing
 CC material originating in mouse anti-HM1.24 antibody. The V regions contain
 CC framework (FR) regions of human origin and complementarity determining
 CC regions (CDR) of mouse origin, leading to a reshaped humanised antibody.
 CC The C regions are human Ck (L-chain) and human C gamma (especially C
 CC gamma 1) (H-chain). The FR regions of the L chain V region are derived
 CC from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions

CC of the H chain V region are derived from human subtype HSG1 (e.g. FR1-3
 CC from human antibody HG3 and FR4 from human antibody JH6). The present
 CC sequence represents a PCR primer used in an example from the present
 CC invention. The antibodies are used for the treatment of myeloma,
 CC especially by injection, intravenously, intramuscularly or
 CC subcutaneously. The antibodies are used at 0.01-1000 (especially 5-100)
 CC mg/kg body weight. The humanised antibody has low antigenicity and is
 CC therefore effective therapeutically in humans
 XX

SQ Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 U; 0 Other;

Query Match 56.8%; Score 14.2; DB 2; Length 39;
 Best Local Similarity 84.2%; Pred. No. 5.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCA 19
 DB 19 GGTGTGCCAAGCAGATTCA 37

RESULT 19
 AAX59432
 ID AAX59432 standard; DNA; 39 BP.
 XX AC
 XX AAX59432;
 XX DT 16-JUL-1999 (first entry)
 XX DE Primer used in construction of humanised anti-HM1.24 antibody.
 XX KW Reconstituted human antibody; peptide antigen HM1.24; framework region;
 KW complementary determining region; CDR; anti-HM1.24 antibody; myeloma;
 KW humanised antibody; primer; ss.
 XX OS Synthetic.
 XX WO9918212-A1.
 XX PD 15-APR-1999.
 XX PF 02-OCT-1998; 98WO-JP004469.
 XX PR 03-OCT-1997; 97JP-00271726.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Tsuchiya M;
 WPI; 1999-277273/23.
 XX Reconstituted human antibody useful in the treatment of myeloma.
 XX Disclosure; Page 114; 256pp; Japanese.

The specification describes a reconstituted human antibody recognizing
 CC the peptide antigen HM1.24. This human antibody contains natural human
 CC framework regions modified by amino acid substitutions to provide
 CC homogeneity with a previously designed framework region (which may arise
 CC from a human or non-human source); and complementary determining regions
 CC (CDR) derived from a non-human anti-HM1.24 antibody. The reconstituted
 CC antibody is useful in the treatment of diseases in which the surface
 CC antigen HM1.24 is implicated such as myeloma. The present sequence is
 CC used in the creation of the antibodies of the invention
 XX

SQ Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 U; 0 Other;

Query Match 56.8%; Score 14.2; DB 2; Length 39;
 Best Local Similarity 84.2%; Pred. No. 5.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCA 19
 DB 19 GGTGTGCCAAGCAGATTCA 37

```

DE XX Light chain primer EL.
KW KW Probe; myeloma; Y3-Ag 1.2.3; primer; rat; monoclonal; antibody; COS;
KW YFC51.1.1; CD18; humanised; antigen; leukocyte; lung; sepsis; asthma;
KW endotoxin shock; adult respiratory distress syndrome; inflammation;
KW immunotoxin; transient expression; PCR; polymerase chain reaction; ss.
XX OS Synthetic.
XX OS
XX FN WO9302191-A1.
XX XX
XX PD 04-FEB-1993.
XX XX
XX PF 15-JUL-1992; 92WO-GB001289.
XX PR 16-JUL-1991; 91GB-00015364.
XX XX
XX PA (WELL ) WELLCOME FOUND LTD.
XX PI Waldmann H, Sims M, Crowe S;
XX DR WPI; 1993-058788/07.
XX XX
XX PT New humanised antibody specific for human CD-18 antigen - inhibits influx
XX of leukocytes into the lungs, useful for treating endotoxic shock, adult
XX respiratory distress syndrome, asthma, etc.
XX PS Disclosure; Page 47; 59pp; English.
XX CC
XX CC The sequences given in AAQ35180-87 are primers which were used to amplify
XX and humanise the light chain isolated from the rat antibody YFC51.1.1.
XX CC The light chain of YFC51.1.1 was isolated using a non-radioactively
XX labelled clone of the light chain from rat myeloma Y3-Ag 1.2.3. The
XX CC isolated sequences were amplified, humanised and constructed into the
XX light chain genes using these primers. The gene construction, and a
XX CC corresponding into COS cells which transiently expressed the humanised
XX YFC51.1.1. YFC51.1.1 is a CD18 antibody which was used as a basis for the
XX production of a humanised antibody with specificity for CD18 antigen. The
XX antibody may be useful in treating leukocyte-mediated conditions, such as
XX inhibiting influx of leukocytes into the lung and other organs during
XX sepsis, endotoxin shock or adult respiratory distress syndrome. The
XX CC antibodies may also be used to treat asthma and inflammation and may form
XX part of an immunotoxin. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 41 BP; 9 A; 8 C; 12 G; 12 T; 0 U; 0 Other;
Query Match 56.8%; Score 14.2; DB 2; Length 41;
Best Local Similarity 84.2%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GCTGAGCCTAGCAGATTCA 19
Db 22 GGTGTGCCAAGCAGATTCA 40
RESULT 22
AAQ34502/c
ID AAL34502 standard; DNA; 50 BP.
XX XX
XX AC AAL34502;
XX XX
XX DT 24-JAN-2002 (first entry)
XX XX
XX DE Human SNP oligonucleotide #7710.
XX XX
XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX amyloid protein; angiopoietin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; cholestase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
KW

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RESULT 20
AAQ24659
ID AAQ24659 standard; DNA; 41 BP.
XX AC AAQ24659;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 10-NOV-1992 (first entry)
XX XX
XX DE PCR primer EL for CAMPATH-1H light chain.
XX XX
XX KW Polymerase chain reaction; humanised antibody; CAMPATH-1H;
KW rat anti-human CD18 light chain; YFC51.1.1; human IgG1 heavy chain;
KW PCR grafting; ss.
XX OS Synthetic.
XX OS
XX FN WO9207075-A1.
XX XX
XX PD 30-APR-1992.
XX XX
XX PF 08-OCT-1991; 91WO-GB001744.
XX PR 10-OCT-1990; 90GB-00022011.
XX XX
XX PA (WELL ) WELLCOME FOUND LTD.
XX XX
XX PI Crowe JS, Lewis AP;
XX XX
XX DR WPI; 1992-167155/20.
XX XX
XX PT Prepn. of chimeric humanised antibodies - using a new polymerase chain
XX reaction technique.
XX PS Example 2; Page 45; 67pp; English.
XX XX
XX CC The YFC51.1.1 rat anti-human -CD18 light chain was humanised as follows:
XX Primer EL (AAQ24659) was used with primer FL (AAQ24660) in a PCR reaction
XX using as template CAMPATH-1H light chain (i.e. humanised CAMPATH-1 on REI
XX framework; Biotechnology 9:64-68 (1991)) to produce fragment EFL. Three
XX other PCR reactions were performed on the same template, generating
XX fragments ABL, CDL and GHL. Fragments EFL and GHL were combined and used
XX as the template for a PCR reaction with primers EL and HL (AAQ24662) to
XX produce fragment EHL. Similarly, fragment ADL was produced from ABL and
XX CDL using the primers AL and DL (AAQ24655 and AAQ24658, respectively).
XX The products ADL and EHL were purified and combined in a recombinant PCR
XX reaction using primers AL and HL. The final humanised light chain
XX product, AHL, was cloned into the HindIII site of pUC18 (primers AL and
XX HL both contain HindIII sites). (Updated on 25-MAR-2003 to correct PN
XX field.)
XX SQ Sequence 41 BP; 9 A; 8 C; 12 G; 12 T; 0 U; 0 Other;
Query Match 56.8%; Score 14.2; DB 2; Length 41;
Best Local Similarity 84.2%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GCTGAGCCTAGCAGATTCA 19
Db 22 GGTGTGCCAAGCAGATTCA 40
RESULT 21
AAQ35184
ID AAQ35184 standard; cDNA; 41 BP.
XX AC AAQ35184;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 08-JUN-1993 (first entry)
XX XX

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XX 17-MAY-2002; 2002JP-00143185.
PR 17-OCT-2002; 2002JP-00303528.
XX (RIKE) RIKEN KK.
PA (NAKA/) NAKAMURA Y.
PA (SEKI/) SEKINE A.
PA (IIDA/) IIDA A.
PA (SAIT/) SAITO S.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX WPI; 2004-012542/01.
XX
XX Detecting gene polymorphism for single nucleotide polymorphism analysis
PT and drug selection.
XX
XX Claim 2; SEQ ID NO 400; 166pp; Japanese.
XX
XX The invention comprises a method for detecting gene polymorphisms, the
CC method involves constructing an oligonucleotide primer and/or probe
CC containing the polymorphism site in a receptor gene or its complementary
CC sequence, amplifying that part and detecting it with the probe and/or
CC primer. The method of the invention is useful for the analysis of SNPs
CC and in drug selection. The present DNA sequence represents a primer/probe
CC of the invention.
XX
XX Sequence 41 BP; 14 A; 11 C; 8 G; 7 T; 0 U; 1 Other;
SQ
Query Match 56.0%; Score 14; DB 12; Length 41;
Best Local Similarity 87.5%; Pred. No. 7e+03;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY 4 GAGCCTAGCAGATTCA 19
DB 20 GRCCTAGCAGAGTCA 35
|:|||||
RESULT 24
ADH91221
ID ADH91221 standard; DNA; 41 BP.
XX
XX ADH91221;
XX
XX 06-MAY-2004 (first entry)
XX
XX 1-beta-methylcarbaenem compound-related human DNA sequence #400.
DE
XX
XX 1-beta-methylcarbaenem compound; antimicrobial; bacterial infection;
KW respiratory infection; human; ds.
KW
XX
XX Homo sapiens.
OS
XX
XX WO2003095454-A1.
XX
XX 20-NOV-2003.
XX
XX 14-MAY-2003; 2003WO-JP006028.
PP
XX
XX 14-MAY-2002; 2002JP-00138448.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Kobayashi Y, Ashida Y, Uchida T, Kojima K;
PI
XX
XX WPI; 2004-081882/08.
XX
XX New carbaenem compounds resistant to beta-lactamase (except metallo-beta
PT -lactamase), useful for treating microbial infections especially
PT respiratory infections.
XX
XX Disclosure; SEQ ID NO 400; 726pp; Japanese.
XX
XX

CC The invention comprises 1-beta-methylcarbapenem compounds which are
CC useful as antimicrobials to treat bacterial infections, especially
CC respiratory infections in warm-blooded animals (e.g. humans). The present
CC human DNA sequence is included in the sequence listing of this patent.

SQ Sequence 41 BP; 14 A; 11 C; 8 G; 7 T; 0 U; 1 Other;

Query Match 56.0%; Score 14; DB 12; Length 41;

Best Local Similarity 87.5%; Pred. No. 7e+03; Mismatches 1; Indels 0; Gaps 0;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGCCTAGCAGATTCA 19

DB 20 GRGCTAGCAGAGTCA 35

RESULT 25

AAZ52556

ID AAZ52556 standard; DNA; 47 BP.

XX AC AAZ52556;

XX 30-JUN-1999 (first entry)

XX Human genome biallelic marker 24.

XX Biallelic marker; human; high density disequilibrium map; disease; trait;

XX identification; Alzheimer's disease; drug response; drug efficacy;

XX drug toxicity; ss.

XX Homo sapiens.

XX WO9904038-A2.

XX 28-JAN-1999.

XX 17-JUL-1998; 98WO-IB001193.

XX 18-JUL-1997; 97EP-00401740.

XX 21-APR-1998; 98US-0082614P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Tchoumakov I;

XX WPI; 1999-132278/11.

XX Production of biallelic markers - by obtaining a genomic DNA library,

XX determining the order and sequence of DNA fragments and identifying

XX nucleotides which vary between individuals.

XX Example 6; Page 134; 288pp; English.

XX This invention describes a novel method for obtaining a set of biallelic

XX markers represented in AAX52533-X52632 and AAX52833-X52843 for use in

XX constructing a high density equilibrium map of the human genome. The

XX method involves (a) obtaining a nucleic acid library comprising genomic

XX DNA fragments comprising the full genome or a portion (b) determining the

XX order of genomic DNA fragments in the genome, (c) determining the

XX sequence of selected regions of the genomic DNA fragments and (d)

XX identifying nucleotides in the genomic DNA fragments which vary between

XX individuals, thereby defining a set of biallelic markers. The methods can

XX be used for identifying traits such as disease (e.g. Alzheimer's

XX disease), drug response, drug efficacy and drug toxicity. They can be

XX used for selecting an individual for inclusion in a clinical trial. The

XX method is used to map the position of genes in a genome (preferably the

XX human genome). The sequences described in AAX52633-X52832 and AAX52844-

XX X52868 represent primers used in the method of the invention

XX Sequence 47 BP; 13 A; 11 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 47;

Best Local Similarity 77.3%; Pred. No. 7.2e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 GAGCCTAGCAGATTCA 25

DB 3 GAGCCTGGAGCTTTCATGAC 24

RESULT 26

AAZ68752

ID AAZ68752 standard; DNA; 47 BP.

XX AC AAZ68752;

XX 10-SEP-2001 (first entry)

XX Human map-related biallelic marker SEQ ID NO:3104.

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotyping; hybridisation; identification; characterisation; diagnosis;

XX single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX variation replace(24,T)

XX FT /*tag= a

XX FT /standard_name= "single nucleotide polymorphism"

XX PN WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium

XX map of the human genome.

XX Claim 3; Page 892; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

XX invention, which contain a polymorphic base at position 24 of their

XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

XX primers for the biallelic markers. The biallelic markers of the invention

XX have a variety of uses; they can be used for high density mapping of the

XX human genome, and in complex association studies and haplotyping studies

XX which are useful in determining the genetic basis for disease states.

XX Compositions and methods of the invention can also be useful for the

XX identification of the targets for the development of pharmaceutical

XX agents and diagnostic methods, as well as the characterisation of the

XX differential efficacious responses to and side effects from

XX pharmaceutical agents acting on a disease as well as other treatment.

XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

XX 3367, are not actually given a sequence in the Sequence Listing from the

XX present invention

XX Sequence 47 BP; 13 A; 11 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 56.0%; Score 14; DB 3; Length 47;

Best Local Similarity 77.3%; Pred. No. 7.2e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 GAGCCTAGCAGATTCA 25

DB 3 GAGCCTGGAGCTTTCATGAC 24

```
Db      3 GAGCCTTGGAAGTTCATGACAC 24

RESULT 27
RAL28480/C
ID      AAL28480 standard; DNA; 50 BP.
XX
AC      AAL28480;
XX
DT      24-JAN-2002 (first entry)
XX
DE      Human SNP oligonucleotide #1688.
XX
KW      Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW      neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW      amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW      cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW      complement related protein; cytochrome; kinesin; cytokine; interferon;
KW      interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW      multifactorial disease; autoimmune disease; infection;
KW      nervous system disease; ss.
XX
OS      Homo sapiens.
XX
PN      WO200147944-A2.
XX
PD      05-JUL-2001.
XX
PF      28-DEC-2000; 2000WO-US035498.
XX
PR      28-DEC-1999; 99US-0173419P.
PR      27-DEC-2000; 2000US-00173419.
XX
PA      (CURA-) CURAGEN CORP.
XX
PI      Shimkets RA, Leach M;
XX
DR      WPI; 2001-465210/50.
XX
PT      Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT      oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT      autoimmune diseases and infections.
XX
PS      Claim 1; Page 1863; 4143pp; English.
XX
CC      The present invention relates to oligonucleotides encoding polymorphic
CC      variants of proteins related to amylases, amyloid proteins, angiotensin,
CC      apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC      histones, kinases, colony stimulating factors, complement related
CC      proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC      protein coupled receptors and thioesterases. The present sequence is one
CC      such oligonucleotide. The oligonucleotides and the peptides encoded by
CC      them may be used in the prevention, diagnosis and treatment of diseases
CC      associated with inappropriate expression of the proteins listed above.
CC      Disorders that may be prevented, diagnosed and/or treated include
CC      multifactorial diseases with a genetic component, such as autoimmune
CC      diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC      systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC      (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC      leukaemia), diseases of the nervous system and an infection of pathogenic
CC      organisms
XX
SQ      Sequence 50 BP; 13 A; 22 C; 8 G; 7 T; 0 U; 0 Other;

Query Match      56.0%; Score 14; DB 4; Length 50;
Best Local Similarity 77.3%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      1 GCTGAGCCTAGCAGATTCATGG 22
      |||||
Db      26 GCTGGGCTAGCAGCAGATGG 5

us-10-788-779-10.rng

RESULT 28
ABZ05333
ID      ABZ05333 standard; DNA; 50 BP.
XX
AC      ABZ05333;
XX
DT      09-JAN-2003 (first entry)
XX
DE      Human leukocyte gene expression profiling probe SEQ ID NO 5324.
XX
KW      T7; leukocyte; gene expression profiling; allograft rejection;
KW      atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW      rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW      ss.
XX
OS      Homo sapiens.
XX
PN      WO200257414-A2.
XX
PD      25-JUL-2002.
XX
PF      22-OCT-2001; 2001WO-US047856.
XX
PR      20-OCT-2000; 2000US-0241994P.
PR      08-JUN-2001; 2001US-0296764P.
XX
PA      (BIOC-) BIOCARDIA INC.
XX
PI      Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI      Ly N, Woodward R, Quettermous T, Johnson F;
XX
DR      WPI; 2002-636525/68.
XX
PT      New system for leukocyte expression profiling, diagnosing a disease, or
PT      monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT      or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS      Claim 1; Page 500; Opp; English.
XX
CC      The invention relates to a system for detecting gene expression, which
CC      comprises one or two isolated DNA molecules that detect expression of a
CC      gene, where the gene corresponds to any of 8143 oligonucleotides
CC      (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC      for leukocyte expression profiling. It is particularly useful for
CC      diagnosing a disease, monitoring (rate of) progression of a disease,
CC      predicting therapeutic outcome, determining prognosis for a patient,
CC      predicting disease complications in an individual or monitoring response
CC      to treatment in an individual. The diseases include cardiac allograft
CC      rejection, kidney allograft rejection, liver allograft rejection,
CC      atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC      rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ      Sequence 50 BP; 14 A; 14 C; 10 G; 12 T; 0 U; 0 Other;

Query Match      56.0%; Score 14; DB 6; Length 50;
Best Local Similarity 77.3%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      3 TGAGCCTAGCAGATTCATGGCA 24
      |||||
Db      3 TGAGCCAGGGGTTTCATGACA 24

RESULT 29
ABK70835
ID      ABK70835 standard; DNA; 21 BP.
XX
AC      ABK70835;
XX
DT      15-JUL-2002 (first entry)
XX
DE      PCR primer for human gene CHST4 #2.
XX
```

KW Human; sulphuric acid conjugation: ss; PCR; CHST1; CHST3; primer; CHST4;
 KW CHST5; CST; HNK-1ST; SULTAL; SULTB1; SULTX3; STE; TPST2.

OS Homo sapiens.

PN JP2002085067-A.

XX 26-MAR-2002.

XX 07-SEP-2000; 2000JP-00272229.

XX 07-SEP-2000; 2000JP-00272229.

XX (SAKA) OTSUKA SEIYAKU KOGYO KK.

XX WPI; 2002-378272/41.

PT Determination of enzymes participating in sulfuric acid conjugation in
 PT humans, useful for confirmation of safety of investigational drugs,
 PT comprises using oligonucleotide probes.

PS Claim 8; Page 11; 13pp; Japanese.

XX The invention relates to classification and quantitative determination of
 CC enzymes participating in sulphuric acid conjugation comprising using
 CC oligonucleotide probes hybridising to the following regions: (a) 885-911
 CC region of CHST1 gene; (b) 174-197 region of CHST3 gene; (c) 1003-1032
 CC region of CHST4 gene; (d) 322-346 region of CHST5 gene; (e) 737-765
 CC region of CST gene; (f) 703-732 region of HNK-1ST gene; (g) 299-325
 CC region of SULT2A1 gene; (h) 358-382 region of SULT2B1 gene; (i) 554-582
 CC region of SULTX3 gene; (j) 451-478 region of STE gene; and (k) 652-677
 CC region of TPST2 gene. Also included are PCR primers for the above genes,
 CC kits and methods for determination. The probes, primers and the method
 CC are used in the determination of sulphuric acid conjugation for
 CC confirmation of the safety of investigational drugs. The present sequence
 CC is a PCR primer for one of the above listed genes

SQ Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 55.2%; Score 13.8; DB 6; Length 21;

Best Local Similarity 88.2%; Pred. No. 7.8e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATG 21

Db 5 AGCCGAGCAATTCATG 21

RESULT 30

ACK02180

ID ACK02180 standard; DNA; 25 BP.

XX

AC ACK02180;

XX

DT 14-OCT-2003 (first entry)

XX

DE Human microarray DNA oligonucleotide SEQ ID NO 102161.

XX

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;

KW genetic variation; biallelic marker; polymorphism; human;

KW cross-species comparison.

XX

OS Homo sapiens.

XX

XX US2003104410-A1.

XX

XX 05-JUN-2003.

XX

PF 15-MAR-2002; 2002US-00098263.

XX

XX 16-MAR-2001; 2001US-0276759P.

XX

XX (AFFY-) AFFYMETRIX INC.

XX

PI Mittmann MP;

XX

DR WPI; 2003-567953/53.

XX

PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX

PS Claim 1; SEQ ID NO 102161; 9pp; English.

XX

CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 5 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 55.2%; Score 13.8; DB 9; Length 25;

Best Local Similarity 88.2%; Pred. No. 8e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TAGCAGATTCATGGCAC 25

Db 2 TAGCGATTAAATGGCAC 18

RESULT 31

ADC21315/c

ID ADC21315 standard; DNA; 33 BP.

XX

AC ADC21315;

XX

DT 18-DEC-2003 (first entry)

XX

DE Plasmid pMOXp36 PCR primer #3.

XX

XX expression construct; vaccine; intradermal injection;

KW type 1 cell-mediated immune response; antiviral; hepatotropic;

KW antiinflammatory; protozoacide; MIDGE;

KW minimalistic immunologically defined gene expression vector;

KW hepatitis B surface antigen; p36 antigen; Leishmania major; ss; primer;

XX PCR.

XX

OS Synthetic.

XX

XX WO2003031469-A2.

XX

XX 17-APR-2003.

XX

XX 02-OCT-2002; 2002WO-DE003798.

XX

XX 02-OCT-2001; 2001DE-01048697.

XX

XX 12-NOV-2001; 2001DE-01056678.

```

XX PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
XX PA (LOPE/) LOPEZ S M.
XX PA (JIME/) JIMENEZ M T.
XX PI Lopez SM, Jimenez MT;
XX DR WPI; 2003-372085/35.
XX PT Use of a DNA expression construct encoding one or more antigens and
XX PT covalently linked to oligopeptides for preparing intradermal vaccine,
XX PT useful for treating e.g. hepatitis and leishmaniasis.
XX PS Example 4; SEQ ID NO 9; 32pp; German.
XX CC This invention describes a novel DNA expression construct, functional in
XX CC eukaryotic cells, to prepare a vaccine, for intradermal injection, to
XX CC generate a type 1 cell-mediated immune response. The construct encodes
XX CC one or more antigens (Ag) under control of a promoter and, to improve
XX CC transfection efficiency, is covalently linked to one or more
XX CC oligopeptides. The products of the invention have antiviral,
XX CC hepatotropic, antiinflammatory and protozoacide activity. Mice were
XX CC immunized intradermally (twice at an interval of 11 weeks) with a MIDGE
XX CC (minimalistic immunologically defined gene expression vector) that
XX CC encoded hepatitis B surface antigen. The resulting antibody titer
XX CC (expressed as optical density in enzyme linked immunosorbent assay) was
XX CC about 0.45, about the same as when using a plasmid for expression. When
XX CC the MIDGE used was modified by binding the Tat protein-derived peptide
XX CC Tyr-Gly-Arg-(lys)_2-(Arg)_2-Gln-(Arg)_3 the optical density was over 0.9.
XX CC The constructs are used, particularly in human medicine, to generate a
XX CC type 1 cell-mediated immune response, specifically against hepatitis B
XX CC virus surface antigen, but also against the p36 antigen of Leishmania
XX CC major. Attachment of the oligopeptides increases transport of the
XX CC construct to the nucleus, resulting in a stronger immune response. This
XX CC sequence represents a PCR primer used in the construction of construct
XX CC pMOKp36 used to make the vaccines described in the disclosure of the
XX CC invention.
XX SQ Sequence 33 BP; 10 A; 7 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 55.2%; Score 13.8; DB 10; Length 33;
Best Local Similarity 72.0%; Pred. No. 8.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GCTGAGCCTAGCAGATTTCATGGCAC 25
DB 32 GGTGACCCCTCGTATGTTTCATGTAC 8
RESULT 32
ID ADC21313/c
XX AC ADC21313;
XX DT 18-DEC-2003 (first entry)
XX DE Plasmid pMOKp36 PCR primer #1.
XX KW expression construct; vaccine; intradermal injection;
XX KW type 1 cell-mediated immune response; antiviral; hepatotropic;
XX KW antiinflammatory; protozoacide; MIDGE;
XX KW minimalistic immunologically defined gene expression vector;
XX KW hepatitis B surface antigen; p36 antigen; Leishmania major; ss; primer;
XX KW PCR.
XX OS Synthetic.
XX OS WO2003031469-A2.
XX FN 17-APR-2003.
XX PD 02-OCT-2002; 2002WO-DE003799.
XX PF
XX PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
XX PA (LOPE/) LOPEZ S M.
XX PA (JIME/) JIMENEZ M T.
XX PI Lopez SM, Jimenez MT;
XX DR WPI; 2003-372085/35.
XX PT Use of a DNA expression construct encoding one or more antigens and
XX PT covalently linked to oligopeptides for preparing intradermal vaccine,
XX PT useful for treating e.g. hepatitis and leishmaniasis.
XX PS Example 4; SEQ ID NO 7; 32pp; German.
XX CC This invention describes a novel DNA expression construct, functional in
XX CC eukaryotic cells, to prepare a vaccine, for intradermal injection, to
XX CC generate a type 1 cell-mediated immune response. The construct encodes
XX CC one or more antigens (Ag) under control of a promoter and, to improve
XX CC transfection efficiency, is covalently linked to one or more
XX CC oligopeptides. The products of the invention have antiviral,
XX CC hepatotropic, antiinflammatory and protozoacide activity. Mice were
XX CC immunized intradermally (twice at an interval of 11 weeks) with a MIDGE
XX CC (minimalistic immunologically defined gene expression vector) that
XX CC encoded hepatitis B surface antigen. The resulting antibody titer
XX CC (expressed as optical density in enzyme linked immunosorbent assay) was
XX CC about 0.45, about the same as when using a plasmid for expression. When
XX CC the MIDGE used was modified by binding the Tat protein-derived peptide
XX CC Tyr-Gly-Arg-(lys)_2-(Arg)_2-Gln-(Arg)_3 the optical density was over 0.9.
XX CC The constructs are used, particularly in human medicine, to generate a
XX CC type 1 cell-mediated immune response, specifically against hepatitis B
XX CC virus surface antigen, but also against the p36 antigen of Leishmania
XX CC major. Attachment of the oligopeptides increases transport of the
XX CC construct to the nucleus, resulting in a stronger immune response. This
XX CC sequence represents a PCR primer used in the construction of construct
XX CC pMOKp36 used to make the vaccines described in the disclosure of the
XX CC invention.
XX SQ Sequence 33 BP; 10 A; 7 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 55.2%; Score 13.8; DB 10; Length 33;
Best Local Similarity 72.0%; Pred. No. 8.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GCTGAGCCTAGCAGATTTCATGGCAC 25
DB 32 GGTGACCCCTCGTATGTTTCATGTAC 8
RESULT 33
ID ADC21307/c
XX AC ADC21307;
XX DT 18-DEC-2003 (first entry)
XX DE Plasmid pMOKp36 PCR primer #3.
XX KW immunization; leishmaniasis; vaccine; protozoacide; p36 antigen;
XX KW TAT peptide; ss; primer; PCR.
XX OS Synthetic.
XX OS WO2003031470-A2.
XX FN 17-APR-2003.
XX PD 02-OCT-2002; 2002WO-DE003799.
XX PF

```


DR WPI; 2004-552653/53.
XX
XX Analyzing multiple targets in polynucleotide, by providing multiple
PT primers with target nucleic acids, digesting nucleic acid products with
PT cognate restriction enzymes, amplifying digested products, and detecting
XX amplified products.
PS Example 1; SEQ ID NO 39; 65pp; English.
XX
XX The invention relates analysing multiple targets in polynucleotide.
CC involves providing a set or sets of multiple primers with target nucleic
CC acids in separate reactions of primer extension or amplification, where
CC the reactions produce nucleic acid products in that each nucleic acid
CC fragments comprise at least one restriction site, digesting nucleic acid
CC products of the separate reactions on the restriction sites with cognate
CC restriction enzymes, joining digested products derived from the separate
CC reactions together, where randomly joining nucleic acid fragments from
CC the separated reactions are created, amplifying the joined products, and
CC detecting the amplified products. Also included are an oligonucleotide
CC primer for detecting target nucleic acid sequence (comprising a 3'
CC complementary portion and 5' non-complementary portion, where the 5' non-
CC complementary portion comprises a restriction enzyme site, where the
CC restriction site acts as detection marker in the process of detecting
CC target nucleic acid sequence, where the detection signal generated from
CC enzymatic manipulation on restriction site of reaction product is
CC indicative of the presence of target nucleic acid sequence) and a kit for
CC use in analysis and detection of multiple targets in a polynucleotide
CC (comprising a set or sets of multiple primers, universal primers,
CC restriction enzymes, DNA ligase, DNA polymerase, ddNTP, buffers for all
CC enzymes, and dNTPs). The method is useful for analysing multiple targets
CC in a polynucleotide and for genotyping mutations, preferably single
CC nucleotide polymorphisms (SNPs), and for analysing differential gene
CC expression profiles, genomic methylation patterns and any specific
CC nucleic acids from any source. The method enables analysis of multiple
CC targets quantitatively. An experiment was performed, using the method of
CC the invention, where 8 SNPs were detected in human genomic DNA,
CC simultaneously. The present sequence is a primer used in the above
XX experiment.
SQ Sequence 49 BP; 15 A; 11 C; 13 G; 10 T; 0 U; 0 Other;
Query Match 55.2%; Score 13.8; DB 13; Length 49;
Best Local Similarity 88.2%; Pred. No. 9.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGG 22
Db 28 GACTAGCAGATTCACGG 44
RESULT 36
AAL28734
ID AAL28734 standard; DNA; 50 BP.
XX AC
XX AAL28734;
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #1942.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
OS
XX WO200147944-A2.
XX

PD 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
PA
XX Shimkets RA, Leach M;
PI
XX WPI; 2001-465210/50.
DR
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Claim 1; Page 1936; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 50 BP; 6 A; 15 C; 19 G; 10 T; 0 U; 0 Other;
Query Match 55.2%; Score 13.8; DB 4; Length 50;
Best Local Similarity 72.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
Db 17 GCTTGGCCACAGCAGCTCCAGGGCCC 41
RESULT 37
ADQ31582
ID ADQ31582 standard; DNA; 50 BP.
XX AC
XX ADQ31582;
DT 21-OCT-2004 (first entry)
XX
DE Multiplex detection of human SNPs, primer F10G.
XX
KW Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP;
KW single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
XX US2004146866-A1.
PN
XX 29-JUL-2004.
PD
XX 24-JAN-2003; 2003US-00349780.
PF
XX 24-JAN-2003; 2003US-00349780.
PR
XX (FUGG/) FU G.
PA
XX FU G;
PI

```

XX WPI; 2004-552653/53.
DR
XX Analyzing multiple targets in polynucleotide, by providing multiple
PT primers with target nucleic acids, digesting nucleic acid products with
PT cognate restriction enzymes, amplifying digested products, and detecting
PT amplified products.
XX
XX Example 1; SEQ ID NO 40; 65pp; English.
PS
XX The invention relates analysing multiple targets in polynucleotide,
CC involves providing a set or sets of multiple primers with target nucleic
CC acids in separate reactions of primer extension or amplification, where
CC the reactions produce nucleic acid products in that each nucleic acid
CC fragments comprise at least one restriction site, digesting nucleic acid
CC products of the separate reactions on the restriction sites with cognate
CC restriction enzymes, joining digested products derived from the separate
CC reactions together, where randomly joining nucleic acid fragments from
CC the separated reactions are created, amplifying the joined products, and
CC detecting the amplified products. Also included are an oligonucleotide
CC primer for detecting target nucleic acid sequence (comprising a 3'
CC complementary portion and 5' non-complementary portion, where the 5' non-
CC complementary portion comprises a restriction enzyme site, where the
CC restriction site acts as detection marker in the process of detecting
CC target nucleic acid sequence, where the detection signal generated from
CC enzymatic manipulation on restriction site of reaction product is
CC indicative of the presence of target nucleic acid sequence) and a kit for
CC use in analysis and detection of multiple targets in a polynucleotide
CC (comprising a set or sets of multiple primers, universal primers,
CC restriction enzymes, DNA ligase, DNA polymerase, ddNTP, buffers for all
CC enzymes, and dNTPs). The method is useful for analysing multiple targets
CC in a polynucleotide and for genotyping mutations, preferably single
CC nucleotide polymorphisms (SNPs), and for analysing differential gene
CC expression profiles, genomic methylation patterns and any specific
CC nucleic acids from any source. The method enables analysis of multiple
CC targets quantitatively. An experiment was performed, using the method of
CC the invention, where 8 SNPs were detected in human genomic DNA.
CC simultaneously. The present sequence is a primer used in the above
CC experiment.
XX
SQ Sequence 50 BP; 16 A; 10 C; 15 G; 9 T; 0 U; 0 Other;
Query Match 55.2%; Score 13.8; DB 13; Length 50;
Best Local Similarity 88.2%; Pred. No. 9.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 6 GCCTAGCAGATTCATGG 22
Db 29 GACTAGCAGATTCACGG 45

RESULT 38
ABI94601/c
ID ABI94601 standard; DNA; 20 BP.
XX
AC ABI94601;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#1688 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW detection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
XX WO200179548-A2.
XX
XX 25-OCT-2001.
XX
XX

```

```

PP 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
PI
XX WPI; 2002-034366/04.
DR
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.
PT
XX Example 5; Fig 29; 30pp; English.
PS
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridize with little mismatch, where
XX (I) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX Epstein-Barr virus and polio virus, and parasitic infectious agents
XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX medinensis. The method is also useful for detecting genetic diseases such
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX involved in DNA amplification, replication, recombination or repair, the
XX cancer is specifically associated with a gene selected from BRCA1 gene,
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX method is also used for environmental monitoring, forensics and the food
XX and feed industry, detecting comprises scanning (using e.g. a scanning
XX electron microscope and infrared microscope) the support at the
XX particular sites and identifying if ligation of the oligonucleotide probe
XX sets occurred and correlating (using a computer) identified ligation to a
XX presence or absence of the target nucleotide sequences. ABI82074 to
XX ABI97546 represent oligonucleotide sequences used in the exemplification
XX of the present invention
XX
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 54.4%; Score 13.6; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 9.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 6 GCCTAGCAGATTCATGGCAC 25
Db 20 GTCCCGCAGATTCAGGCAC 1

RESULT 39
AAZ26929/c
ID AAZ26929 standard; DNA; 21 BP.
XX
AC AAZ26929;
XX
DT 18-NOV-1999 (first entry)
XX
DE Human chromosome 11 linked CHD1 gene mutation screening PCR primer #67.
XX
KW Human; coronary heart disease susceptibility gene; CHD1; mutation;
KW chromosome 11; diagnosis; screening; PCR primer; metabolic disorder;
KW detection; hypophosphatemia; familial combined hyperlipidaemia;
KW insulin resistant syndrome X; multiple metabolic disorder; obesity;
KW diabetes; dyslipidaemic hypertension; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
XX WO9945112-A2.
XX
XX 10-SEP-1999.
XX

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XX PF 04-MAR-1999; 98WO-US004682.
XX PF 04-MAR-1998; 98US-00034941.
XX PR 06-APR-1998; 98US-0080934P.
XX XX (MYRI-) MYRIAD GENETICS INC.
XX PF Ballinger DG, Ding W, Wagner S, Hess MA;
XX WPI; 1999-540844/45.
XX PF New isolated coronary heart disease susceptibility gene, used to develop
XX PT products for diagnosis and treatment of coronary heart disease and
XX PT metabolic disorders.
XX PS Example 6; Page 98; 297pp; English.
XX CC The present invention describes the human chromosome 11-linked coronary
XX CC heart disease susceptibility gene (CHD1). Mutations in the CHD1 locus in
XX CC the germline are indicative of a predisposition to coronary heart disease
XX CC or to metabolic disorders related to lipid metabolism. Products from the
XX CC present invention can be used in the diagnosis of predisposition to
XX CC coronary heart disease and to metabolic disorders, including
XX CC hypochalipoproteinaemia, familial combined hyperlipidaemia, insulin
XX CC resistant syndrome X or multiple metabolic disorder, obesity, diabetes
XX CC and dyslipidaemic hypertension. CHD1 proteins can be used for treating
XX CC coronary heart disease and metabolic disorders. The products can also be
XX CC used for detection and drug screening. AAZ26832 to AAZ26841 and AAZ27027
XX CC to AAZ27029 represent human CHD1 nucleotide sequences. AAZ29917 to
XX CC AAZ29926 represent human CHD1 proteins and protein sequences used in the
XX CC exemplification of the present invention. AAZ26842 to AAZ26862 represent
XX CC primers used in the identification of human CHD1; AAZ26863 to AAZ27014
XX CC represent PCR primers used in the screening of mutations in human CHD1;
XX CC AAZ27015 to AAZ27026 represent oligonucleotides used in the
XX CC exemplification of the present invention
XX SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 54.4%; Score 13.6; DB 2; Length 21;
Best Local Similarity 80.0%; Pred. No. 9.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 21 GCTTAGAGAGTGTGTCAC 2

RESULT 40
AAF95928/c
ID AAF95928 standard; DNA; 21 BP.
XX AC AAF95928;
XX DT 18-NOV-2004 (revised)
XX DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #689.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX KW polymorphism; vascular disease; coronary artery disease; forensics;
XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX KW pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX OS Unidentified.
XX PH Key Location/Qualifiers
XX FT variation 11
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX PN WO200118250-A2.

```

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XX PD 15-MAR-2001.
XX PF 07-SEP-2000; 2000WO-US024503.
XX PR 10-SEP-1999; 99US-0153357P.
XX PR 26-JUL-2000; 2000US-0220947P.
XX PR 16-AUG-2000; 2000US-0225724P.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX PT Nucleic acids comprising single nucleotide polymorphisms, useful in
XX PT applications such as forensics, paternity testing, medicine, genetic
XX PT analysis and phenotype correlations to diseases such as diabetes and
XX PT atherosclerosis.
XX PS Example; Page 95; 242pp; English.
XX CC The present invention provides a method of diagnosing a vascular disease
XX CC in an individual, involving determining the sequence at various
XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX CC genes. The sequences at a number of polymorphic sites are also provided
XX CC in the specification. In particular, the method can be used in the
XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX CC useful in forensics, paternity testing, genetic analysis and phenotype
XX CC correlations to diseases. The present sequence is an example of one of
XX CC the human gene SNPs shown in the specification
XX CC Revised record issued on 18-NOV-2004 : The variantion feature was
XX CC incorrectly given a captial V
XX SQ Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 54.4%; Score 13.6; DB 4; Length 21;
Best Local Similarity 80.0%; Pred. No. 9.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCA 24
Db 21 AGCCTAGCAGATGATGCA 2

Search completed: November 18, 2005, 11:52:38
Job time : 175.148 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1195.82 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-10

Perfect score: 25

Sequence: 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	60.0	49	1	AI789860 ue65d12.r
2	14.2	56.8	44	1	AI256664 ui29h04.y
3	13.8	55.2	50	1	AI102770 AU102770
4	13.8	55.2	50	1	AI102772 AU102772
5	13.4	53.6	23	1	AL932459 AL932459
6	13.2	52.8	34	8	AZ829250 2M0106X17
7	13.2	52.8	47	7	D12221 HUM000S362
8	13	52.0	30	8	AZ782156 2M0022X09
9	13	52.0	35	9	AL757317 Arabidops
10	13	52.0	50	1	AI103585 AU103585
11	13	52.0	50	4	BI824288 603040689
12	12.8	51.2	30	8	BH790466 SALK 0571
13	12.8	51.2	33	9	TA317P10Q
14	12.8	51.2	39	2	BE732614 601571185
15	12.8	51.2	46	1	AA715909 nv76904.r
16	12.8	51.2	50	1	AI105049 AU105049
17	12.8	51.2	50	1	AI105060 AU105060
18	12.8	51.2	50	1	AI105083 AU105083
19	12.8	51.2	50	1	AI105084 AU105084
20	12.8	51.2	50	1	AI105091 AU105091
21	12.6	50.4	28	8	AZ480878 T. brucei
22	12.6	50.4	45	9	TA372A04P
23	12.4	49.6	36	7	T65804 ycl1h12.gi
24	12.4	49.6	38	8	AZ824424 2M0099D06

25	12.4	49.6	39	9	AL938370 Arabidops
26	12.4	49.6	42	7	H97155 yv91f07.gi
27	12.4	49.6	44	8	AZ491459 LM0325R05
28	12.4	49.6	50	4	BG405996 sac40901.
29	12.2	48.8	43	1	AI182198 uc64f11.r
30	12.2	48.8	50	1	AU102762 AU102762
31	12.2	48.8	50	1	AU102764 AU102764
32	12.2	48.8	50	1	AU102765 AU102765
33	12.2	48.8	50	1	AU102768 AU102768
34	12.2	48.8	50	1	AU102771 AU102771
35	12.2	48.8	50	1	AU102773 AU102773
36	12.2	48.8	50	1	AU102775 AU102775
37	12.2	48.8	50	1	AU102777 AU102777
38	12.2	48.8	50	1	AU102778 AU102778
39	12.2	48.8	50	1	AU102782 AU102782
40	12.2	48.8	50	1	AU102784 AU102784
41	12.2	48.8	50	1	AU102785 AU102785
42	12.2	48.8	50	1	AU102786 AU102786
43	12.2	48.8	50	1	AU102787 AU102787
44	12.2	48.8	50	1	AU102788 AU102788
45	12.2	48.8	50	1	AU102789 AU102789

ALIGNMENTS

RESULT 1
AI789860
LOCUS
DEFINITION
AI789860 49 bp mRNA linear EST 02-JUL-1999
IMAGE:1495991 5', similar to SW:KClA_CHICK P70065 CASEIN KINASE I,
ALPHA ISOFORM ;, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AI789860
ue65d12.r1 Soares_mammary_gland_NLMG Mus musculus cDNA clone
IMAGE:1495991 5', similar to SW:KClA_CHICK P70065 CASEIN KINASE I,
ALPHA ISOFORM ;, mRNA sequence.
AI789860
AI789860.1 GI:5337576
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.
1 (bases 1 to 49)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:933595
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1495991"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/clone_lib="Soares mammary_gland_NLMG"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

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Query Match      60.0%; Score 15; DB 1; Length 49;
Best Local Similarity 78.3%; Pred. No. 3e+04; 5; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GCTGAGCCTACGAGATTCATGGC 23
    ||||| ||||| ||||| |||||
Db 3 GCTGGGCCCGAGGATCCATGCAC 25

RESULT 2
AI256664
LOCUS      44 bp mRNA linear EST 12-NOV-1998
DEFINITION clone IMAGE:1852759 5' similar to gb:M9438 TRANSDUCIN-LIKE
            ENHANCER PROTEIN 3 (HUMAN);, mRNA sequence.
ACCESSION AI256664
VERSION    AI256664.1 GI:3864189
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE   1 (bases 1 to 44)
AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,P., Underwood,K., Moore,B.,
            Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,K. and
            Waterston,R.
TITLE      The WashU-HMMI Mouse EST Project
JOURNAL    Unpublished (1996)
COMMENT    Contact: Marra M/Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through L1NL; contact the
            IMAGE Consortium (info@image.l1nl.gov) for further information.
            MGI:968187
Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
FEATURES   Location/Qualifiers
            source          1..44
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /db_xref="taxon:10090"
                        /clone="IMAGE:1852759"
                        /sex="equal ratio of male:female"
                        /tissue_type="urogenital ridge (embryonic)"
                        /dev_stage="fetal, mixture of 11.5 and 12.5 dpc"
                        /lab_host="DH10B"
                        /clone_lib="Soares mouse urogenital ridge NMUR"
                        /note="Organ: gonad; Vector: pT7m3D-Pac (Pharmacia) with a
                        modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                        strand cDNA was primed with a Not I - oligo(dT) primer [5',
                        TGTACCAACTGAAGTGGAGCGCGCATCTCTTTTCTTTTCTTTTCTTTTCTTTT
                        T 3']; double-stranded cDNA was ligated to Eco RI
                        adaptors (Pharmacia), digested with Not I and cloned into
                        the Not I and Eco RI sites of the modified pT7T3 vector.
                        Library went through two rounds of normalization, and was
                        constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match      56.8%; Score 14.2; DB 1; Length 44;
Best Local Similarity 84.2%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCA 24
    ||||| ||||| ||||| |||||
Db 9 GCCTTGGGATACATGGCA 27

us-10-788-779-10.rst
RESULT 3
AI102770/c
LOCUS      50 bp mRNA linear EST 28-JAN-2004
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS02715, mRNA sequence.
ACCESSION AI102770
VERSION    AI102770.1 GI:13552291
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE   1 (bases 1 to 50)
AUTHORS    Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE      Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE    21270072
PUBMED     11375929
COMMENT    Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997)
FEATURES   Location/Qualifiers
            source          1..50
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="CAS02715"
                        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      55.2%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 28 GCGGAGACTCGCGGATACAGAGCAC 4

us-10-788-779-10.rst
RESULT 4
AI102772/c
LOCUS      50 bp mRNA linear EST 28-JAN-2004
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS03205, mRNA sequence.
ACCESSION AI102772
VERSION    AI102772.1 GI:13552293
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE   1 (bases 1 to 50)
AUTHORS    Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE      Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE    21270072
PUBMED     11375929
COMMENT    Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo

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Qy      2 CTGAGCCTAGCAGATTCA 19
      ||||| ||||| ||||| |||||
Db      21 CAGAGCATAGCAGATGCA 4

RESULT 7
D12221/c
LOCUS      D12221
DEFINITION HUN000S362 Liver HepG2 cell line. Homo sapiens cDNA clone #362,
            mRNA sequence.
ACCESSION  D12221
VERSION    D12221.1 GI:2148401
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 47)
AUTHORS   Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima,A., Kojima,Y.
            and Matsubara,K.
TITLE     Large scale cDNA sequencing for analysis of quantitative and
            qualitative aspects of gene expression
JOURNAL    Nat. Genet. 2, 173-179 (1992)
MEDLINE    94258199
PUBMED     1345164
COMMENT    Contact: Kousaku Okubo, Nachiro Hori, Ryo Matoba, Toshiyuki
            Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
            Institute for Molecular and Cellular Biology
            Osaka University
            1-3 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES             source
    Location/Qualifiers
        1..47
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="GDB:D05772E"
            /db_xref="taxon:9606"
            /clone="s362"
            /lab_host="E.coli"
            /clone_lib="Liver HepG2 cell line."
            /note="3'-directed regional cDNA library. Cleaved by MboI
            and transformed into E.coli."

ORIGIN
Query Match      52.8%; Score 13.2; DB 7; Length 47;
Best Local Similarity 83.3%; Pred. No. 2.2e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      8 CTAGCAGATTTCATGGCAC 25
      ||||| ||||| ||||| |||||
Db      41 CTAGACCTTTCATGGAC 24

RESULT 8
AZ782156/c
LOCUS      AZ782156
DEFINITION 2M0022K09F Mouse 10kb plasmid UUC1M library Mus musculus genomic
            clone UUC2M002K09 F, genomic survey sequence.
ACCESSION  AZ782156
VERSION    AZ782156.1 GI:12915573
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 30)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss

Qy      5 AGCCTAGCAGATTTCATGGCAC 25
      ||||| ||||| ||||| |||||
Db      27 ACCCTAGCCGACTCAGCAGAC 7

RESULT 9
AL757317/c
LOCUS      AL757317
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-120G10-012516,
            genomic survey sequence.
ACCESSION  AL757317
VERSION    AL757317.1 GI:21495665
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE  1
AUTHORS   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
            GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
            Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL    22755829
MEDLINE    12874060
PUBMED

Qy      52.0%; Score 13; DB 8; Length 30;
Best Local Similarity 76.2%; Pred. No. 2.6e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      5 AGCCTAGCAGATTTCATGGCAC 25
      ||||| ||||| ||||| |||||
Db      27 ACCCTAGCCGACTCAGCAGAC 7

RESULT 9
AL757317/c
LOCUS      AL757317
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-120G10-012516,
            genomic survey sequence.
ACCESSION  AL757317
VERSION    AL757317.1 GI:21495665
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE  1
AUTHORS   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
            GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
            Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL    22755829
MEDLINE    12874060
PUBMED

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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0022 row: K column: 09
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.

FEATURES

source

1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M002K09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 13; DB 8; Length 30;
Best Local Similarity 76.2%; Pred. No. 2.6e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTTCATGGCAC 25

Db 27 ACCCTAGCCGACTCAGCAGAC 7

RESULT 9

AL757317/c

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-120G10-012516,
genomic survey sequence.

ACCESSION AL757317

VERSION AL757317.1 GI:21495665

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1

Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.

GABI-Kat Simplesearch: a flanking sequence tag (FST) database for

the identification of T-DNA insertion mutants in Arabidopsis

thaliana

Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL 22755829

MEDLINE 12874060

PUBMED


```

REFERENCE
AUTHORS      Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
              Weisshaar,B.
TITLE        An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
              flanking sequence tag-based reverse genetics
JOURNAL      Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE      23117147
PUBMED       14756321
REFERENCE
AUTHORS      Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
              Weisshaar,B.
TITLE        High-throughput generation of sequence indexes from T-DNA
              mutagenized Arabidopsis thaliana lines
JOURNAL      Biotechniques 35 (6), 1164-1168 (2003)
PUBMED       14682050
REFERENCE
AUTHORS      Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
TITLE        Direct Submission
JOURNAL      Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
              Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT      It indicates an insertion close to or within gene Atig05890.
              Details on the protocols used for generation of the sequence are
              described in References 1-3. The sequences are generated at the MPI
              for Plant Breeding Research in the context of the GABI-Kat project.
              GABI-Kat is part of the German Plant Genomics program designated
              'GABI'. Information on line availability can be found at:
              http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
source
Location/Qualifiers
1. .35
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."
ORIGIN
Query Match      52.0%; Score 13; DB 9; Length 35;
Best Local Similarity 76.2%; Pred. NO. 2.6e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5 AGCCTAGCAGATTCATGGCAC 25
|||||
Db 25 AGCTTAGCAGATTCATGGCAC 5
|||||

RESULT 10
LOCUS      AUI03585/c
DEFINITION AUI03585 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP02395, mRNA sequence.
ACCESSION  AUI03585
VERSION     AUI03585.1 GI:13553106
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taiba,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isoga,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

```

```

EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP02395"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      52.0%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. NO. 2.7e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5 AGCCTAGCAGATTCATGGCAC 25
|||||
Db 24 AGCCCGGAGAGTCATGGGAC 4
|||||

RESULT 11
LOCUS      BI824288
DEFINITION  BI824288 50 bp mRNA linear EST 04-OCT-2001
mRNA sequence.
ACCESSION  BI824288
VERSION     BI824288.1 GI:15935838
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11452 row: b column: 23
High quality sequence stop: 50.
FEATURES
source
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5181238"
/lab_host="DH10B"
/clone_lib="NIH MGC 115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.

```

Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 52.0%; Score 13; DB 4; Length 50;
Best Local Similarity 76.2%; Pred. No. 2.7e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATG 21
|||||
Db 4 GCGGCGCCACGACAGATCAGG 24

RESULT 12

BH790466 30 bp DNA linear GSS 02-APR-2002
LOCUS SALK_057108.32.55.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_057108.32.55.x, genomic survey sequence.

ACCESSION BH790466 GI:19883564
VERSION BH790466
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 30)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

AUTHORS

Arabidopsis Genome

JOURNAL

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of Atg14330.

Class: TDNA tagged.

FEATURES

source

1. .30
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_057108.32.55.x"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.2%; Score 12.8; DB 8; Length 30;
Best Local Similarity 70.8%; Pred. No. 3.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGCA 24
|||||
Db 2 GCTGAGCCCAACACATCGGA 25

RESULT 13

TA317F100 33 bp DNA linear GSS 13-DEC-2000
LOCUS TA317F100
DEFINITION T. brucei sheared genomic DNA clone 317F10, reverse sequence,

genomic survey sequence.

AL491482

AL491482.1 GI:11867130

GSS.

Trypanosoma brucei

Trypanosoma brucei

Eukaryotes; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 33)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

1. .33

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="317f10"

Query Match 51.2%; Score 12.8; DB 9; Length 33;

Best Local Similarity 70.8%; Pred. No. 3.2e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGCA 24

|||||

Db 5 GCTGATCATTCGATTTCTTGCCA 28

RESULT 14

BE732614/c

LOCUS BE732614

DEFINITION 601571185F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3925725 5',

mRNA sequence.

ACCESSION BE732614

BE732614.1 GI:10146606

EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 39)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: L1CM752 row: i column: 22.

Location/Qualifiers

```

source
1. .39
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3925725"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected by
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 51.2%; Score 12.8; DB 2; Length 39;
Best Local Similarity 70.8%; Pred. No. 3.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 CTGAGCCTAGCAGATTCTTGGCAC 25
34 CCGTACCTGCCCGATTCTTGGCAC 11

Db

RESULT 15
AA715909
LOCUS
DEFINITION
nv76904.r1 NCI CGAP Br4 Homo sapiens cDNA clone IMAGE:1235766
similar to SW:NUAM GORGO P03907 NADH-UBIQUINONE OXIDOREDUCTASE
CHAIN 4 ; mRNA sequence.

ACCESSION
AA715909
VERSION
AA715909.1 GI:2728183
KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 46)
Sakaki, Y., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
Ph.D. student, Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtp/image/image.html

Trace considered overall poor quality
Insert Length: 562 Std Error: 0.00
Seq primer: -28m13 rev1 Ert from Amersham
High quality sequence stop: 1.

Location/Qualifiers
1. 46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1235766"
/sex="female"
/tissue_type="normal ductal tissue"
/lab_host="DH10B"
/clone_lib="NCI CGAP Br4"
/note="Organ: breast; Vector: pAMP10; mRNA made from
normal breast ductal tissue, cDNA made by oligo-dT

FEATURES
source

ORIGIN

Query Match 51.2%; Score 12.8; DB 1; Length 46;
Best Local Similarity 87.5%; Pred. No. 3.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGCCTAGCAGATTCA 19
10 GTGCCTAGCAGATCA 25

Db

RESULT 16
AU105049/c
LOCUS
DEFINITION
AU105049 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00293, mRNA sequence.

ACCESSION
AU105049
VERSION
AU105049.1 GI:13554570
KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE
21270072

PUBMED
11375929

COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT00293"
/clone_lib="Sugano Homo sapiens cDNA library"

FEATURES
source

ORIGIN

Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 CTGAGCCTAGCAGATTCTTGGCAC 25
25 CTGAGCCTAGCAGATTCTTGGCAC 2

Db

RESULT 17
AU105060/c
LOCUS
DEFINITION
AU105060 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT04574, mRNA sequence.

ACCESSION
AU105060
VERSION
AU105060.1 GI:13554581
KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT04574"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CTGAGCCTTAGCAGATTTCATGGCAC 25
Db 25 CTCACGCTGTACCTTCATGGCAC 2

RESULT 18
AUI05083/c
LOCUS
DEFINITION AUI05083 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT10532, mRNA sequence.
ACCESSION AUI05083
VERSION AUI05083.1 GI:13554604
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT10532"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CTGAGCCTTAGCAGATTTCATGGCAC 25
Db 25 CTCACGCTGTACCTTCATGGCAC 2

RESULT 19
AUI05084/c
LOCUS
DEFINITION AUI05084 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT10642, mRNA sequence.
ACCESSION AUI05084
VERSION AUI05084.1 GI:13554605
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT10642"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CTGAGCCTTAGCAGATTTCATGGCAC 25
Db 25 CTCACGCTGTACACATTCATAGCAC 2

RESULT 20
AUI05091/c
LOCUS
DEFINITION AUI05091 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSE01778, mRNA sequence.
ACCESSION AUI05091
VERSION AUI05091.1 GI:13554612
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)

```

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)

FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT10642"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CTGAGCCTTAGCAGATTTCATGGCAC 25
Db 25 CTCACGCTGTACACATTCATAGCAC 2

RESULT 20
AUI05091/c
LOCUS
DEFINITION AUI05091 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSE01778, mRNA sequence.
ACCESSION AUI05091
VERSION AUI05091.1 GI:13554612
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)

```

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuk@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

LOCATION/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="ADSR01778"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 CTGAGCCTAGCAGATTTCATGGCAC 25
||| ||| ||| ||| ||| ||| |||
Db 26 CTCACGCTGTGCAGTTTATAGCAC 3

RESULT 21
AZ480878 28 bp DNA linear GSS 04-OCT-2000
LOCUS IM0302122R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0302122 R, genomic survey sequence.

ACCESSION AZ480878
VERSION .
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
UNIVERSITY University of Utah Genome Center
COMMENT Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: I column: 22
Seq primer: CACACAGGAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"

/db_xref="taxon:10090"
/clone="UUGC1M0302122"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus CS7BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [GI14732114|95|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E.coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 50.4%; Score 12.6; DB 8; Length 28;
Best Local Similarity 78.9%; Pred. No. 3.9e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CTGAGCCTAGCAGATTTCAT 20
||| ||| ||| ||| ||| ||| |||
Db 6 CTTAGCTTTGGAGATTTCAT 24

RESULT 22
TA372A04P/c 45 bp DNA linear GSS 13-DEC-2000
LOCUS TA372A04P
DEFINITION T. brucei sheared genomic DNA clone 372a04, forward sequence, genomic survey sequence.

ACCESSION AL496098
VERSION AL496098.1 GI:11872137
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 45)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
Location/Qualifiers
1..45
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"

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Best Local Similarity 59.6%; Pred. No. 5e+05;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY
2 CTGAGCCTAGCAGATTCATGCGCA 24
||||| ||||| ||||| |||||
Db
36 CTCCGCTCCANATTCACGCCA 14

RESULT 24
AZ824424 38 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION
2M009D06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M009D06 F, genomic survey sequence.
ACCESSION
VERSION AZ824424.1 GI:12994332
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: D column: 06
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 38.

FEATURES
source
1. .38
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M009D06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 49.6%; Score 12.4; DB 8; Length 38;

Best Local Similarity 50.4%; Score 12.6; DB 9; Length 45;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
4 GAGCCTAGCAGATTCATGG 22
||||| ||||| |||||
Db
35 GTGGCTAGCAGCATCATGG 17

RESULT 23
T65804/c
LOCUS
DEFINITION
T65804 36 bp mRNA linear EST 20-FEB-1995
yc1h12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:80423 3' similar to gb|W87927|HUMALCE44 Human carcinoma
cell-derived Alu RNA transcript, (rRNA); gb:D5272 !!! ALU CLASS A
WARNING ENTRY !!!! (HUMAN);, mRNA sequence.
ACCESSION
VERSION T65804.1 GI:674849
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,G., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 232
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNL This clone is available royalty-free
through LNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Possible reversed clone: polyt not found
Insert Length: 232 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 1.

FEATURES
source
1. .36
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:484040"
/db_xref="taxon:9606"
/clone="IMAGE:80423"
/sex="male"
/dev_stages="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene lung (#937210)"
/note="Organ: lung; Vector: pBluescript SK-; Site:1:
EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. normal lung. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match 49.6%; Score 12.4; DB 7; Length 36;

```

Best Local Similarity 72.7%; Pred. No. 5.1e+05; Mismatches 6; Indels 0; Gaps 0;
Matches 16; Conservative 0;

QY 1 GCTGAGCCTAGCAGATTCATGG 22
|||||
Db 10 GCTGAGAAATCCAGATGCATGG 31
|||||

RESULT 25
AL938370
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-234D12-014337,
genomic survey sequence.

ACCESSION
AL938370.1 GI:24370164

VERSION
GSS.

KEYWORDS
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
1
Li, Y., Rosso M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL
MEDLINE
PUBMED
22755829
12874060

REFERENCE
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weishaar, B.

TITLE
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL
MEDLINE
PUBMED
23117147
14756321

REFERENCE
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weishaar, B.

TITLE
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

JOURNAL
PUBMED
BioTechniques 35 (6), 1164-1168 (2003)

REFERENCE
4 (bases 1 to 39)

ROSSO, M.G., LI, Y., STRIZHOV, N. and WEISHAAR, B.

TITLE
Direct Submission
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At3g56610.

DETAILS on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
Location/Qualifiers

1..39

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-234D12-014337"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 49.6%; Score 12.4; DB 9; Length 39;
Best Local Similarity 72.7%; Pred. No. 5.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCATGG 22

|||||
Db 8 GATGAGACTAAACACTCATGG 29
|||||

RESULT 26

H97155/c

LOCUS

DEFINITION

H97155 42 bp mRNA linear EST 11-DEC-1995

YV91f07.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone

IMAGE:250117 3' similar to gb:XS4156_rnal CELLULAR TUMOR ANTIGEN

P53 (HUMAN);, mRNA sequence.

ACCESSION
H97155

VERSION
H97155.1 GI:1114198

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (Bases 1 to 42)

AUTHORS
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsone, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, B., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
The WashU-Merck EST Project

JOURNAL
Unpublished (1995)

COMMENT
Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1247 Std Error: 0.00

Seq primer: Promega -2ml3

High quality sequence stop: 1.

Location/Qualifiers

1..42

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3867823"

/db_xref="taxon:9606"

/clone="IMAGE:250117"

/sex="Male"

/tissue type="melanocyte"

/lab host="DH10B (ampicillin resistant)"

/clone_lib="Soares melanocyte 2NbHM"

/note="Vector: pT73D (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5',

TGTTACCAATCTGAAGTGGAGCGCGCAGTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT73 vector

(Pharmacia). Library constructed by Bento Soares and

M.Fatima Bonaldo. RNA from normal foreskin melanocytes

(FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 49.6%; Score 12.4; DB 7; Length 42;
Best Local Similarity 72.7%; Pred. No. 5.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;


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Qy      3  TGAGCCTAGCAGATTTCATGGCA 24
      ||| ||| ||| ||| ||| ||| |||
Db      30  TGAGCCCGAGGAGTTTGAGGCCA 9

RESULT 27
LOCUS   AZ491459/c
DEFINITION AZ491459F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
          clone UUGC1M0325H05 F, genomic survey sequence.
ACCESSION AZ491459
VERSION   AZ491459.1 GI:10663188
KEYWORDS  GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 44)
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D., Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: dunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0325 Row: H Column: 05
          Seq primer: CGTTGTAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 44.
          Location/Qualifiers
            1..44
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0325H05"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /notes="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 [G14732114|gb|AF129072.1], a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

FEATURES             source
    source
    1..50
       /organism="Glycine max"
       /mol_type="mRNA"
       /cultivar="Raiden"
       /db_xref="taxon:3847"
       /clone="GENOME SYSTEMS CLONE ID: Gm-cl062-2594"
       /tissue_type="stem tissue of greenhouse grown plants"
       /dev_stage="1 month old"
       /lab_host="DH10B"
       /clone_lib="Gm-cl062"
       /notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
       XhoI; The cDNA library was constructed from mRNA isolated
       from stem tissue of 1 month old greenhouse grown plants
       for the cultivar Raiden. Complementary DNA was
       synthesized from mRNA using a primer consisting of a
       poly(dT) sequence with a XhoI restriction site. EcoRI
       adaptors were ligated to the blunt-ended cDNA fragments
       followed by XhoI digestion. The cDNA fragments were
       directionally cloned into the EcoRI-XhoI restriction site
       of the pBluescript vector. The ligated cDNA fragments were
       transformed into DH10B host cells (GibcoBRL). This library
       was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN
Query Match      49.6%; Score 12.4; DB 8; Length 44;
Best Local Similarity 92.9%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4  GAGCCTAGCAGATTTCATGGCAC 25
      ||| ||| ||| ||| ||| ||| |||
Db      25  GAGATGAGGAGATCATGGCTC 46

RESULT 28
LOCUS   BG405996
DEFINITION BG405996 ssc40g01.y1 Gm-cl062 Glycine max cDNA clone GENOME SYSTEMS CLONE
          ID: Gm-cl062-2594 5', mRNA sequence.
ACCESSION BG405996
VERSION   BG405996.1 GI:13312345
KEYWORDS  EST.
SOURCE   Glycine max (soybean)
ORGANISM Glycine max
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
          Glycine.
REFERENCE 1 (bases 1 to 50)
AUTHORS  Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
          Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
          Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
          Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
          Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
          McCann,R., Waterston,R. and Wilson,R.
TITLE    Public Soybean EST Project
JOURNAL  Unpublished (1999)
COMMENT  Contact: Shoemaker R/Public Soybean EST Project
          Public Soybean EST Project
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          When it has been determined, an EST from the other end of this
          clone is listed in the 'Other ESTs on clone' field. This clone is
          available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
          57006 USA (phone: 800 423 4163; email:
          info@biogeneticservices.com).
          Location/Qualifiers
            1..50
               /organism="Glycine max"
               /mol_type="mRNA"
               /cultivar="Raiden"
               /db_xref="taxon:3847"
               /clone="GENOME SYSTEMS CLONE ID: Gm-cl062-2594"
               /tissue_type="stem tissue of greenhouse grown plants"
               /dev_stage="1 month old"
               /lab_host="DH10B"
               /clone_lib="Gm-cl062"
               /notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
               XhoI; The cDNA library was constructed from mRNA isolated
               from stem tissue of 1 month old greenhouse grown plants
               for the cultivar Raiden. Complementary DNA was
               synthesized from mRNA using a primer consisting of a
               poly(dT) sequence with a XhoI restriction site. EcoRI
               adaptors were ligated to the blunt-ended cDNA fragments
               followed by XhoI digestion. The cDNA fragments were
               directionally cloned into the EcoRI-XhoI restriction site
               of the pBluescript vector. The ligated cDNA fragments were
               transformed into DH10B host cells (GibcoBRL). This library
               was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN
Query Match      49.6%; Score 12.4; DB 4; Length 50;
Best Local Similarity 72.7%; Pred. No. 5.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      4  GAGCCTAGCAGATTTCATGGCAC 25
      ||| ||| ||| ||| ||| ||| |||
Db      25  GAGATGAGGAGATCATGGCTC 46

```



```

RESULT 29
A1182198/c
LOCUS
DEFINITION uc54f11.r1 Soares mammary_gland NbMMG Mus musculus cDNA clone
IMAGE:1430445 5' similar to TR:Q90574 Q90574 FILAMIN. i, mRNA
sequence.
ACCESSION A1182198
VERSION A1182198
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:914513
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..43
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1430445"
/sex="male"
/tissue_type="mammary gland"
/dev_stages="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary_gland NbMMG"
/notes="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo (dT) primer [5',
TGTTACCAATCTGAAGTGGGCGCGCCGGAATGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
ORIGIN
Query Match 48.8%; Score 12.2; DB 1; Length 43;
Best Local Similarity 82.4%; Pred. No. 6.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 7 CCTAGCAGATTCATGGC 23
Db 31 CTTACCAGATTCCTGGC 15
RESULT 30
A1182198/c
LOCUS
DEFINITION uc54f11.r1 Soares mammary_gland NbMMG Mus musculus cDNA clone
IMAGE:1430445 5' similar to TR:Q90574 Q90574 FILAMIN. i, mRNA
sequence.
ACCESSION A1182198
VERSION A1182198
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:914513
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..43
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1430445"
/sex="male"
/tissue_type="mammary gland"
/dev_stages="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary_gland NbMMG"
/notes="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo (dT) primer [5',
TGTTACCAATCTGAAGTGGGCGCGCCGGAATGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
ORIGIN
Query Match 48.8%; Score 12.2; DB 1; Length 43;
Best Local Similarity 82.4%; Pred. No. 6.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 7 CCTAGCAGATTCATGGC 23
Db 31 CTTACCAGATTCCTGGC 15

```

```

LOCUS
DEFINITION AUI02762 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS00532, mRNA sequence.
ACCESSION AUI02762
VERSION AUI02762
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS00532"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
Db 30 GCGGAGACTGGAGGATACAGAGCAC 6
RESULT 31
AUI02764/c
LOCUS
DEFINITION AUI02764 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS01012, mRNA sequence.
ACCESSION AUI02764
VERSION AUI02764
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

```

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01012"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Db 28 GCGGAGACTGGAGTACAGAGCAC 4

RESULT 32

AU102765/c

LOCUS

DEFINITION AU102765 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS01084, mRNA sequence.

ACCESSION

VERSION AU102765

KEYWORDS

SOURCE AU102765.1 GI:13552286

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Construction and

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES

source
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01084"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Db 31 GCGGAGACTGGAGTACAGAGCAC 7

RESULT 33

AU102768/c

LOCUS

DEFINITION AU102768 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

CAS01704, mRNA sequence.

ACCESSION

VERSION AU102768

KEYWORDS

SOURCE AU102768.1 GI:13552289

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Construction and

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES

source

Location/Qualifiers

1. 50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CAS01704"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 48.8%; Score 12.2; DB 1; Length 50;

Best Local Similarity 68.0%; Pred. No. 6.5e+05;

Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Db 29 GCGGAGACTGCGGATACAGAGCAC 5

RESULT 34

AU102771/c

LOCUS

DEFINITION AU102771 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

CAS03060, mRNA sequence.

ACCESSION AU102771

VERSION AU102771.1 GI:13552292

KEYWORDS EST.

SOURCE AU102771.1 GI:13552292

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Construction and

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yezuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

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FEATURES
  source
    149-156 (1997).
      Location/Qualifiers
        1..50
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="CAS03060"
          /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
  Query Match      48.8%; Score 12.2; DB 1; Length 50;
  Best Local Similarity 68.0%; Pred. No. 6.5e+05;
  Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
    |||||
Db 30 GCGGAGACTGGAGGATACAGAGCAC 6

RESULT 35
AUI02773/c
LOCUS
DEFINITION AUI02773 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS03358, mRNA sequence.
ACCESSION AUI02773
VERSION AUI02773.1 GI:13552294
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
          Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
          EMBO Rep. 2 (5), 388-393 (2001)
          21270072
          PUBMED
          COMMENT
            Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES
  source
    1..50
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="CAS04123"
      /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
  Query Match      48.8%; Score 12.2; DB 1; Length 50;
  Best Local Similarity 68.0%; Pred. No. 6.5e+05;
  Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
    |||||
Db 29 GCGGAGACTGGAGGATACAGAGCAC 5

RESULT 37
AUI02777/c
LOCUS
DEFINITION AUI02777 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS05434, mRNA sequence.
ACCESSION AUI02777
VERSION AUI02777.1 GI:13552298
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
          Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
          EMBO Rep. 2 (5), 388-393 (2001)
          21270072
          PUBMED
          COMMENT
            Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES
  source
    1..50
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="CAS03358"
      /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
  Query Match      48.8%; Score 12.2; DB 1; Length 50;
  Best Local Similarity 68.0%; Pred. No. 6.5e+05;
  Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
    |||||
Db 29 GCGGAGACTGCCGATACAGAGCAC 5

RESULT 36
AUI02775/c
LOCUS
DEFINITION AUI02775 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS04123, mRNA sequence.
ACCESSION AUI02775
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```

source      1. .50
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clones="CAS05434"
            /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTACGAGTTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 28 GCGGAGACTGGAGGATACAGGCAC 4

RESULT 38
AU102778/c
LOCUS AU102778 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS06130, mRNA sequence.
ACCESSION AU102778
VERSION AU102778.1 GI:13552299
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
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REFERENCE
1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source      1. .50
            /organism="Homo sapiens"
            /mol_type="mRNA"
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            /clone_lib="Sugano Homo sapiens cDNA library"

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Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTACGAGTTCATGGCAC 25
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Db 28 GCGGAGACTGGAGGATACAGGCAC 4

RESULT 39
AU102782/c
LOCUS AU102782 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS06130, mRNA sequence.
ACCESSION AU102782
VERSION AU102782.1 GI:13552303
KEYWORDS EST.

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 50)
            Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
            21270072
            PUBMED 11375929
            COMMENT Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
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            /organism="Homo sapiens"
            /mol_type="mRNA"
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            /clone_lib="Sugano Homo sapiens cDNA library"

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Query Match      48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTACGAGTTCATGGCAC 25
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Db 29 GCGGAGACTGCCGATACAAAGCAC 5

RESULT 40
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LOCUS AU102784 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS08174, mRNA sequence.
ACCESSION AU102784
VERSION AU102784.1 GI:13552305
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 50)
            Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
            21270072
            PUBMED 11375929
            COMMENT Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
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source      1. .50
            /organism="Homo sapiens"

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ORIGIN

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Query Match      48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy      1  GCTGAGCCTAGCAGATTTCATGGCAC 25
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Db      28  GCGGAGACTGGAGGATACAGAGCAC 4

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Job time : 1196.82 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 48.5741 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-10

Perfect score: 25

Sequence: 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	25	100.0	25	1	US-07-989-160-10
2	14.6	58.4	29	4	US-10-039-659A-24
3	14.2	56.8	38	3	US-08-646-265A-37
4	14.2	56.8	39	4	US-09-269-921-50
5	14.2	56.8	41	2	US-08-039-198B-17
6	14.2	56.8	41	2	US-08-182-067-22
7	14.2	56.8	41	2	US-08-465-313-22
8	14.2	56.8	41	4	US-09-378-967-22
9	14.2	56.8	49	4	US-08-407-620A-41
10	14	56.0	25	4	US-09-396-196G-24574
11	13.8	55.2	25	4	US-09-396-196G-43320
12	13.8	55.2	25	4	US-09-396-196G-43321
13	13.8	55.2	25	4	US-09-396-196G-43332
14	13.8	55.2	25	4	US-09-396-196G-61733
15	13.8	55.2	25	4	US-09-396-196G-110219
16	13.6	54.4	21	3	US-09-262-773-104
17	13.6	54.4	25	4	US-09-866-108A-5529
18	13.6	54.4	25	4	US-09-866-108A-5530
19	13.6	54.4	25	4	US-09-866-108A-5531
20	13.6	54.4	25	4	US-09-866-108A-5532
21	13.6	54.4	25	4	US-09-866-108A-5533
22	13.6	54.4	25	4	US-09-866-108A-5534
23	13.6	54.4	25	4	US-09-396-196G-24817
24	13.6	54.4	25	4	US-09-396-196G-65707
25	13.6	54.4	25	4	US-09-396-196G-104940
26	13.6	54.4	47	4	US-09-422-978-3104
27	13.4	53.6	25	4	US-09-396-196G-22130

c 28	13.4	53.6	25	4	US-09-396-196G-22131	Sequence 22131, A
c 29	13.4	53.6	25	4	US-09-396-196G-54320	Sequence 54320, A
c 30	13.4	53.6	33	4	US-09-826-509-105	Sequence 105, App
c 31	13.4	53.6	49	3	US-08-916-576B-33	Sequence 33, Appl
c 32	13.4	53.6	49	4	US-10-078-337-33	Sequence 33, Appl
c 33	13.2	52.8	21	4	US-09-657-472-693	Sequence 693, App
c 34	13.2	52.8	25	4	US-09-647-563-17	Sequence 17, Appl
c 35	13.2	52.8	25	4	US-09-396-196G-104928	Sequence 104928, A
c 36	13.2	52.8	25	4	US-09-396-196G-104929	Sequence 104929, A
c 37	13.2	52.8	33	3	US-09-136-605-26	Sequence 26, Appl
c 38	13.2	52.8	36	2	US-08-484-993B-56	Sequence 56, Appl
c 39	13.2	52.8	36	2	US-08-484-158B-56	Sequence 56, Appl
c 40	13.2	52.8	36	2	US-08-484-596A-56	Sequence 56, Appl
c 41	13.2	52.8	36	2	US-08-480-150A-56	Sequence 56, Appl
c 42	13.2	52.8	36	3	US-08-458-731-56	Sequence 56, Appl
c 43	13.2	52.8	36	3	US-08-149-223A-56	Sequence 56, Appl
c 44	13	52.0	18	4	US-09-422-978-4829	Sequence 4829, Ap
c 45	13	52.0	25	4	US-09-396-196G-21353	Sequence 21353, A

ALIGNMENTS

RESULT 1
US-07-989-160-10
; Sequence 10, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-989-160-10

Query Match 100.0%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-10-039-659A-24
; Sequence 24, Application US/10039659A
; Patent No. 6723520
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Antibodies that bind chemokine TECK
; FILE REFERENCE: DX0589KIB US
; CURRENT APPLICATION NUMBER: US/10/039,659A
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: exon 3-specific CRAM primer
US-10-039-659A-24

Query Match      58.4%; Score 14.6; DB 4; Length 29;
Best Local Similarity 81.0%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 3
US-08-646-265A-37
; Sequence 37, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763

US-10-039-198B-17
; Sequence 17, Application US/08039198B
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER

; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-646-265A-37

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Best Local Similarity 84.2%; Pred. No. 9.8e+02;
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; Sequence 50, Application US/09269921
; Patent No. 6699974
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-269-921-50

Query Match      56.8%; Score 14.2; DB 4; Length 39;
Best Local Similarity 84.2%; Pred. No. 9.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
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Db      19 GGTGTGCCAAGCAGATTCA 37

RESULT 5
US-08-039-198B-17
; Sequence 17, Application US/08039198B
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
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; REFERENCE/DOCKET NUMBER: LYNX91-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-465-313-22

Query Match 56.8%; Score 14.2; DB 2; Length 41;
Best Local Similarity 84.2%; Pred. NO. 1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 19
Db 22 GGTGTGCCAAGCAGATTCA 40

RESULT 8
US-09-378-967-22
; Sequence 22, Application US/09378967
; Patent No. 6689869
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN J.
; APPLICANT: CROWE, J. SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILLITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,967
; FILING DATE: 23-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,313
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,067
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01289
; FILING DATE: 15-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9115364.3
; FILING DATE: 16-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WENDLER, HELEN E.
; REFERENCE/DOCKET NUMBER: 37,964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-378-967-22

Query Match 56.8%; Score 14.2; DB 4; Length 41;
Best Local Similarity 84.2%; Pred. NO. 1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 19
Db 22 GGTGTGCCAAGCAGATTCA 40

RESULT 9
US-08-407-620A-41
; Sequence 41, Application US/08407620A
; Patent No. 6569430
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: CLARK, MICHAEL R.
; APPLICANT: WINTER, GREGORY P.
; APPLICANT: RIECHMANN, LUTZ
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,620A
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,705
; FILING DATE: 29-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,480
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,601
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/424,233
; FILING DATE: 12-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 88036228
; FILING DATE: 12-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8804464
; FILING DATE: 25-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-325
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-407-620A-41

Query Match 56.8%; Score 14.2; DB 4; Length 49;
Best Local Similarity 84.2%; Pred. No. 1.e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 19
Db 12 GGTGTCCCAAGCAGATTCA 30

RESULT 10
US-09-396-196G-24574/c
; Sequence 24574, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24574
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24574

Query Match 56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 77.3%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 22
Db 25 GCAGACAAGCAGACCCATGG 4

RESULT 11
US-09-396-196G-43320
; Sequence 43320, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-43320

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTC 18
Db 5 CTGAGCCAGCAGCTTC 21

RESULT 12
US-09-396-196G-43321
; Sequence 43321, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-43321

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTC 18
Db 3 CTGAGCCAGCAGCTTC 19

RESULT 13
US-09-396-196G-43332
; Sequence 43332, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43332
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-43332

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTC 18
Db 1 CTGAGCCAGCAGCTTC 17

RESULT 14
US-09-396-196G-61733/c
; Sequence 61733, Application US/09396196G
; Patent No. 6821724

```
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61733
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-61733

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGCCTAGCAGATCA 19
Db 21 TGAGCCTAGAGATCCA 5

RESULT 15
US-09-396-196G-110219/c
; Sequence 110219, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110219
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-110219

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CCTAGCAGATTCATGGC 23
Db 25 CCTCCAGATTCATGGC 9

RESULT 16
US-09-262-773-104/c
; Sequence 104, Application US/09262773
; Patent No. 6225451
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ding, Wei
; APPLICANT: Wagner, Susanne
; APPLICANT: Hesse, Mark A.
; TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
; FILE REFERENCE: Myriad 3
; CURRENT APPLICATION NUMBER: US/09/262,773

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5529
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5529

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCTTAGCAGATTCATGGCAC 25
Db 21 GCTTAGAAGAGTGTGGCAC 2

RESULT 17
US-09-866-108A-5529/c
; Sequence 5529, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5529
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5529

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCTTAGCAGATTCATGGCAC 25
Db 25 GCCCAGCATCTCCATGGCAC 6
```

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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 686188
; SEQ ID NO 5531
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-5531

Query Match          54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      6  GCCTAGCAGATTCATGGCAC 25
      ||| ||| ||| ||| ||| ||| |||
Db      23  GCCAGCATCTCATGGCAC 4

RESULT 20
US-09-866-108A-5532/c
; Sequence 5532 Application US/09866108A
; Patent No. 686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

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; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Acomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 5532

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-5532

Query Match 54.4%; Score 13.6; DB 4; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25

Db 22 GCCCAGCATCTCCATGGCAC 3

RESULT 21

US-09-866-108A-5533/c

; Sequence 5533, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Acomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 5533

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-5533

Query Match 54.4%; Score 13.6; DB 4; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25

Db 21 GCCCAGCATCTCCATGGCAC 2

RESULT 22

US-09-866-108A-5534/c

; Sequence 5534, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Acomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 5534

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-5534

Query Match 54.4%; Score 13.6; DB 4; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25

Db 20 GCCCAGCATCTCCATGGCAC 1

RESULT 23

US-09-396-196G-24817

; Sequence 24817, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 24817
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24817

Query Match      54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGAGCCTAGCAGATTCATGGG 22
Db 1 TTAGCCTGCCAGATTTAGGG 20

RESULT 24
US-09-396-196G-65707/c
; Sequence 65707, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65707
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65707

Query Match      54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCA 24
Db 24 AGTCTAGCTCATTTCAGGCA 5

RESULT 25
US-09-396-196G-104940/c
; Sequence 104940, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104940
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104940

Query Match      54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTCATGGC 23
Db 24 GCGACCGACGAGCTTCATGGC 5

RESULT 26
US-09-422-978-3104
; Sequence 3104, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3104
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2342-217 : polymorphic base C or T
US-09-422-978-3104

Query Match      54.4%; Score 13.6; DB 4; Length 47;
Best Local Similarity 72.7%; Pred. No. 2.1e+03;
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTCATGGCAC 25
Db 3 GAGCCTTGGAGCTTTTCATGACAY 24

RESULT 27
US-09-396-196G-22130/c
; Sequence 22130, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-22130

Query Match      53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AGCAGATTCATGGCA 24
Db 10 AGCAGATTCATGGCA 24
```

```
Db      22 AGCAGATTCATGGAA 8

RESULT 28
US-09-396-196G-22131/c
; Sequence 22131, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22131
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-22131

Query Match      53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 AGCAGATTCATGGCA 24
        |||||
Db      16 AGCAGATTCATGGAA 2

RESULT 29
US-09-396-196G-54320/c
; Sequence 54320, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-54320

Query Match      53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 CTGAGCCTAGCAGATTCATGGCA 24
        |||||
Db      24 CTGAGCAGAGCTGATGACGGAA 2

RESULT 30
US-09-826-509-105
; Sequence 105, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinema, Karin

; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: Protein-Coupled Receptors
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 105
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-105

Query Match      53.6%; Score 13.4; DB 4; Length 33;
Best Local Similarity 73.9%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCATGGC 23
        |||||
Db      6 GCTTGCCCAAGAGTGTCTATGGC 28

RESULT 31
US-08-916-576B-33/c
; Sequence 33, Application US/08916576B
; Patent No. 6171816
; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: EBER, REINHARD
; APPLICANT: ENDRESS, GREGORY A.
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,576B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,347
; FILING DATE: 23-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0500001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-916-576B-33
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Query Match 53.6%; Score 13.4; DB 3; Length 49;
Best Local Similarity 73.9%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGC 23
|||||
Db 33 GCTGAGTGTAGCATCATGGC 11

RESULT 32

US-10-078-337-33/c
; Sequence 33, Application US/10078337
; Patent No. 6818412
; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG
; DILLON, PATRICK J.
; EBER, REINHARD
; ENDRESS, GREGORY A.
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/078,337
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/916,576
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0500001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Query Match 53.6%; Score 13.4; DB 4; Length 49;
Best Local Similarity 73.9%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGC 23
|||||
Db 33 GCTGAGTGTAGCATCATGGC 11

RESULT 33

US-09-657-472-693/c
; Sequence 693, Application US/09657472
; Patent No. 672063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George O.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-693

Query Match 52.8%; Score 13.2; DB 4; Length 21;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCA 24
|||||
Db 21 AGCCTAGCAGATTCATGGCA 2

RESULT 34

US-09-647-563-17/c
; Sequence 17, Application US/09647563
; Patent No. 6706475
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America
; TITLE OF INVENTION: Oligonucleotide Probes for Detecting Enterobacteriaceae
; FILE REFERENCE: 6395-57017
; CURRENT APPLICATION NUMBER: US/09/647,563
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-09-647-563-17

Query Match 52.8%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGC 23
|||||
Db 25 GCCTAGTACGTTTCATGGC 8

RESULT 35

US-09-396-196G-104928/c
; Sequence 104928, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678

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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104928
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104928

Query Match      52.8%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGC 23
Db      25 GACCAGCAGCTTCATGGC 8

RESULT 36
US-09-396-196G-104929/c
; Sequence 104929, Application US/09396196G
; GENERAL INFORMATION:
; PATENT NO. 6821724
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Afymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104929
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104929

Query Match      52.8%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGC 23
Db      24 GACCAGCAGCTTCATGGC 7

RESULT 37
US-09-136-605-26
; Sequence 26, Application US/09136605A
; Patent No. 6140052
; GENERAL INFORMATION:
; APPLICANT: He, Tong-Chuan
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to
; TITLE OF INVENTION: Prevent Cancer
; FILE REFERENCE: 1107.75741
; CURRENT APPLICATION NUMBER: US/09/136.605A
; CURRENT FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 08/821,355
; EARLIER FILING DATE: 1997-03-20
; EARLIER APPLICATION NUMBER: 09/003,687
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-136-605-26
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104928
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104928

Query Match      52.8%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGC 23
Db      25 GACCAGCAGCTTCATGGC 8

RESULT 36
US-09-396-196G-104929/c
; Sequence 104929, Application US/09396196G
; GENERAL INFORMATION:
; PATENT NO. 6821724
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Afymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104929
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104929

Query Match      52.8%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGC 23
Db      24 GACCAGCAGCTTCATGGC 7

RESULT 37
US-09-136-605-26
; Sequence 26, Application US/09136605A
; Patent No. 6140052
; GENERAL INFORMATION:
; APPLICANT: He, Tong-Chuan
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to
; TITLE OF INVENTION: Prevent Cancer
; FILE REFERENCE: 1107.75741
; CURRENT APPLICATION NUMBER: US/09/136.605A
; CURRENT FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 08/821,355
; EARLIER FILING DATE: 1997-03-20
; EARLIER APPLICATION NUMBER: 09/003,687
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-136-605-26
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104928
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104928

Query Match      52.8%; Score 13.2; DB 3; Length 33;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5 AGCCTAGCAGATTCATGG 22
Db      12 AGCCTAGCAGGTCGGGG 29

RESULT 38
US-08-484-993B-56
; Sequence 56, Application US/08484993B
; Patent No. 5837497
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immunococontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,993B
; FILING DATE: 09-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-484-993B-56

Query Match      52.8%; Score 13.2; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      8 CTAGCAGATTCATGGCAC 25
Db      5 CTAGCAGATTCATGGCG 22

RESULT 39
US-08-484-158B-56
; Sequence 56, Application US/08484158B
; Patent No. 5976545
```

GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Pharmaceutical Compositions for
TITLE OF INVENTION: Immunococontraception
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484.158B
FILING DATE: 07-JUNE-95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,223
FILING DATE: 09-NOV-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-92
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 32794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-484-158B-56

Query Match 52.8%; Score 13.2; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 8 CTAGCAGATTCATGGCAC 25
Db 5 CTAGCAGATCTATGGCGC 22

RESULT 40
US-08-484-596A-56
Sequence 56, Application US/08484596A
Patent No. 5981228
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunococontraception
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago

STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484.596A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,223
FILING DATE: 11-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31745
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-484-596A-56
Query Match 52.8%; Score 13.2; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 5 CTAGCAGATCTATGGCGC 22
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 336.027 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-10

Perfect score: 25

Sequence: 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

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Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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- 21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
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- 26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	8	US-08-469-172-10
2	25	100.0	25	20	US-10-788-779-10
3	16.8	67.2	25	26	US-11-036-317-506713
4	16.6	66.4	25	26	US-11-060-756-179689
5	16.2	64.8	25	24	US-10-719-956-625525

6	16.2	64.8	25	26	US-11-060-756-203326	Sequence 203326,
7	16.2	64.8	25	26	US-11-060-756-203327	Sequence 203327,
8	15.8	63.2	25	24	US-10-719-956-696370	Sequence 696370,
9	15.6	62.4	25	26	US-11-036-317-644145	Sequence 644145,
10	15.6	62.4	25	26	US-11-036-317-738392	Sequence 738392,
11	15.2	60.8	25	22	US-10-719-900-30711	Sequence 30711, A
12	15.2	60.8	25	22	US-10-719-900-841582	Sequence 841582,
13	15.2	60.8	25	22	US-10-956-157-161796	Sequence 161796,
14	15.2	60.8	25	24	US-10-719-956-320514	Sequence 320514,
15	15.2	60.8	25	24	US-10-719-956-460571	Sequence 460571,
16	15.2	60.8	25	24	US-10-719-956-625734	Sequence 625734,
17	15.2	60.8	25	26	US-11-036-317-506712	Sequence 506712,
18	15.2	60.8	25	26	US-11-036-317-743982	Sequence 743982,
19	15.2	60.8	25	26	US-11-060-756-185070	Sequence 185070, A
20	15	60.0	25	22	US-10-719-900-81247	Sequence 81247, A
21	15	60.0	25	22	US-10-719-900-384887	Sequence 384887,
22	15	60.0	25	22	US-10-719-900-616192	Sequence 616192,
23	15	60.0	25	24	US-10-719-956-40306	Sequence 40306, A
24	15	60.0	25	24	US-10-719-956-513171	Sequence 513171,
25	15	60.0	25	26	US-11-036-317-567135	Sequence 567135,
26	15	60.0	50	18	US-10-131-827-1185	Sequence 1185, Ap
27	14.8	59.2	25	22	US-10-719-900-21139	Sequence 21139, A
28	14.8	59.2	25	22	US-10-719-900-853965	Sequence 853965,
29	14.8	59.2	25	24	US-10-719-956-369596	Sequence 369596,
30	14.6	58.4	25	20	US-10-623-500-10	Sequence 10, Appl
31	14.6	58.4	25	22	US-10-719-900-697665	Sequence 697665,
32	14.6	58.4	25	22	US-10-956-157-16200	Sequence 16200, A
33	14.6	58.4	25	22	US-10-956-157-16201	Sequence 16201, A
34	14.6	58.4	25	22	US-10-956-157-16202	Sequence 16202, A
35	14.6	58.4	25	22	US-10-956-157-16203	Sequence 16203, A
36	14.6	58.4	25	22	US-10-956-157-16206	Sequence 16206, A
37	14.6	58.4	25	24	US-10-719-956-625526	Sequence 625526, A
38	14.6	58.4	25	26	US-11-036-317-30872	Sequence 30872, A
39	14.6	58.4	25	26	US-11-036-317-435368	Sequence 435368,
40	14.6	58.4	25	26	US-11-036-317-482048	Sequence 482048,
41	14.6	58.4	29	20	US-10-754-071-24	Sequence 24, Appl
42	14.6	58.4	29	22	US-10-759-860-24	Sequence 394784,
43	14.4	57.6	25	22	US-10-719-900-906265	Sequence 906265,
44	14.4	57.6	25	24	US-10-719-956-643918	Sequence 643918,
45	14.4	57.6	25	24	US-10-719-956-643918	Sequence 643918,

ALIGNMENTS

RESULT 1
US-08-469-172-10
; Sequence 10, Application US/08469172
; Publication No. US200300543A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-469-172-10

Query Match 100.0%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
Db 1 GCTGAGCCTAGCAGATTCATGGCAC 25

RESULT 2
US-10-788-779-10
; Sequence 10, Application US/10788779
; Publication No. US2004015212A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-788-779-10

Query Match 100.0%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
Db 1 GCTGAGCCTAGCAGATTCATGGCAC 25

RESULT 3
US-11-036-317-506713/c
; Sequence 506713, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 506713
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-506713

Query Match 67.2%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTCATGGC 23
Db 22 GAGCCTAGTAGATTCATGGC 3

RESULT 4
US-11-060-756-179689
; Sequence 179689, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TARGET GENES
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179689
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-179689

Query Match 66.4%; Score 16.6; DB 26; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGC 23
Db 3 GCGGAGCCTAGCAGACTCAGGCC 25
```

```
RESULT 5
US-10-719-956-625525
; Sequence 625525, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 625525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-625525

Query Match      64.8%; Score 16.2; DB 24; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| |||||
Db 2 GCTGAGCCAGCTGATGCATG 22
   ||||| ||||| ||||| |||||

RESULT 6
US-11-060-756-203326
; Sequence 203326, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 203326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-203326

Query Match      64.8%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| |||||
Db 4 GCGGAGCCTAGCAGACTCAGG 24
   ||||| ||||| ||||| |||||

RESULT 7
US-11-060-756-203327
; Sequence 203327, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 203327
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-203327

Query Match      64.8%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| |||||
Db 4 GCGGAGCCTAGCAGACTCAGG 24
   ||||| ||||| ||||| |||||

RESULT 8
US-10-719-956-696370/c
; Sequence 696370, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 696370
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-696370

Query Match      63.2%; Score 15.8; DB 24; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTCAT 20
   ||||| ||||| ||||| |||||
Db 23 CTGAGCCAGCAGATCAT 5
   ||||| ||||| ||||| |||||

RESULT 9
US-11-036-317-644145/c
; Sequence 644145, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 644145
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-644145

Query Match      62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGG 22
   ||||| ||||| ||||| |||||
Db 24 GCTGTGCCGCGCAGATCATGG 3
   ||||| ||||| ||||| |||||
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RESULT 10
US-11-036-317-738392
; Sequence 738392, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 738392
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-738392

Query Match      62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGG 22
    ||||| ||||| ||||| |||||
Db 4 GCTGTGACTAGAGATTCATGG 25

RESULT 11
US-10-719-900-30711/c
; Sequence 30711, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30711
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-30711

Query Match      60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTCATG 21
    ||||| ||||| ||||| |||||
Db 22 CTAAGGCTAGCAGAATCATG 3

RESULT 12
US-10-719-900-841582/c
; Sequence 841582, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 841582
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-841582

Query Match      60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTCATG 21
    ||||| ||||| ||||| |||||
Db 25 CTAAGGCTAGCAGAATCATG 6

RESULT 13
US-10-956-157-161796
; Sequence 161796, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161796
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-161796

Query Match      60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCA 24
    ||||| ||||| ||||| |||||
Db 2 AGCCTGGCAGATGCTGGCA 21

RESULT 14
US-10-719-956-320514
; Sequence 320514, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320514
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-320514

Query Match      60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 1 GACCAGCAGATTCCTTGGCAC 20
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; SEQ ID NO 841582
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-841582

Query Match      60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTCATG 21
    ||||| ||||| ||||| |||||
Db 25 CTAAGGCTAGCAGAATCATG 6

RESULT 13
US-10-956-157-161796
; Sequence 161796, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161796
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-161796

Query Match      60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCA 24
    ||||| ||||| ||||| |||||
Db 2 AGCCTGGCAGATGCTGGCA 21

RESULT 14
US-10-719-956-320514
; Sequence 320514, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320514
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-320514

Query Match      60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 1 GACCAGCAGATTCCTTGGCAC 20
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```
RESULT 15
US-10-719-956-460571/c
; Sequence 460571, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 460571
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-460571

Query Match      60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      22 GCCTAGCAGAGCCTTGGCAC 3

RESULT 16
US-10-719-956-625734/c
; Sequence 625734, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 625734
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-625734

Query Match      60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5 AGCTTAGCAGATTCATGGCA 24
Db      23 AGCTTCTCAGATTCATGGCA 4

RESULT 17
US-11-036-317-506712/c
; Sequence 506712, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 506712
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-506712

Query Match      60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GAGCCTAGCAGATTCATGGC 23
Db      22 GAGCCTAGTGTGATTCATGGC 3

RESULT 18
US-11-036-317-743982
; Sequence 743982, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 743982
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-743982

Query Match      60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 TGAGCCTAGCAGATTCATGG 22
Db      6 TTAGCCTAGCAGATGTATGG 25

RESULT 19
US-11-060-756-185070
; Sequence 185070, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 185070
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-185070

Query Match      60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GAGCCTAGCAGATTCATGGC 23
Db      2 GAGCAGAGGAGATTCATGGC 21
```

```
RESULT 20
US-10-719-900-81247/c
; Sequence 81247, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81247
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-81247

Query Match          60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 CTGAGCCTAGCAGATTTCATGGCA 24
    ||||| ||||| ||||| |||||
Db  25 CTCAGCTGGGAGATTCTTGCCA 3

RESULT 21
US-10-719-900-384887
; Sequence 384887, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 384887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-384887

Query Match          60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6 GCCTAGCAGATTTCAT 20
    ||||| ||||| |||||
Db  7 GCCTAGCAGATTTCAT 21

RESULT 22
US-10-719-900-616192
; Sequence 616192, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 616192
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-616192

Query Match          60.0%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 TGAGCCTAGCAGATTTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db  23 TGTGCTTGGCAGATTTCATCCAC 1
```

```
; SEQ ID NO 616192
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-616192

Query Match          60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 GCTGAGCCTAGCAGATTTCATGGC 23
    ||||| ||||| ||||| |||||
Db  2 GCCGAGCATAGCAGTTTCTTGGC 24

RESULT 23
US-10-719-956-40306/c
; Sequence 40306, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 40306
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-40306

Query Match          60.0%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 GCTGAGCCTAGCAGATTTCATGGC 23
    ||||| ||||| ||||| |||||
Db  25 GCTGAGGCGAGCCACATTTCATGGC 3

RESULT 24
US-10-719-956-513171/c
; Sequence 513171, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 513171
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-513171

Query Match          60.0%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 TGAGCCTAGCAGATTTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db  23 TGTGCTTGGCAGATTTCATCCAC 1
```

```
RESULT 25
US-11-036-317-567135/c
; Sequence 567135, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 567135
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-567135

Query Match          60.0%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTTCATGCG 23
    ||||| ||||| ||||| ||||| |||||
Db 25 GCTGAGCCTCGTAGATGCACTGC 3

RESULT 26
US-10-131-827-1185
; Sequence 1185, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1185
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1185

Query Match          60.0%; Score 15; DB 18; Length 50;
Best Local Similarity 78.3%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGAGCCTAGCAGATTTCATGCGCAC 25
    ||||| ||||| ||||| ||||| |||||
Db 14 TGAGCCGAGCAGTTTCAAGACAC 36

RESULT 27
US-10-719-900-21199/c
; Sequence 21199, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21199
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-21199

Query Match          59.2%; Score 14.8; DB 22; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTTCATGG 22
    ||||| ||||| ||||| |||||
Db 24 AGCCTACCACATTCATGG 7

RESULT 28
US-10-719-900-853965
; Sequence 853965, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 853965
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-853965

Query Match          59.2%; Score 14.8; DB 22; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTTC 18
    ||||| ||||| ||||| |||||
Db 4 GCTGGCCTAGTAGATTC 21

RESULT 29
US-10-719-956-369596/c
; Sequence 369596, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 369596
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-369596

Query Match          59.2%; Score 14.8; DB 24; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 7 CCTAGCAGATTCATGGCA 24
| | | | | | | | | | | | | | | |
Db 20 CCTAGGAGATTCATGACA 3

RESULT 30

US-10-623-500-10/c
; Sequence 10, Application US/10623500
; Publication No. US20040133945A1
; GENERAL INFORMATION:
; APPLICANT: Bayer BioScience N.V.
; APPLICANT: Greet, Vanderkimpfen
; APPLICANT: Gerben, Van Eldik
; APPLICANT: Frank, Meulewaeter
; TITLE OF INVENTION: Corn root preferential promoters and uses thereof
; FILE REFERENCE: 021565-119
; CURRENT APPLICATION NUMBER: US/10/623.500
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 60/399383
; PRIOR FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer GVK30
US-10-623-500-10

Query Match 58.4%; Score 14.6; DB 20; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTCATGGCA 24
| | | | | | | | | | | | | | | |
Db 23 GAGCATAGTCGATCATGGCA 3

RESULT 31

US-10-719-900-697665
; Sequence 697665, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719.900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 697665
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-697665

Query Match 58.4%; Score 14.6; DB 22; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGAGCCTAGCAGATTCATGGC 23
| | | | | | | | | | | | | | | |
Db 2 TGACCTGATCAGATTCATGGC 22

RESULT 32

US-10-956-157-16200/c
; Sequence 16200, Application US/10956157
; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16200
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-16200

Query Match 58.4%; Score 14.6; DB 22; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCAC 25
| | | | | | | | | | | | | | | |
Db 23 AGCCTCTCAGATTCATTGAAC 3

RESULT 33

US-10-956-157-16201/c
; Sequence 16201, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16201
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-16201

Query Match 58.4%; Score 14.6; DB 22; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCAC 25
| | | | | | | | | | | | | | | |
Db 24 AGCCTCTCAGATTCATTGAAC 4

RESULT 34

US-10-956-157-16202/c
; Sequence 16202, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-16202

```
Query Match      58.4%; Score 14.6; DB 22; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTCATGGCAC 25
   ||||| ||||| ||||| ||||| |||||
DB 21 AGCCTCTCAGATTCATTGAAC 1

RESULT 35
US-10-956-157-16203/c
; Sequence 16203, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-16203

Query Match      58.4%; Score 14.6; DB 22; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTCATGGCAC 25
   ||||| ||||| ||||| ||||| |||||
DB 22 AGCCTCTCAGATTCATTGAAC 2

RESULT 36
US-10-956-157-16206/c
; Sequence 16206, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16206
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-16206

Query Match      58.4%; Score 14.6; DB 22; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTCATGGCAC 25
   ||||| ||||| ||||| ||||| |||||
DB 25 AGCCTCTCAGATTCATTGAAC 5

RESULT 37
US-10-719-956-625526
; Sequence 625526, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 625526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-625526

Query Match      58.4%; Score 14.6; DB 24; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| ||||| |||||
DB 2 GCTGAGCCCGAGTGATGCATG 22

RESULT 38
US-11-036-317-30872
; Sequence 30872, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30872
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-30872

Query Match      58.4%; Score 14.6; DB 26; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| ||||| |||||
DB 4 GCTGAGCCTGGGAGTTTCCTG 24

RESULT 39
US-11-036-317-435368
; Sequence 435368, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 435368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
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US-11-036-317-435368

Query Match 58.4%; Score 14.6; DB 26; Length 25;
 Best Local Similarity 81.0%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCATG 21
 |||||
 Db 4 GCTGAGCCTGGGAGTTTCTG 24

RESULT 40

US-11-036-317-482048/c
 ; Sequence 482048, Application US/11036317
 ; Publication No. US20050214823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Alan
 ; APPLICANT: Blume, John
 ; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 ; FILE REFERENCE: 3654.1
 ; CURRENT APPLICATION NUMBER: US/11/036,317
 ; CURRENT FILING DATE: 2005-01-13
 ; PRIOR APPLICATION NUMBER: US 60/536,639
 ; PRIOR FILING DATE: 2004-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 482048
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-482048

Query Match 58.4%; Score 14.6; DB 26; Length 25;
 Best Local Similarity 81.0%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTCATGGCAC 25
 |||||
 Db 24 AGCCTAGCCCGTTCATGTCAC 4

Search completed: November 18, 2005, 15:41:10
 Job time : 336.027 secs